



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 180153

TO: Patricia Duffy
Location: REM-3B05/3C18
Art Unit: 1645
Wednesday, March 01, 2006
Case Serial Number: 09/955502

From: Kristine Hensle
Location: Biotech-Chem Library
REM-1B69
Phone: (571) 272-4161

Kristine.Hensle@uspto.gov

Search Notes

Examiner Duffy,

See attached results.

If you have any questions about this search feel free to contact me at any time.

Thank you for using STIC search services!

Kristine Hensle
Librarian
STIC Biotech/Chem Library
(571)272-4161

part 1205

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STIC-Biotech/ChemLib

180153

From: Pak, Michael
Sent: Wednesday, February 22, 2006 9:37 AM
To: STIC-Biotech/ChemLib
Cc: Duffy, Patricia
Subject: FW: multiple short protein search each <100 AA long 09/955,502
Importance: High

Dear STIC,

Please search the multiple sequence search request set forth below.

Thanks,

Mike Pak

-----Original Message-----

From: Duffy, Patricia
Sent: Tuesday, February 21, 2006 4:54 PM
To: Pak, Michael
Subject: multiple short protein search each <100 AA long 09/955,502
Importance: High

Mike,

Please approve multiple short protein sequences.

All sequences used in method claims. Genus claim free of the art. All species claimed.

Thanks,

Pat d.

Dear Stic,

Please search SEQ ID NOS:2-45.

Please print out top 25 hits in each category.

Please perform both an interference and commercial database search.

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search
NA# _____ AA#: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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Thanks.

Patricia A. Duffy, Ph.D.
Primary Patent Examiner
571-272-0855,
Remsen 3B05,
Mailbox: 3C18

Searcher: _____
Searcher Phone: _____
Date Searcher Picked up: _____
Date completed: _____
Searcher Prep Time: _____
Online Time: _____

Type of Search

NA# _____ AA# _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure #: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other (Specify): _____

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 19.4713 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467
Sequence: 1 MARMVFCVKLNKEAEGMKRP.....QMEGYFFGDDGADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	221	47.3	93	2	US-09-543-681A-5443 Sequence 5443, Ap
4	207	44.3	122	2	US-09-991A-23355 Sequence 23355, A
5	182	39.0	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	68.5	14.7	361	2	US-09-252-991A-25005 Sequence 25005, A
7	67.5	14.5	466	2	US-09-252-991A-32761 Sequence 32761, A
8	66	14.1	418	2	US-09-489-039A-13155 Sequence 13155, A
9	65.5	14.0	649	2	US-09-107-532A-4298 Sequence 4298, Ap
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12	64.5	13.8	361	2	US-09-955-518-21 Sequence 21, Appl
13	63	13.5	351	2	US-09-248-796A-19129 Sequence 19129, A
14	63	13.5	461	1	US-08-672-571A-3 Sequence 3, Appli
15	63	13.5	490	1	US-08-672-571A-1 Sequence 1, Appli
16	62.5	13.4	263	2	US-09-252-991A-22230 Sequence 22230, A
17	62	13.3	360	2	US-09-543-681A-7067 Sequence 7067, Ap
18	62	13.3	671	2	US-09-252-991A-18020 Sequence 18020, A
19	61.5	13.2	422	2	US-09-198-452A-377 Sequence 377, App
20	61.5	13.2	423	2	US-09-438-185A-363 Sequence 363, App
21	60.5	13.0	478	2	US-09-489-039A-7300 Sequence 7300, Ap
22	60.5	13.0	596	2	US-09-902-540-10121 Sequence 10121, A
23	60	12.8	621	2	US-09-489-039A-10378 Sequence 10378, A
24	60	12.8	2186	1	US-08-822-445-2 Sequence 2, Appli
25	60	12.8	2186	2	US-09-396-540-2 Sequence 2, Appli
26	59.5	12.7	315	2	US-09-461-325-297 Sequence 297, App
27	59.5	12.7	315	2	US-10-012-542-297 Sequence 297, App

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
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30	59.5	12.7	420	2	US-09-902-540-16463	Sequence 16463, A
31	59.5	12.7	431	2	US-09-461-325-146	Sequence 146, App
32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
33	59.5	12.7	431	2	US-09-311-021-178	Sequence 178, App
34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	848	2	US-09-538-092-33	Sequence 33, Appl
36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
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64	57.5	12.3	180	2	US-09-640-211A-834	Sequence 834, App
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68	57.5	12.3	210	2	US-09-438-185A-88	Sequence 88, Appl
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73	57	12.2	157	2	US-09-902-540-15203	Sequence 15203, A
74	57	12.2	384	2	US-10-094-944-19	Sequence 19, Appl
75	57	12.2	412	2	US-09-538-092-709	Sequence 709, App

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:44:45 ; Search time 57.1494 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467
Sequence: 1 MARMVFCVKLNKEAGMKFP.....QMEQYFFGDGADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	339	72.6	87	3	US-09-955-502-30 Sequence 30, Appl
6	294	63.0	87	3	US-09-955-502-31 Sequence 31, Appl
7	290	62.1	87	3	US-09-955-502-2
8	290	62.1	87	3	US-09-955-502-3
9	272.5	58.4	86	3	US-09-955-502-4
10	258	55.2	88	3	US-09-955-502-33 Sequence 33, Appl
11	243	52.0	87	3	US-09-955-502-32 Sequence 32, Appl
12	240	51.4	90	3	US-09-955-502-10 Sequence 10, Appl
13	235	50.3	87	3	US-09-955-502-8 Sequence 8, Appl
14	230	49.3	88	3	US-09-955-502-9 Sequence 9, Appl
15	228	48.8	91	3	US-09-955-502-5 Sequence 5, Appl
16	227	48.6	87	3	US-09-955-502-7 Sequence 7, Appl
17	219	46.9	87	3	US-09-955-502-24 Sequence 24, Appl
18	217	46.5	87	3	US-09-955-502-6 Sequence 6, Appl
19	213	45.6	91	3	US-09-955-502-11 Sequence 11, Appl
20	213	45.6	91	3	US-09-955-502-12 Sequence 12, Appl
21	213	45.6	91	3	US-09-955-502-13 Sequence 13, Appl
22	211	45.2	88	3	US-09-955-502-15 Sequence 15, Appl
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25	211	45.2	91	3	US-09-955-502-17 Sequence 17, Appl
26	210	45.0	78	3	US-09-955-502-19 Sequence 19, Appl
27	207	44.3	87	3	US-09-955-502-25 Sequence 25, Appl

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30	198	42.4	90	3	US-09-955-502-20	Sequence 20, Appl
31	198	42.4	90	3	US-09-955-502-23	Sequence 23, Appl
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63	63.5	13.6	288	5	US-10-472-928-132	Sequence 132, App
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75	62	13.3	1025	4	US-10-424-599-149485	Sequence 149485,

ALIGNMENTS

RESULT 1
US-09-955-502-26
; Sequence 26, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:45:38 ; Search time 5.56322 Seconds
(without alignments)
235.489 Million cell updates/sec

Title: US-09-955-502A-42

Perfect score: 467
Sequence: 1 MARMVFCVKLNKBAEGMKFP.....QMEQYFFGDGADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	60	12.8	1092	6	US-10-821-234-999 Sequence 999, App
3	58	12.4	380	6	US-10-525-674-28 Sequence 28, Appl
4	58	12.4	614	7	US-11-165-576-2 Sequence 2, Appli
5	58	12.4	614	7	US-11-165-576-4 Sequence 4, Appli
6	57.5	12.3	200	6	US-10-793-626-1186 Sequence 1186, Ap
7	57.5	12.3	200	6	US-10-793-626-2390 Sequence 2390, Ap
8	57.5	12.3	204	7	US-11-098-686-10498 Sequence 10498, A
9	57.5	12.3	655	7	US-11-098-686-10464 Sequence 10464, A
10	57	12.2	384	7	US-11-219-282-19 Sequence 19, Appl
11	57	12.2	620	6	US-10-131-826A-324 Sequence 324, Appl
12	56.5	12.1	575	7	US-11-098-686-10635 Sequence 10635, A
13	56.5	12.1	688	7	US-11-165-226-124 Sequence 124, App
14	56	12.0	1124	7	US-11-090-617-688 Sequence 688, App
15	56	12.0	1375	6	US-10-995-561-809 Sequence 809, App
16	56	12.0	1376	7	US-11-100-640-32 Sequence 32, Appl
17	55.5	11.9	403	7	US-11-009-658-14 Sequence 14, Appl
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21	55	11.8	261	6	US-10-467-657-400 Sequence 400, Appl
22	55	11.8	611	6	US-10-454-437-54 Sequence 54, Appl
23	55	11.8	633	7	US-11-193-561-13 Sequence 13, Appl
24	55	11.8	633	7	US-11-193-771-13 Sequence 13, Appl
25	55	11.8	633	7	US-11-193-789-13 Sequence 13, Appl

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, Appl
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, Appl
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, Appl
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, Appli
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, Appli
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, Appl
32	54	11.6	307	6	US-10-793-626-522	Sequence 522, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, A
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, Appl
35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
36	53.5	11.5	310	7	US-11-055-163-7	Sequence 7, Appli
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, Appli
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, Appli
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, Appli
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, Appli
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, Ap
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, Ap
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, Appli
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, Ap
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, Appl
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appli
56	52.5	11.2	4128	6	US-10-770-726-77	Sequence 77, Appl
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
60	52	11.1	390	7	US-11-219-282-112	Sequence 12, Appl
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 94, Appl
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 2, Appli
64	51.5	11.0	403	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 2343, Ap
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, Appl
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, Appli
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, A
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, Appl
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 10, Appl
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwln9, version 1.04

GenCore version 5.1.7
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OM protein - proteain search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 73.25 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502A-43
Perfect score: 471
Sequence: 1 MSRMVQCVKLGHEAEGLDLP.....KQMBAYFRGDGAQSPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	471	100.0	87	5	ABB78176 Amino aci
2	310	65.8	87	5	ABB78175 Amino aci
3	304	64.5	87	5	ABB78174 Amino aci
4	294	62.4	88	5	ABB78171 Amino aci
5	294	62.4	88	5	ABB78172 Amino aci
6	294	62.4	88	5	ABB78173 Amino aci
7	294	62.4	88	6	ABP77219 N. gonorr
8	291	61.8	87	5	ABB78177 Amino aci
9	286	60.7	88	5	ABB78178 Amino aci
10	286	60.7	89	9	AEBA1576 L. pneumo
11	286	60.7	95	9	AEBA1576 L. pneumo
12	275	58.4	87	5	ABB78148 Amino aci
13	275	58.4	87	5	ABB78147 Amino aci
14	257.5	54.7	86	5	ABB78149 Amino aci
15	242	51.4	87	5	ABB78170 Amino aci
16	242	51.4	122	7	ABO74609 Pseudomon
17	237	50.3	87	5	ABB78169 Amino aci
18	225.5	47.9	92	6	ADA34169 Acinetoba
19	219	46.5	90	5	ABB78168 Amino aci
20	213	45.2	88	5	ABB78154 Amino aci
21	211	44.8	87	5	ABB78153 Amino aci
22	208.5	44.3	90	5	ABB78167 Amino aci
23	208	44.2	91	5	ABB78150 Amino aci
24	208	44.2	93	7	ADF05158 Bacterial

25	208	44.2	107	7	ABO65445	Ab065445 Klebsiell
26	204	43.3	90	5	ABB78155	Abb78155 Amino aci
27	202	42.9	87	5	ABB78152	Abb78152 Amino aci
28	200	42.5	87	5	ABB78151	Abb78151 Amino aci
29	200	42.5	91	5	ABB78158	Abb78158 Amino aci
30	200	42.5	91	5	ABB78157	Abb78157 Amino aci
31	200	42.5	91	5	ABB78156	Abb78156 Amino aci
32	197	41.8	88	5	ABB78160	Abb78160 Amino aci
33	197	41.8	91	5	ABB78161	Abb78161 Amino aci
34	197	41.8	91	5	ABB78159	Abb78159 Amino aci
35	196	41.6	91	5	ABB78162	Abb78162 Amino aci
36	196	41.6	78	5	ABB78164	Abb78164 Amino aci
37	190	40.3	91	5	ABB78163	Abb78163 Amino aci
38	186	39.5	90	5	ABB78165	Abb78165 Amino aci
39	177	37.6	110	8	ADL05173	Adl05173 M. catarr
40	166	35.2	76	5	ABB78166	Abb78166 Amino aci
41	72.5	15.4	2285	4	ABB63057	Abb63057 Drosophil
42	71.5	15.2	387	7	ABO82328	Ab082328 Pseudomon
43	71	15.1	523	4	AAU35394	Aau35394 Haemophil
44	71	15.1	523	6	ABU30183	Abu30183 Protein e
45	71	15.1	568	8	ADN22552	Adn22552 Bacterial
46	69	14.6	1263	2	AAW22052	Aaw22052 DNA polym
47	69	14.6	1263	2	AAW97098	Aaw97098 Pfu DNA p
48	69	14.6	1263	3	AAV51659	Aay51659 Pyrococcu
49	69	14.6	1263	3	AAV52030	Aay52030 P. furios
50	68.5	14.5	249	8	ADS28293	Ads28293 Bacterial
51	68	14.4	536	6	ABU40906	Abu40906 Protein e
52	68	14.4	569	7	ADF06692	Adf06692 Bacterial
53	67	14.2	188	9	AEA50037	Aea50037 Rice glob
54	67	14.2	319	6	ADA56784	Ada56784 Human sec
55	67	14.2	319	6	ADA40633	Ada40633 Human sec
56	67	14.2	319	6	ABR47664	AbR47664 Human sec
57	67	14.2	319	6	ABR00028	AbR00028 Human sec
58	67	14.2	319	7	ADB91477	Adb91477 Human sec
59	67	14.2	319	2	ADC74042	Adc74042 Human sec
60	67	14.2	320	7	AAV30730	Aay30730 Amino aci
61	67	14.2	561	6	ADA54803	Ada54803 Human pro
62	67	14.2	907	5	ABG91058	Abg91058 Neisseria
63	67	14.2	915	2	AAV51770	Aay51770 N. gonorr
64	67	14.2	915	2	AAV07476	Aay07476 N. gonorr
65	67	14.2	915	3	AAV80374	Aay80374 N. gonorr
66	67	14.2	915	5	AAE20190	Aae20190 Neisseria
67	67	14.2	950	4	AAU35678	Aau35678 Haemophil
68	67	14.2	950	6	ABU30652	Abu30652 Protein e
69	67	14.2	1798	8	ADN46771	Adn46771 Thermococ
70	66.5	14.1	204	9	AEA50033	Aea50033 Rice glo
71	66.5	14.1	972	4	ABB70158	Abb70158 Drosophil
72	66	14.0	387	7	ADF58994	Adf58994 Human pol
73	65.5	13.9	186	7	ADC07962	Adc07962 Rice prot
74	65.5	13.9	186	7	ADC07948	Adc07948 Rice prot
75	65.5	13.9	198	4	ABG23100	Abg23100 Novel hum

ALIGNMENTS

RESULT 1
ABB78176
ID ABB78176 standard; protein; 87 AA.
XX ABB78176;
AC
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Acidithiobacillus ferrooxidans.
XX
PN US2002072118-A1.

XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-009555502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 471; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRMVQCVKLGHEAEGLDPRPPYFGALGARITYQEVSKAWQWLGKHQTMLINEYRLSPIDP 60
Db 1 MSRMVQCVKLGHEAEGLDPRPPYFGALGARITYQEVSKAWQWLGKHQTMLINEYRLSPIDP 60
OY 61 KSRTFLEKQMBAYFFGDGAQSPGEGYVP 87
Db 61 KSRTFLEKQMBAYFFGDGAQSPGEGYVP 87

RESULT 2
ABB78175
ID ABB78175 standard; protein; 87 AA.
XX
AC ABB78175;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-009555502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX

PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 65.8%; Score 310; DB 5; Length 87;
Best Local Similarity 64.4%; Pred. No. 4.4e-31;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

OY 1 MSRMVQCVKLGHEAEGLDPRPPYFGALGARITYQEVSKAWQWLGKHQTMLINEYRLSPIDP 60
Db 1 MARMIHCARKGEAEGLDPRPPLPGELGKRLYESVSKQAWQDWLKHQTMLINEYRLMADP 60
OY 61 KSRTFLEKQMBAYFFGDGAQSPGEGYVP 87
Db 61 RARQYIMKQTEKYPFGEADQASGYVP 87

RESULT 3
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
AC ABB78174;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-009555502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.75 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502A-43
Perfect score: 471
Sequence: 1 MSRMVQCVKLGHEAEGLDRP.....KQMEAYFFGDGAQSPGCVVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	294	62.4	88	2 H81014	conserved hypothet
2	242	51.4	90	2 H83003	conserved hypothet
3	215	45.6	105	2 C82624	conserved hypothet
4	204	43.3	90	2 C82320	conserved hypothet
5	202	42.9	90	2 C64013	hypothetical prote
6	200	42.5	91	2 A85954	hypothetical prote
7	200	42.5	91	2 A65082	hypothetical prote
8	200	42.5	91	2 F91108	hypothetical prote
9	197	41.8	91	2 AH0879	conserved hypothet
10	186	39.5	90	2 AH0116	conserved hypothet
11	166	35.2	93	2 E84994	hypothetical prote
12	71.5	15.2	383	2 F83321	hypothetical prote
13	71	15.1	523	1 I64055	GMP synthase (glut
14	71	15.1	568	2 T25162	Frizzled-1 protein
15	70	14.9	1197	2 I39613	pyruvate (flavodox
16	70	14.9	1199	2 AD2156	pyruvate-flavodoxi
17	69.5	14.8	501	2 T35009	probable phospholi
18	69	14.6	1263	2 T43934	DNA-directed DNA p
19	68.5	14.5	249	2 A83963	hypothetical prote
20	67.5	14.3	564	2 T49322	related to RNA-bin
21	67	14.2	915	2 A43335	transferrin-bindin
22	67	14.2	950	2 B64135	oxoglutarate dehyd
23	66	14.0	604	2 S36493	E1 protein - human
24	65.5	13.9	186	1 WMR219	19K globulin precu
25	65.5	13.9	186	2 JC4784	alpha-globulin pre
26	65.5	13.9	368	2 T31103	probable GMP synth
27	65	13.8	159	2 AD0348	probable membrane
28	65	13.8	1434	2 G71232	hypothetical prote
29	64.5	13.7	914	2 T17233	hypothetical prote

30	64.5	13.7	4273	2 C69679	polyketide synthas
31	64	13.6	205	2 AD0788	heme exporter prot
32	64	13.6	205	2 AC0960	heme exporter prot
33	64	13.6	306	2 A97249	Zn-binding lipopro
34	64	13.6	364	2 C48376	orf2 5' to phbC -
35	64	13.6	598	2 A75531	hypothetical prote
36	63.5	13.5	376	2 C82310	sulfate ABC transp
37	63.5	13.5	609	2 S36481	E1 protein - human
38	63.5	13.5	1199	2 S77082	pyruvate (flavodox
39	63.5	13.5	1243	2 JC5615	membrane-associate
40	63	13.4	265	2 T46733	citr protein (impo
41	63	13.4	443	2 T48593	hypothetical prote
42	63	13.4	468	2 F87359	leucine aminopepti
43	63	13.4	705	2 S18733	glutenin high mole
44	63	13.4	1455	2 E75199	DNA-directed DNA p
45	62.5	13.3	243	2 JQ1427	hypothetical 27K p
46	62.5	13.3	289	2 T46370	hypothetical prote
47	62.5	13.3	393	2 T49257	protein kinase-lik
48	62.5	13.3	475	2 S54993	reverse transcript
49	62.5	13.3	475	2 S54994	reverse transcript
50	62.5	13.3	510	2 A96735	hypothetical prote
51	62.5	13.3	513	2 AB1921	hypothetical prote
52	62.5	13.3	605	2 S36469	E1 protein - human
53	62	13.2	316	2 C91272	hypothetical prote
54	62	13.2	316	2 C86113	hypothetical prote
55	62	13.2	503	2 AF2029	hypothetical prote
56	62	13.2	512	1 FOMVGS	gag polyprotein -
57	62	13.2	520	1 FOLJGL	gag polyprotein -
58	62	13.2	662	2 T41215	probable acetate-C
59	61	13.0	254	2 T15187	hypothetical prote
60	61	13.0	316	2 B37318	delta(2)-isopenten
61	61	13.0	430	2 B96031	hypothetical prote
62	61	13.0	450	2 S73419	signal recognition
63	61	13.0	457	1 JC4993	biphenyl dioxygena
64	61	13.0	525	1 SYECGU	GMP synthase (glut
65	61	13.0	525	1 F85894	GMP synthase (gl
66	61	13.0	525	2 AD0820	GMP synthase (glut
67	61	13.0	525	2 A91050	GMP synthetase [lm
68	61	13.0	535	2 AF0103	probable sulfatase
69	61	13.0	915	2 F81196	transferrin-bindin
70	60.5	12.8	359	2 T26813	hypothetical prote
71	60.5	12.8	475	2 S54996	reverse transcript
72	60.5	12.8	475	2 S54998	reverse transcript
73	60	12.7	342	2 T19021	probable inositol
74	60	12.7	352	2 D69410	cell division cont
75	60	12.7	375	2 T39364	probable galactosy

ALIGNMENTS

RESULT 1

H81014
Conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58)
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tettelin, H.; Saunders, N.J.; Jeffries, A.C.; Nelson, K.B.; Bisen, J.T.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.,
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandl, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; V
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g722727279; PIDN
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgens, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 65.75 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502a-43

Perfect score: 471
Sequence: 1 MSRMVQCVKLGHAEGLDRP.....KQMEAYFFGDGAQSPGTYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	331	70.3	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
2	319	67.7	90	1	PETP_CHRVO	Q7N874 chromobacte
3	313	66.5	90	1	PETP_NITEU	Q82xf2 nitrosomona
4	310	65.8	91	1	PETP_BURMA	Q62iu9 burkholderi
5	310	65.8	91	1	PETP_BURPS	Q63sj4 burkholderi
6	309	65.6	91	1	PETP_RALSO	Q8Y010 ralstonia s
7	294	62.4	88	1	PETP_NEIGI	Q5f553 neisseria g
8	294	62.4	88	1	PETP_NEIMA	P67615 neisseria m
9	294	62.4	88	1	PETP_NEIMB	P67616 neisseria m
10	291	61.8	90	1	PETP_METCA	Q60af7 methylococc
11	286	60.7	89	1	PETP_LEGPA	Q5x3x9 legionella
12	286	60.7	89	1	PETP_LEGPH	Q5zu80 legionella
13	286	60.7	90	1	PETP_COXBU	Q83d06 coxiella bu
14	284	60.3	89	1	PETP_LEGPL	Q5wvc4 legionella
15	275	58.4	90	1	PETP_BORBR	Q7wh06 bordetella
16	275	58.4	90	1	PETP_BORPA	Q7w9q2 bordetella
17	275	58.4	90	1	PETP_BORPE	Q7wvc4 bordetella
18	261	55.4	91	1	PETP_XANAC	Q8Djh7 xanthomonas
19	255	54.1	92	1	PETP_XANOR	Q5gy22 xanthomonas
20	252	53.5	92	1	PETP_XANCP	Q8p829 xanthomonas
21	252	53.5	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
22	249	52.9	92	2	Q4NM04_9DELT	Q4nmw4 anaeromyxob
23	242	51.4	90	1	PETP_PSEAE	Q9hu36 pseudomonas
24	238	50.5	90	1	PETP_IDILO	Q5gy58 idiomarina
25	237	50.3	90	1	PETP_PSEBP	Q88r49 pseudomonas
26	231	49.0	90	2	Q4JZ28_AZOVI	Q4j228 azotobacter
27	229	48.6	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
28	224.5	47.7	90	1	PETP_ACIAI	Q6ffb3 acinetobact
29	222	47.1	90	1	PETP_XYLLT	Q87d06 xyella fas
30	222	47.1	90	2	Q4KU72_PSEFS	Q4kjt2 pseudomonas
31	220	46.7	90	1	PETP_VIBFI	Q5e7c0 vibrio fisc

32	219	46.5	90	1	PETP_PSESM	Q87uf5 pseudomonas
33	219	46.5	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
34	218	46.3	90	1	PETP_PHOLL	Q7n711 photorhabdu
35	215	45.6	90	1	PETP_XYLFA	Q9pc73 xyella fas
36	213	45.2	92	1	PETP_SHEON	Q8ebx6 shewanella
37	211	44.8	90	1	PETP_VIBVU	Q8dcs5 vibrio vuln
38	211	44.8	90	1	PETP_VIBVY	Q7mb14 vibrio vuln
39	211	44.8	94	1	PETP_HAEDU	Q7vxb6 haemophilus
40	208	44.2	90	1	PETP_VIBPA	Q871i5 vibrio para
41	204	43.3	90	1	PETP_VIBCH	Q9kur4 vibrio chol
42	203	43.1	87	1	PETP_FRATT	Q5nhj8 francisella
43	202	42.9	90	1	PETP_HAEIN	P44048 haemophilus
44	202	42.9	90	2	Q4QMD9_HAE18	Q4qmd9 haemophilus
45	200	42.5	90	1	PETP_PASMU	Q9clb9 pasteurella
46	200	42.5	91	1	PETP_MANSM	Q6svr7 manheimia
47	197	41.8	90	1	PETP_ERWCT	Q6d8j9 erwinia car
48	195	41.4	90	1	PETP_ECOLI	P0a8p4 escherichia
49	195	41.4	90	1	PETP_SHIFL	P0a8p3 escherichia
50	195	41.4	90	1	PETP_YERPS	P0a8p5 shigella fl
51	194	41.2	90	1	PETP_YERPS	Q66fm3 yersinia ps
52	192	40.8	90	1	PETP_PHOPR	Q6lmk7 photobacter
53	192	40.8	90	1	PETP_SALCH	Q57K04 salmonella
54	192	40.8	90	1	PETP_SALPA	Q5pmm1 salmonella
55	192	40.8	90	1	PETP_SALTI	P67618 salmonella
56	192	40.8	90	1	PETP_SALTY	P67617 salmonella
57	191	40.6	90	1	PETP_ECOL6	Q8fe19 escherichia
58	186	39.5	90	1	PETP_YERPE	Q8zhe7 yersinia pe
59	179	38.0	78	1	PETP_BUCAP	Q8K925 buchnera ap
60	172	36.5	78	1	PETP_WIGBR	Q8d3cs wiggleswort
61	172	36.5	79	1	PETP_CANBR	Q7vrg9 candidatus
62	167	35.5	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
63	166	35.2	77	1	PETP_BUCAI	P57618 buchnera ap
64	142	30.1	87	1	PETP_BUCBP	Q89a44 buchnera ap
65	78.5	16.7	825	1	AOXB_ALCPA	Q7sif4 alcaligenes
66	78.5	16.7	826	2	Q6WB60_ALCPA	Q6wb60 alcaligenes
67	72.5	15.4	484	2	Q6MQ14_BDEBA	Q6mq14 bdellovibri
68	72.5	15.4	2308	2	Q9VP17_DROME	Q9vp17 drosophila
69	72	15.3	514	2	Q8VNU2_DESDE	Q8vnu2 desulfovibr
70	71.5	15.2	359	2	Q4N608_THERA	Q4n608 theileria p
71	71.5	15.2	383	2	Q910P0_PSEAE	Q910p0 pseudomonas
72	71.5	15.2	1200	2	Q4NU62_9DELT	Q4nu62 anaeromyxob
73	71.5	15.2	1322	2	Q7SHA9_ORYSA	Q7sha9 oryza sativ
74	71	15.1	523	1	GUAA_HAEIN	P44335 haemophilus
75	71	15.1	523	2	Q4QNW4_HAE18	Q4qnw4 haemophilus

ALIGNMENTS

RESULT 1
Q4LS19_9BURK
ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Ibrani S., Pictuck S., Richardson P.,
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/Genbank/DBJ databases.
RN [2]
NUCLEOTIDE SEQUENCE.

RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000021; EAM18958.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match 70.3%; Score 331; DB 2; Length 91;
Best Local Similarity 70.1%; Pred. No. 4.1e-29;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCIVLGHAEAGLDPRPPYALGARIYQEVSKAWQGLKHQTMLINEYRLSPIDP 60
Db 1 MARMIQCALGKAEAGLDPPPLPGLGKRIYESVSKAWQGLKHQTMLINEYRLSPIDP 60
61 KSRTPLEKQMEAYFFGDGAQSPGEGYVP 87
61 RARQYLMKQTEKTFPGDGADQASGYVP 87

RESULT 2
FETP_CHRVO
ID_FETP_CHRVO STANDARD; PRT; 90 AA.
AC Q7NSR4;
DT 05-JUL-2004 (Rel. 44, Last Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=CV3356;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burtley H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeliro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meisener R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE016922; AAQ61020.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10095 MW; 60492ED67A9ABE78 CRC64;

Query Match 67.7%; Score 319; DB 1; Length 90;
Best Local Similarity 65.5%; Pred. No. 8.8e-28;
Matches 57; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCIVLGHAEAGLDPRPPYALGARIYQEVSKAWQGLKHQTMLINEYRLSPIDP 60
Db 1 MSRTVNCIKLGHAEAGLDPPPLPGLGKRIYESVSKAWQGLKHQTMLINEYRLSPIDP 60
61 KSRTPLEKQMEAYFFGDGAQSPGEGYVP 87
61 RARQYIASQLDAYFFGQADADAGYTP 87

RESULT 3
FETP_NITEU
ID_FETP_NITEU STANDARD; PRT; 90 AA.
AC Q82XF2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=NE0322;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdn J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whitaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea.";
RL J. Bacteriol. 185:2759-2773(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX321857; CAD84233.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 19.25 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-43

Perfect score: 471
Sequence: 1 MSRMVQCCKLGHBAEGIDRP.....KQMBAYFFGDGAQSPGYPV 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	242	51.4	122	2	US-09-252-991A-23355
2	225.5	47.9	92	2	US-09-328-352-5456
3	208	44.2	93	2	US-09-543-681A-5443
4	208	44.2	107	2	US-09-489-039A-11962
5	177	37.6	110	2	US-09-540-236-2859
6	71.5	15.2	387	2	US-09-252-991A-31074
7	69	14.6	1263	2	US-09-446-504-6
8	69	14.6	1263	2	US-09-712-266-6
9	69	14.6	1263	2	US-09-091-889A-4
10	68	14.4	569	2	US-09-543-681A-6977
11	67	14.2	320	2	US-09-716-129-77
12	67	14.2	353	2	US-09-716-129-169
13	67	14.2	915	1	US-08-487-890A-96
14	67	14.2	915	1	US-08-363-124A-2
15	67	14.2	915	1	US-08-478-435-96
16	67	14.2	915	1	US-08-337-483-96
17	67	14.2	915	1	US-08-478-373-96
18	67	14.2	915	2	US-08-474-671-96
19	67	14.2	915	2	US-08-483-577A-96
20	67	14.2	915	2	US-08-613-009A-18
21	67	14.2	915	2	US-08-897-438-96
22	67	14.2	915	2	US-08-637-654-96
23	67	14.2	915	2	US-08-649-518-96
24	67	14.2	915	2	US-08-778-570B-24
25	67	14.2	915	2	US-09-059-584-24
26	67	14.2	917	2	US-08-753-750B-11
27	64.5	13.7	225	2	US-10-104-047-3107

28	64.5	13.7	502	2	US-09-904-615-69	Sequence 69, Appl
29	64.5	13.7	502	2	US-10-054-988-69	Sequence 69, Appl
30	64	13.6	125	2	US-09-640-211A-762	Sequence 762, App
31	64	13.6	313	2	US-09-513-151A-68	Sequence 68, Appl
32	63.5	13.5	600	2	US-09-540-236-2965	Sequence 2965, Ap
33	63	13.4	162	2	US-09-248-796A-21408	Sequence 21408, A
34	63	13.4	452	2	US-09-284-768A-22	Sequence 22, Appl
35	63	13.4	608	2	US-09-284-768A-4	Sequence 4, Appli
36	63	13.4	657	2	US-09-284-768A-7	Sequence 7, Appli
37	62.5	13.3	225	2	US-09-107-532A-5865	Sequence 5865, Ap
38	62.5	13.3	259	2	US-09-134-000C-4934	Sequence 4934, Ap
39	62.5	13.3	672	2	US-09-949-016-9511	Sequence 9511, Ap
40	62	13.2	632	2	US-09-902-540-11147	Sequence 11147, A
41	62	13.2	1047	2	US-10-104-047-2408	Sequence 2408, Ap
42	61.5	13.1	680	2	US-09-252-991A-29223	Sequence 29223, A
43	61	13.0	582	2	US-09-902-540-11161	Sequence 11161, A
44	60.5	12.8	425	2	US-09-252-991A-32805	Sequence 32805, A
45	60.5	12.8	1244	2	US-08-938-291A-5	Sequence 5, Appli
46	60.5	12.8	1244	2	US-09-589-619-5	Sequence 5, Appli
47	60	12.7	317	2	US-09-489-039A-8503	Sequence 8503, Ap
48	60	12.7	407	2	US-09-252-991A-25606	Sequence 25606, A
49	59.5	12.6	436	2	US-09-583-110-4694	Sequence 4694, Ap
50	59.5	12.6	2005	2	US-08-836-325-7	Sequence 3819, Ap
51	59.5	12.6	2005	2	US-09-457-571-7	Sequence 7, Appli
52	59.5	12.6	510	1	US-08-097-829-2	Sequence 2, Appli
53	59	12.5	510	1	US-08-577-403-2	Sequence 2, Appli
54	59	12.5	837	2	US-09-564-805-228	Sequence 228, App
55	59	12.5	230	2	US-09-270-767-46697	Sequence 46697, A
56	58.5	12.4	401	2	US-09-543-681A-5084	Sequence 5084, Ap
57	58.5	12.4	444	2	US-10-104-047-2690	Sequence 2690, Ap
58	58.5	12.4	510	2	US-09-852-067-2	Sequence 2, Appli
59	58.5	12.4	526	2	US-09-949-016-6263	Sequence 6263, Ap
60	58.5	12.4	145	2	US-09-902-540-13774	Sequence 13774, A
61	58.5	12.4	506	2	US-08-888-998-2	Sequence 2, Appli
62	58	12.3	506	2	US-09-877-476-2	Sequence 2, Appli
63	58	12.3	506	2	US-09-877-476-26	Sequence 26, Appl
64	58	12.3	506	2	US-09-877-476-30	Sequence 30, Appl
65	58	12.3	506	2	US-09-877-476-36	Sequence 36, Appl
66	58	12.3	506	2	US-09-877-476-38	Sequence 38, Appl
67	58	12.3	506	2	US-09-877-476-40	Sequence 40, Appl
68	58	12.3	1302	1	US-08-232-537-2	Sequence 2, Appli
69	58	12.3	378	2	US-09-252-991A-21060	Sequence 21060, A
70	58	12.3	393	2	US-09-634-238-274	Sequence 274, App
71	58	12.3	727	2	US-09-134-000C-6290	Sequence 6290, Ap
72	57.5	12.2				
73	57.5	12.2				
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75	57.5	12.2				

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:44:45 ; Search time 56.5 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-43

Perfect score: 471
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	294	62.4	88	3	US-09-955-502-27
6	294	62.4	88	3	US-09-955-502-28
7	291	61.8	87	3	US-09-955-502-32
8	286	60.7	88	3	US-09-955-502-33
9	275	58.4	87	3	US-09-955-502-2
10	275	58.4	87	3	US-09-955-502-3
11	257.5	54.7	86	3	US-09-955-502-4
12	242	51.4	87	3	US-09-955-502-25
13	237	50.3	87	3	US-09-955-502-24
14	219	46.5	90	3	US-09-955-502-23
15	215	45.6	89	3	US-09-955-502-22
16	213	45.2	88	3	US-09-955-502-9
17	211	44.8	87	3	US-09-955-502-8
18	208	44.2	91	3	US-09-955-502-5
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20	202	42.9	87	3	US-09-955-502-7
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28	197	41.8	91	3	US-09-955-502-17	Sequence 17, Appl
29	196	41.6	78	3	US-09-955-502-19	Sequence 19, Appl
30	190	40.3	91	3	US-09-955-502-18	Sequence 18, Appl
31	186	39.5	90	3	US-09-955-502-20	Sequence 20, Appl
32	166	35.2	76	3	US-09-955-502-21	Sequence 21, Appl
33	78	16.6	289	4	US-10-437-963-109722	Sequence 109722,
34	72.5	15.4	2285	6	US-11-097-143-15963	Sequence 15963, A
35	71	15.1	523	3	US-09-815-242-10987	Sequence 10987, A
36	71	15.1	523	3	US-10-282-122A-58107	Sequence 58107, A
37	71	15.1	568	4	US-10-369-493-5205	Sequence 5205, Ap
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39	68.5	14.5	249	4	US-10-369-493-17326	Sequence 17326, A
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44	67	14.2	319	5	US-10-472-533-317	Sequence 317, App
45	67	14.2	353	4	US-10-632-983-169	Sequence 169, App
46	67	14.2	561	4	US-10-094-749-2371	Sequence 2371, Ap
47	67	14.2	907	4	US-10-467-534-82	Sequence 82, Appl
48	67	14.2	915	3	US-09-332-226-2	Sequence 2, Appli
49	67	14.2	915	4	US-10-043-344-96	Sequence 96, Appl
50	67	14.2	950	3	US-09-815-242-11271	Sequence 11271, A
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70	64.5	13.7	501	4	US-10-181-108-14	Sequence 14, Appl
71	64.5	13.7	501	6	US-11-079-743-14	Sequence 14, Appl
72	64.5	13.7	502	3	US-09-739-254-69	Sequence 69, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiobacillus ferrooxidans

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502A-43
Perfect score: 471
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Total number of hits satisfying chosen parameters: 318885

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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6	294	62.4	88	5	US-09-955-502A-27 Sequence 27, Appl
7	294	62.4	88	5	US-09-955-502A-28 Sequence 28, Appl
8	294	62.4	88	5	US-09-955-502A-42 Sequence 42, Appl
9	291	61.8	87	5	US-09-955-502A-32 Sequence 32, Appl
10	286	60.7	88	5	US-09-955-502A-33 Sequence 33, Appl
11	275	58.4	87	5	US-09-955-502A-2
12	275	58.4	87	5	US-09-955-502A-3
13	267	56.7	84	5	US-09-955-502A-44
14	257.5	54.7	86	5	US-09-955-502A-4
15	242	51.4	87	5	US-09-955-502A-25
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18	237	50.3	87	5	US-09-955-502A-41
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21	215	45.6	89	5	US-09-955-502A-45
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23	213	45.2	88	5	US-09-955-502A-39
24	211	44.8	87	5	US-09-955-502A-8
25	208	44.2	91	5	US-09-955-502A-5

26	204	43.3	90	5	US-09-955-502A-10	Sequence 10, Appl
27	202	42.9	87	5	US-09-955-502A-7	Sequence 7, Appl
28	202	42.9	87	5	US-09-955-502A-38	Sequence 38, Appl
29	200	42.5	87	5	US-09-955-502A-6	Sequence 6, Appl
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34	197	41.8	91	5	US-09-955-502A-14	Sequence 14, Appl
35	197	41.8	91	5	US-09-955-502A-17	Sequence 17, Appl
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37	197	41.8	91	5	US-09-955-502A-35	Sequence 35, Appl
38	196	41.6	78	5	US-09-955-502A-19	Sequence 19, Appl
39	190	40.3	88	5	US-09-955-502A-15	Sequence 15, Appl
40	190	40.3	91	5	US-09-955-502A-16	Sequence 16, Appl
41	190	40.3	91	5	US-09-955-502A-18	Sequence 18, Appl
42	186	39.5	90	5	US-09-955-502A-20	Sequence 20, Appl
43	186	39.5	90	5	US-09-955-502A-37	Sequence 37, Appl
44	166	35.2	76	5	US-09-955-502A-21	Sequence 21, Appl
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72	62	13.2	500	8	US-60-752-355-39106	Sequence 39106, A
73	62	13.2	513	8	US-60-742-219-1524	Sequence 1524, Ap
74	62	13.2	534	6	US-10-567-867-1108	Sequence 1108, Ap
75	62	13.2	634	8	US-60-752-355-32764	Sequence 32764, A

ALIGNMENTS

RESULT 1
US-09-955-502A-31
; Sequence 31, Application US/09955502A
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502A
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thlobacillus ferrooxidans
US-09-955-502A-31

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 70.7241 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502a-44
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	278	62.3	87	5	ABB78175 Amino aci
5	272	61.0	87	5	ABB78174 Amino aci
6	267	59.9	87	5	ABB78176 Amino aci
7	265	59.4	88	5	ABB78171 Amino aci
8	265	59.4	88	5	ABB78172 Amino aci
9	265	59.4	88	5	ABB78173 Amino aci
10	265	59.4	88	6	ABP77219 N. gonorr
11	252	56.5	87	5	ABB78177 Amino aci
12	242	54.3	91	5	ABB78150 Amino aci
13	238	53.4	88	5	ABB78154 Amino aci
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22	231	51.8	91	5	ABB78161 Amino aci
23	231	51.8	91	5	ABB78159 Amino aci
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25	231	51.8	91	5	ABB78163	Abb78163 Amino aci
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29	221	49.6	87	5	ABB78153	Abb78153 Amino aci
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31	218	48.9	78	5	ABB78164	Abb78164 Amino aci
32	218	48.9	87	5	ABB78170	Abb78170 Amino aci
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66	64.5	14.5	207	9	ADW94758	Adw94758 Prolifera
67	64.5	14.5	503	2	AAW24140	Aaw24140 Thermosta
68	64.5	14.5	702	8	ADR6184	Adr6184 Aspergill
69	64.5	14.5	1240	6	ABU29661	Abu29661 Protein e
70	64.5	14.5	1242	7	ADC95614	Adc95614 E. faeciu
71	64.5	14.5	3346	9	AEB22178	Aeb22178 Plasmodiu
72	64	14.3	117	9	ADX40159	Adx40159 HIV Rev p
73	64	14.3	244	3	AAAB42492	Aab42492 Human ORF
74	64	14.3	272	4	AAAB36605	Aab36605 Human FLE
75	64	14.3	373	4	AAAB95352	Aab95352 Human pro

ALIGNMENTS

RESULT 1	ABB78149	standard; protein; 86 AA.	Abb78163 Amino aci
ID	ABB78149		Abb78151 Amino aci
AC	ABB78149;		Adf05158 Bacterial
XX			Ab065445 Klebsiell
DT	05-NOV-2002	(first entry)	Abb78153 Amino aci
XX			Ada34169 Acinetoba
DE		Amino acid sequence of a YggX homologue.	Abb78164 Amino aci
XX			Ab074609 Pseudomon
KW		Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	Abb78178 Amino aci
XX		hydroxyl radical; DNA damage; YggX homologue.	Abb78165 Amino aci
OS		Bordetella bronchiseptica.	Abb78167 Amino aci
XX			Abb78166 Amino aci
PN			Abb78168 Amino aci
XX			Adl05173 M. catar
XX			Abm94402 M. xanthu
XX			Adb06106 Alloiococ
XX			Abm70179 Photorhab
XX			Abb54524 Lactococc
XX			Adg66727 Novel hum
XX			Adx40209 HIV Rev p
XX			Aao20498 Human amy
XX			Aao80170 Human pro
XX			Abu40908 Protein e
XX			Adf05593 Bacterial
XX			Abu49707 Protein e
XX			Aab41703 Human ORF
XX			Aeb40319 L. pneumo
XX			Aeb36958 L. pneumo
XX			Aaw85085 Esterase
XX			Ab062233 Klebsiell
XX			AbR39820 Human SCA
XX			Aae26857 Anabaena
XX			Aay57085 Human rho
XX			Adg12800 Human rho
XX			Abb61876 Drosophil
XX			Adx40214 HIV Rev p
XX			Abm73508 Staphyloc
XX			Adv16859 Staphyloc
XX			Adw94758 Prolifera
XX			Aaw24140 Thermosta
XX			Adr6184 Aspergill
XX			Abu29661 Protein e
XX			Adc95614 E. faeciu
XX			Aeb22178 Plasmodiu
XX			Adx40159 HIV Rev p
XX			Aab42492 Human ORF
XX			Aab36605 Human FLE
XX			Aab95352 Human pro

Wed Mar 1 09:15:57 2006

PD 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
PF 22-SEP-2000; 2000US-0234588P.
PR
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PA
XX Downs D, Gralnicks JA;
PI
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 86 AA;

Query Match 97.8%; Score 436; DB 5; Length 86;
Best Local Similarity 98.8%; Pred. No. 2.6e-45;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYNCVYKLRBAEGLDFPPYGGELGTRIWQOISKEAWBEWKQIQTRLVNNENRLNPADA 60
Db 1 MSRIYNCVYKLRBAEGLDFPPYGGELGTRIWQOISKEAWBEWKQIQTRLVNNENRLNPADA 60

QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
Db 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 2
ABB78148 standard; protein; 87 AA.
ID ABB78148 standard; protein; 87 AA.
XX
AC ABB78148;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella parapertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PS (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PA
XX Downs D, Gralnicks JA;
PI

DR WPI; 2002-589476/63.
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 97.8%; Score 436; DB 5; Length 87;
Best Local Similarity 98.8%; Pred. No. 2.7e-45;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYNCVYKLRBAEGLDFPPYGGELGTRIWQOISKEAWBEWKQIQTRLVNNENRLNPADA 60
Db 1 MSRIYNCVYKLRBAEGLDFPPYGGELGTRIWQOISKEAWBEWKQIQTRLVNNENRLNPADA 60

QY 61 RARKYLOQOMERFLFEDGTVEAOG 84
Db 61 RARKYLOQOMERFLFEDGTVEAOG 84

RESULT 3
ABB78147 standard; protein; 87 AA.
ID ABB78147 standard; protein; 87 AA.
XX
AC ABB78147;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella pertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PS (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PA
XX Downs D, Gralnicks JA;
PI
XX WPI; 2002-589476/63.
XX
DR Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.3793 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-44

Perfect score: 446
Sequence: 1 MSRIIVNCVKLKRAEGIDFP.....YLQOMERFLFEDGTEAOG 84

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*

1: pir1:*\n2: pir2:*\n3: pir3:*\n4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	265	59.4	88	2	H81014	conserved hypothet
2	237	53.1	91	2	A85954	hypothetical prote
3	237	53.1	91	2	A65082	hypothetical prote
4	237	53.1	91	2	F91108	hypothetical prote
5	234	52.5	90	2	C64013	hypothetical prote
6	231	51.8	90	2	C82320	conserved hypothet
7	231	51.8	91	2	AH0879	conserved hypothet
8	218	48.9	90	2	H83003	conserved hypothet
9	208	46.6	90	2	A10116	conserved hypothet
10	205	46.0	105	2	C82624	conserved hypothet
11	196	43.9	93	2	E84994	hypothetical prote
12	69.5	15.6	749	2	E86774	hypothetical prote
13	69	15.5	134	2	T37027	hypothetical prote
14	69	15.5	241	2	S19999	hypothetical prote
15	69	15.5	429	2	AB2501	hypothetical prote
16	67.5	15.1	855	2	A45713	Env transmembrane
17	67	15.0	389	2	T14751	hypothetical prote
18	66.5	14.9	680	2	C82437	transketolase 1 VC
19	66.5	14.9	1177	2	AD0438	probable exported
20	65.5	14.7	412	2	F69796	sugar-binding prot
21	65.5	14.7	2291	1	A46147	spectrin beta chai
22	65	14.6	110	2	S77857	probable proline-t
23	65	14.6	506	2	T50211	WD-repeat protein
24	65	14.6	1068	2	S73091	hypothetical prote
25	64.5	14.5	207	2	B89952	conserved hypothet
26	64.5	14.5	622	2	T23804	hypothetical prote
27	64.5	14.5	931	2	C90891	probable peptidase
28	64.5	14.5	931	2	F85726	probable peptidase
29	64.5	14.5	1883	2	G82875	hypothetical prote

30	64	14.3	133	2	G75385	hypothetical prote
31	63.5	14.2	393	2	T49257	protein kinase-lik
32	63.5	14.2	531	2	S75607	glucose-6-phosphat
33	63.5	14.2	714	2	S77385	nitrate reductase
34	63.5	14.2	931	2	A64903	probable zinc prot
35	63	14.1	228	2	C26599	clathrin light cha
36	63	14.1	229	2	B31775	clathrin light cha
37	63	14.1	238	1	LRRTB2	ethylene-forming e
38	63	14.1	320	2	S11879	probable type II r
39	63	14.1	372	2	B81952	hypothetical prote
40	63	14.1	904	2	S45673	hypothetical prote
41	63	14.1	1966	2	T32552	nitrogenase iron p
42	63	14.1	2848	2	T32550	hypothetical prote
43	62.5	14.0	272	2	D86295	transketolase (EC
44	62.5	14.0	332	2	D86295	transketolase (EC
45	62.5	14.0	664	2	AG0113	dynein heavy chain
46	62.5	14.0	897	2	G02529	hypothetical prote
47	62	13.9	107	2	AG1878	hypothetical prote
48	62	13.9	865	2	E84718	zinc proteinase (B
49	62	13.9	989	2	T46183	hypothetical prote
50	61.5	13.8	164	2	E75293	porphobilinogen de
51	61.5	13.8	396	2	H84383	protein disulfide-
52	61.5	13.8	522	1	ISBYSS	transketolase (EC
53	61.5	13.8	667	1	A48660	transketolase 2 is
54	61.5	13.8	667	2	G91044	transketolase 2 is
55	61.5	13.8	667	2	B85889	p97 protein - Toxo
56	61.5	13.8	877	2	T03098	exodeoxyribonuclea
57	61.5	13.8	1069	2	A81050	hypothetical prote
58	61.5	13.8	1464	2	T07050	microtubule-associ
59	61.5	13.8	2774	2	A43359	dynein heavy chain
60	61.5	13.8	4644	1	A38905	general stress pro
61	61	13.7	143	2	D70003	hypothetical prote
62	61	13.7	260	2	AH1639	probable 1-aminocy
63	61	13.7	321	2	T02754	ethylene-forming e
64	61	13.7	323	2	JT0755	hypothetical prote
65	61	13.7	323	2	A86184	hypothetical prote
66	61	13.7	337	2	AG2423	probable transcrip
67	61	13.7	416	2	C47017	RNA polymerase sig
68	61	13.7	416	2	AF2017	hypothetical prote
69	61	13.7	431	2	T32694	glutamine syntheta
70	61	13.7	439	2	A36911	hypothetical prote
71	61	13.7	567	2	B84504	hypothetical prote
72	60.5	13.6	348	2	D85212	hypothetical prote
73	60.5	13.6	388	2	T38810	hypothetical prote
74	60.5	13.6	509	2	T01344	hypothetical prote
75	60.5	13.6	713	2	S56833	nuclear pore prote

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tetteijn, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masiyanti, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:.
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

```

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: F81958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <PAR>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: NMB2021; MMA0419
C/Superfamily: fe(II) trafficking protein YggX

Query Match      59.4%; Score 265; DB 2; Length 88;
Best Local Similarity 58.3%; Pred. No. 4.1e-21;
Matches 49; Conservative 14; Mismatches 21; Indels 0; Gaps 0;

Oy      1 MSRIIVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRNLNPADA 60
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MARWFCVKLNKEAEAGMKFPPLPNELGKRIFENVSGEAWAATRRHQTMILINENRLSLADP 60
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Oy      61 RARKYLQQOMERFLFEDGTVEAOG 84
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 RAREYLAQQOMEQYFFGDGDAVQG 84
        ||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 2
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
A/Perna, N.T.; Plunkett II, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoustis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI000163A04; GB:AB005174; NID:g12517511; R
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: YggX
C/Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 237; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.9e-18;
Matches 46; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

Oy      1 MSRIIVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRNLNPADA 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      1 MSRTIFCTFLQREAEGQDFQLYPGELGKRIYNEISKEMAQWQHQTMLINEKCLNMNNA 60
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

Oy      61 RARKYLQQOMERFLFEDGTVEAOG 84
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      61 EHKKLLQEEMVNFLFEKGKVHIEG 84
        |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
A/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA

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A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g1
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 237; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.9e-18;
Matches 46; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

OY      1 MSRIIVCVKLKREAEGIDFPYPGELGTRIMQISKEAWBEWKQIQTRLVNEKRLNPADA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKKLNMMNA 60

OY      61 RARKYLQQQMERFLPEDGTVEAOG 84
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EHRKLLQEQMVNFLFEGKEVHIEG 84

RESULT 4
F91108
hypothetical protein BCs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: EC83838
C/Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 237; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.9e-18;
Matches 46; Conservative 12; Mismatches 26; Indels 0; Gaps 0;

OY      1 MSRIIVCVKLKREAEGIDFPYPGELGTRIMQISKEAWBEWKQIQTRLVNEKRLNPADA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKKLNMMNA 60

OY      61 RARKYLQQQMERFLPEDGTVEAOG 84
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EHRKLLQEQMVNFLFEGKEVHIEG 84

RESULT 5
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.;
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C/Superfamily: fe(II) trafficking protein YggX

Query Match      52.5%; Score 234; DB 2; Length 90;

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 63.4828 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502A-44
Perfect score: 446
Sequence: 1 MSRTVNCVKLRKREAGLDLP.....YLQQQMERFLPEDGTVAAG 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	436	97.8	90	1	FETP_BORBR
2	436	97.8	90	1	FETP_BORPA
3	436	97.8	90	1	FETP_BORPB
4	291	65.2	91	1	FETP_RALSO
5	282	63.2	91	2	Q4LS19_9BURK
6	278	62.3	91	1	FETP_BURMA
7	278	62.3	91	1	FETP_BURPS
8	276	61.9	90	1	FETP_CHRVO
9	265	59.4	88	1	FETP_NEIGI
10	265	59.4	88	1	FETP_NEIMA
11	265	59.4	88	1	FETP_NEIMB
12	262	58.7	90	1	FETP_NITEU
13	252	56.5	90	1	FETP_METCA
14	238	53.4	92	1	FETP_SHEON
15	237	53.1	90	1	FETP_VIBPA
16	236	52.9	90	1	FETP_IDILO
17	235	52.7	89	1	FETP_LEGPA
18	235	52.7	89	1	FETP_LEGPH
19	235	52.7	91	1	FETP_MANSN
20	234	52.5	89	1	FETP_LEGPI
21	234	52.5	90	1	FETP_HAEIN
22	234	52.5	90	1	FETP_VIBF1
23	234	52.5	90	2	Q4QMD9_HAEI8
24	232	52.0	90	1	FETP_ECO57
25	232	52.0	90	1	FETP_ECOL6
26	232	52.0	90	1	FETP_ECOLI
27	232	52.0	90	1	FETP_PHOLL
28	232	52.0	90	1	FETP_SHIFL
29	232	52.0	90	1	FETP_VIBVU
30	232	52.0	90	1	FETP_VIBVY
31	231	51.8	90	1	FETP_VIBCH

ALIGNMENTS

32	230	51.6	91	1	FETP_XANAC	Q8pjh7 xanthomonas
33	229	51.3	90	1	FETP_PASMU	Q9cib9 pasteurella
34	229	51.3	90	1	FETP_PHOPR	Q6lmk7 photobacter
35	226	50.7	90	1	FETP_SALCH	Q57K04 salmonella
36	226	50.7	90	1	FETP_SALPA	Q5pmn1 salmonella
37	226	50.7	90	1	FETP_SALTI	P67618 salmonella
38	226	50.7	90	1	FETP_SALTY	P67617 salmonella
39	224	50.2	90	2	Q4J228_AZOVI	Q4J228 azotobacter
40	224	50.2	92	1	FETP_XANOR	Q59Y22 xanthomonas
41	221.5	49.7	90	1	FETP_ACIAD	Q6fEb3 acinetobact
42	221	49.6	90	1	FETP_ERWCT	Q6d819 erwina car
43	221	49.6	92	1	FETP_XANCP	Q8p829 xanthomonas
44	221	49.6	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
45	221	49.6	94	1	FETP_HABDU	Q7vkb6 haemophilus
46	218	48.9	90	1	FETP_PSEAE	Q9nu36 pseudomonas
47	216	48.4	78	1	FETP_BUCAP	Q8K925 buchnera ap
48	216	48.4	90	1	FETP_COXBU	Q83d06 coxiella bu
49	216	48.4	90	1	FETP_YERPS	Q66m3 yersinia ps
50	212	47.5	90	1	FETP_XYLEFT	Q87d06 xylella fas
51	209	46.9	79	1	FETP_CANBF	Q7vrg9 candidatus
52	208	46.6	90	1	FETP_YERPE	Q8zhe7 yersinia pe
53	205	46.0	90	1	FETP_XYLEFA	Q9pc73 xylella fas
54	200	44.8	90	1	FETP_PSEBP	Q88r49 pseudomonas
55	196	43.9	77	1	FETP_BUCAI	P57618 buchnera ap
56	196	43.9	90	1	FETP_PSESM	Q87uFs pseudomonas
57	196	43.9	90	2	Q4ZLF3_PSESM	Q4Zlp3 pseudomonas
58	192	43.0	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
59	192	43.0	90	2	Q4KJ72_PSEF5	Q4Kjt2 pseudomonas
60	189	42.4	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
61	185	41.5	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
62	177	39.7	87	1	FETP_FRATT	Q5nhj8 francisella
63	162	36.3	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	153	34.3	87	1	FETP_BUCBP	Q89a44 buchnera ap
65	79.5	17.8	116	2	Q6UPK7_9HIV1	Q6ufk7 human immun
66	77	17.3	330	2	Q5DA35_SCHJA	Q5da35 schistosoma
67	76.5	17.2	786	2	Q4ICH5_GIBZE	Q4ich5 gibberella
68	76.5	17.2	2410	2	Q5AZ49_EMENT	Q5az49 aspergillus
69	75.5	16.9	116	2	Q6WS71_9HIV1	Q6ws71 human immun
70	75.5	16.9	116	2	Q5ESM1_VIBF1	Q5esm1 vibrio fusc
71	73	16.4	509	2	Q5ESM1_VIBF1	Q5esm1 plasmodium
72	71	15.9	2322	2	Q6UDW6_PLAFA	Q6udw6 chlorobium
73	70.5	15.8	272	2	Q8KAR9_CHLTR	Q8kar9 photorhabdu
74	70.5	15.8	307	2	Q7N7T0_PHOLL	Q7n7t0 vibrio para
75	70.5	15.8	663	2	Q87GY4_VIBPA	Q87gy4 vibrio para

RESULT 1

ID	FETP_BORBR	STANDARD;	PRT;	90 AA.
AC	Q5WH06;			
DT	05-JUL-2004 (Rel. 44, Created)			
DT	05-JUL-2004 (Rel. 44, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocustNames=BB3405;			
OS	Bordetella bronchiseptica (Alcaligenes bronchisepticus).			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;			
OC	Alcaligenaceae; Bordetella.			
OX	NCBI_TaxID=518;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=RB50 / ATCC BAA-588;			
RX	MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;			
RA	Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,			
RA	Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,			
RA	Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,			
RA	Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,			
RA	Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,			
RA	Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagsels K.,			
RA	Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,			

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RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
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DR EMBL; BX640447; CAB33897.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.8%; Score 436; DB 1; Length 90;
Best Local Similarity 98.8%; Pred. No. 9.3e-39;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNPADA 60
DB 1 MSRIYVCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNPADA 60

QY 61 PARKYLQOQMERFLFEDGTVEAOG 84
DB 61 PARKYLQOQMERFLFEDGTVEAOG 84

RESULT 2
FETP BORPA
ID FETP BORPA STANDARD; PRT; 90 AA.
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP1703;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Cherevach I.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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-----
DR EMBL; BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.8%; Score 436; DB 1; Length 90;
Best Local Similarity 98.8%; Pred. No. 9.3e-39;
Matches 83; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNPADA 60
DB 1 MSRIYVCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNPADA 60

QY 61 PARKYLQOQMERFLFEDGTVEAOG 84
DB 61 PARKYLQOQMERFLFEDGTVEAOG 84

RESULT 3
FETP BORPE
ID FETP BORPE STANDARD; PRT; 90 AA.
AC Q7WVC4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP2336;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
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CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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-----
DR EMBL; BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 18.5862 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-44
Perfect score: 446
Sequence: 1 MSRIIVNCTVKRRAEGLDFP.....YLQQQMERFLPBDGTVEAGG 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query length	DB ID	Description
1	228	51.1	93	2	US-09-543-681A-5443 Sequence 5443, Ap
2	225	50.4	107	2	US-09-489-039A-11962 Sequence 11962, A
3	220.5	49.4	92	2	US-09-328-352-5456 Sequence 5456, Ap
4	218	48.9	122	2	US-09-252-991A-23355 Sequence 23355, A
5	153.5	34.4	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	72.5	16.3	303	2	US-09-902-540-13601 Sequence 13601, A
7	67	15.0	381	2	US-09-949-016-9788 Sequence 9788, Ap
8	67	15.0	381	2	US-09-964-899-13 Sequence 13, Appl
9	66.5	14.9	665	2	US-09-543-681A-5878 Sequence 5878, Ap
10	66	14.8	503	2	US-09-058-260-26 Sequence 26, Appl
11	66	14.8	726	2	US-09-489-039A-8750 Sequence 8750, Ap
12	64.5	14.5	1242	2	US-09-107-532A-5241 Sequence 5241, Ap
13	64	14.3	1493	2	US-09-713-273A-20 Sequence 20, Appl
14	63.5	14.2	200	2	US-09-710-279-1186 Sequence 1186, Ap
15	63.5	14.2	200	2	US-09-710-279-2390 Sequence 2390, Ap
16	63.5	14.2	208	2	US-09-134-001C-3785 Sequence 3785, Ap
17	63.5	14.2	498	2	US-09-058-260-16 Sequence 16, Appl
18	63.5	14.2	503	1	US-08-781-802-2 Sequence 2, Appl
19	63.5	14.2	503	1	US-08-781-802-10 Sequence 10, Appl
20	63.5	14.2	503	1	US-08-781-802-12 Sequence 12, Appl
21	63.5	14.2	503	2	US-08-694-078-2 Sequence 2, Appl
22	63.5	14.2	503	2	US-09-058-260-2 Sequence 2, Appl
23	63.5	14.2	503	2	US-09-058-260-10 Sequence 10, Appl
24	63.5	14.2	503	2	US-09-058-260-12 Sequence 12, Appl
25	63.5	14.2	503	2	US-09-058-260-28 Sequence 28, Appl
26	63.5	14.2	503	2	US-09-058-260-30 Sequence 30, Appl
27	63.5	14.2	666	2	US-09-270-767-62249 Sequence 62249, A

28	63.5	14.2	721	2	US-09-270-767-46645	Sequence 46645, A
29	63	14.1	581	2	US-09-713-273A-12	Sequence 12, Appl
30	62.5	14.0	1186	2	US-09-543-681A-5514	Sequence 5514, Ap
31	62	13.9	856	2	US-09-252-991A-17850	Sequence 17850, A
32	62	13.9	979	2	US-09-543-681A-5466	Sequence 5466, Ap
33	61.5	13.8	478	2	US-10-000-489-108	Sequence 108, Appl
34	61.5	13.8	504	1	US-08-441-139-18	Sequence 18, Appl
35	61.5	13.8	518	2	US-09-045-360-4	Sequence 4, Appl
36	61.5	13.8	518	2	US-09-746-390-4	Sequence 4, Appl
37	61.5	13.8	521	1	US-08-557-122A-32	Sequence 32, Appl
38	61.5	13.8	521	2	US-09-262-666-32	Sequence 32, Appl
39	61.5	13.8	522	2	US-09-368-588-2	Sequence 2, Appl
40	61.5	13.8	530	1	US-08-557-122A-35	Sequence 35, Appl
41	61.5	13.8	530	2	US-09-262-666-35	Sequence 35, Appl
42	61.5	13.8	1464	2	US-09-045-360-2	Sequence 2, Appl
43	61.5	13.8	1464	2	US-09-713-273A-21	Sequence 21, Appl
44	61.5	13.8	1464	2	US-10-038-224-2	Sequence 2, Appl
45	61.5	13.8	1464	2	US-09-746-390-2	Sequence 2, Appl
46	60.5	13.6	81	2	US-10-290-579A-138	Sequence 138, Appl
47	60.5	13.6	130	2	US-09-270-767-31697	Sequence 31697, A
48	60.5	13.6	130	2	US-09-270-767-46914	Sequence 46914, A
49	60.5	13.6	354	2	US-09-949-016-6929	Sequence 6929, Ap
50	60.5	13.6	427	2	US-09-248-796A-19520	Sequence 19520, A
51	60.5	13.6	440	2	US-09-248-796A-25909	Sequence 25909, A
52	60	13.5	100	2	US-09-732-210-60	Sequence 60, Appl
53	60	13.5	713	2	US-09-540-236-3595	Sequence 3595, Ap
54	59.5	13.3	386	2	US-09-605-703B-1466	Sequence 1466, Ap
55	59.5	13.3	447	2	US-09-902-540-13195	Sequence 13195, A
56	59.5	13.3	591	2	US-09-370-368-8	Sequence 8, Appl
57	59.5	13.3	3080	6	5223423-4	Patent No. 5223423
58	59	13.2	156	2	US-09-134-000C-3451	Sequence 3451, Ap
59	59	13.2	484	2	US-09-605-703B-1468	Sequence 1468, Ap
60	59	13.2	1047	2	US-10-104-047-2408	Sequence 2408, Ap
61	59	13.2	1388	1	US-08-685-576-4	Sequence 4, Appl
62	59	13.2	1388	2	US-09-976-594-296	Sequence 296, Appl
63	58.5	13.1	318	1	US-08-695-412B-12	Sequence 12, Appl
64	58.5	13.1	318	2	US-09-255-154D-12	Sequence 12, Appl
65	58.5	13.1	318	2	US-10-213-452A-12	Sequence 12, Appl
66	58.5	13.1	436	2	US-09-107-532A-5135	Sequence 5135, Ap
67	58.5	13.1	520	2	US-09-328-352-7451	Sequence 7451, Ap
68	58.5	13.1	1469	2	US-09-713-273A-16	Sequence 16, Appl
69	58	13.0	332	2	US-09-605-703B-1422	Sequence 1422, Appl
70	58	13.0	361	2	US-09-252-991A-25005	Sequence 25005, A
71	58	13.0	366	2	US-08-928-213B-59	Sequence 59, Appl
72	58	13.0	530	2	US-09-328-352-5795	Sequence 5795, Ap
73	58	13.0	912	2	US-09-664-958-8	Sequence 8, Appl
74	57.5	12.9	319	2	US-09-248-796A-17948	Sequence 17948, A
75	57.5	12.9	398	2	US-09-710-279-44	Sequence 44, Appl

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:44:45 ; Search time 54.5517 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-44
Perfect score: 446
Sequence: 1 MSRIYNCVTKLKREAEGLDFP.....YLQOQMERFLFEDGTVEAOG 84

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	436	97.8	86	3	US-09-955-502-4
2	436	97.8	87	3	US-09-955-502-2
3	436	97.8	87	3	US-09-955-502-3
4	278	62.3	87	3	US-09-955-502-29
5	278	62.3	87	3	US-09-955-502-30
6	267	59.9	87	3	US-09-955-502-31
7	265	59.4	88	3	US-09-955-502-26
8	265	59.4	88	3	US-09-955-502-27
9	265	59.4	88	3	US-09-955-502-28
10	252	56.5	87	3	US-09-955-502-32
11	242	54.3	91	3	US-09-955-502-5
12	238	53.4	88	3	US-09-955-502-9
13	237	53.1	91	3	US-09-955-502-11
14	237	53.1	91	3	US-09-955-502-12
15	237	53.1	91	3	US-09-955-502-13
16	234	52.5	87	3	US-09-955-502-7
17	231	51.8	88	3	US-09-955-502-15
18	231	51.8	90	3	US-09-955-502-10
19	231	51.8	91	3	US-09-955-502-14
20	231	51.8	91	3	US-09-955-502-16
21	231	51.8	91	3	US-09-955-502-17
22	231	51.8	91	3	US-09-955-502-18
23	229	51.3	87	3	US-09-955-502-6
24	221	49.6	87	3	US-09-955-502-8
25	218	48.9	78	3	US-09-955-502-19
26	218	48.9	87	3	US-09-955-502-25
27	216	48.4	88	3	US-09-955-502-33

28	208	46.6	90	3	US-09-955-502-20	Sequence 20, Appl
29	205	46.0	89	3	US-09-955-502-22	Sequence 22, Appl
30	200	44.8	87	3	US-09-955-502-24	Sequence 24, Appl
31	196	43.9	76	3	US-09-955-502-21	Sequence 21, Appl
32	196	43.9	90	3	US-09-955-502-23	Sequence 23, Appl
33	72.5	16.3	1374	4	US-10-437-963-189670	Sequence 189670,
34	71	15.9	527	5	US-10-501-282-46	Sequence 46, Appl
35	71	15.9	528	5	US-10-501-282-48	Sequence 48, Appl
36	69	15.5	826	4	US-10-437-963-189868	Sequence 189868,
37	69	15.5	852	4	US-10-437-963-189841	Sequence 189841,
38	69	15.5	1588	4	US-10-437-963-189741	Sequence 189741,
39	68.5	15.4	87	4	US-10-424-599-281616	Sequence 281616,
40	68	15.2	317	5	US-10-732-923-10013	Sequence 10013, A
41	68	15.2	648	4	US-10-437-963-189835	Sequence 189835,
42	68	15.2	923	4	US-10-437-963-189730	Sequence 189730,
43	68	15.2	1060	4	US-10-437-963-189614	Sequence 189614,
44	68	15.2	1400	4	US-10-437-963-158675	Sequence 158675,
45	68	15.2	1748	4	US-10-437-963-158726	Sequence 158726,
46	67	15.0	373	4	US-10-437-963-107538	Sequence 107538,
47	67	15.0	381	3	US-09-964-899-13	Sequence 13, Appl
48	67	15.0	381	5	US-10-975-523-13	Sequence 13, Appl
49	67	15.0	837	4	US-10-437-963-189921	Sequence 189921,
50	67	15.0	901	4	US-10-437-963-189632	Sequence 189632,
51	66.5	14.9	361	4	US-10-437-963-181511	Sequence 181511,
52	66.5	14.9	664	4	US-10-282-122A-68832	Sequence 68832, A
53	66.5	14.9	680	4	US-10-282-122A-77631	Sequence 77631, A
54	66.5	14.9	1360	4	US-10-437-963-201860	Sequence 201860,
55	66.5	14.9	1733	4	US-10-437-963-181840	Sequence 181840,
56	66	14.8	235	4	US-10-437-963-173278	Sequence 173278,
57	66	14.8	428	4	US-10-437-963-146305	Sequence 146305,
58	66	14.8	861	4	US-10-437-963-159716	Sequence 159716,
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61	66	14.8	1012	4	US-10-437-963-189765	Sequence 189765,
62	66	14.8	1386	4	US-10-437-963-189627	Sequence 189627,
63	65.5	14.7	231	4	US-10-788-197-23	Sequence 23, Appl
64	65.5	14.7	563	5	US-10-754-473-23	Sequence 23, Appl
65	65.5	14.7	563	5	US-10-437-963-167473	Sequence 167473,
66	65.5	14.7	1136	4	US-10-437-963-180218	Sequence 180218,
67	65.5	14.7	2291	6	US-11-097-143-12420	Sequence 12420, A
68	65	14.6	319	5	US-10-732-923-10012	Sequence 10012, A
69	65	14.6	558	4	US-10-425-115-217061	Sequence 217061,
70	65	14.6	802	4	US-10-437-963-189798	Sequence 189798,
71	65	14.6	1283	4	US-10-437-963-180218	Sequence 180218,
72	65	14.6	1479	4	US-10-437-963-180217	Sequence 180217,
73	64.5	14.5	207	5	US-10-857-625-698	Sequence 698, App
74	64.5	14.5	559	4	US-10-425-115-338828	Sequence 338828,
75	64.5	14.5	752	4	US-10-437-963-159713	Sequence 159713,

ALIGNMENTS

RESULT 1
US-09-955-502-4
; Sequence 4, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:45:38 ; Search time 5.31034 Seconds
(without alignments)
235.489 Million cell updates/sec

Title: US-09-955-502a-44
Perfect score: 446
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	265	59.4	88	US-10-467-657-968	Sequence 968, App
2	73	16.4	1320	US-11-098-686-10831	Sequence 10831, A
3	65.5	14.7	563	US-11-040-218-23	Sequence 23, Appl
4	63.5	14.2	200	US-10-793-626-1186	Sequence 1186, Ap
5	63.5	14.2	200	US-10-793-626-2390	Sequence 2390, Ap
6	63	14.1	384	US-11-098-686-10752	Sequence 10752, A
7	61.5	13.8	478	US-10-689-742-184	Sequence 184, App
8	61.5	13.8	832	US-11-098-686-10182	Sequence 10182, A
9	59.5	13.3	483	US-11-137-465-40	Sequence 40, Appl
10	59	13.2	331	US-11-098-686-10431	Sequence 10431, A
11	59	13.2	1047	US-11-072-512-2408	Sequence 2408, Ap
12	58.5	13.1	123	US-10-467-657-4690	Sequence 4690, Ap
13	58	13.0	240	US-11-044-111-10	Sequence 10, Appl
14	58	13.0	919	US-10-821-234-951	Sequence 951, App
15	57.5	12.9	398	US-10-793-626-44	Sequence 44, Appl
16	57.5	12.9	398	US-10-793-626-1498	Sequence 1498, Ap
17	57.5	12.9	447	US-11-024-959-286	Sequence 286, App
18	57.5	12.9	567	US-11-033-039-1279	Sequence 1279, Ap
19	57.5	12.9	897	US-10-821-234-1523	Sequence 1523, Ap
20	57	12.8	314	US-11-072-512-2917	Sequence 2917, Ap
21	57	12.8	361	US-11-072-512-2833	Sequence 2833, Ap
22	57	12.8	464	US-10-959-322-5	Sequence 5, Appli
23	57	12.8	760	US-10-912-580-4	Sequence 4, Appli
24	57	12.8	804	US-10-912-580-5	Sequence 5, Appli
25	57	12.8	2504	US-10-647-956A-8	Sequence 8, Appli

26	56.5	12.7	694	7	US-11-072-512-2469	Sequence 2469, Ap
27	56.5	12.7	805	7	US-11-108-539-2	Sequence 2, Appli
28	56.5	12.7	1068	6	US-10-467-657-2904	Sequence 2904, Ap
29	56	12.6	310	7	US-11-198-746-88	Sequence 88, Appl
30	56	12.6	310	7	US-11-198-794-88	Sequence 88, Appl
31	56	12.6	313	7	US-11-237-600-68	Sequence 68, Appl
32	56	12.6	315	7	US-11-198-746-91	Sequence 91, Appl
33	56	12.6	315	7	US-11-198-794-91	Sequence 91, Appl
34	56	12.6	322	7	US-11-198-746-89	Sequence 89, Appl
35	56	12.6	322	7	US-11-198-794-89	Sequence 89, Appl
36	56	12.6	528	7	US-11-198-746-90	Sequence 90, Appl
37	56	12.6	528	7	US-11-198-794-90	Sequence 90, Appl
38	56	12.6	548	7	US-11-198-746-86	Sequence 86, Appl
39	56	12.6	548	7	US-11-198-794-86	Sequence 86, Appl
40	56	12.6	695	7	US-11-198-746-87	Sequence 87, Appl
41	56	12.6	695	7	US-11-198-794-87	Sequence 87, Appl
42	56	12.6	832	7	US-11-065-943-100	Sequence 100, App
43	56	12.6	832	7	US-11-007-797A-11	Sequence 11, Appl
44	56	12.6	832	7	US-11-007-642B-11	Sequence 11, Appl
45	56	12.6	832	7	US-11-198-746-4	Sequence 4, Appli
46	56	12.6	832	7	US-11-198-794-4	Sequence 4, Appli
47	56	12.6	832	7	US-11-242-730-1	Sequence 1, Appli
48	56	12.6	833	7	US-11-198-746-85	Sequence 85, Appl
49	56	12.6	833	7	US-11-198-794-85	Sequence 85, Appl
50	55.5	12.4	1659	7	US-11-072-175-205	Sequence 205, App
51	55.5	12.4	3353	7	US-11-037-243-64	Sequence 64, Appl
52	55	12.3	212	7	US-11-044-111-6	Sequence 6, Appli
53	55	12.3	212	7	US-11-044-111-26	Sequence 26, Appli
54	55	12.3	239	7	US-11-044-111-5	Sequence 5, Appli
55	55	12.3	239	7	US-11-044-111-25	Sequence 25, Appl
56	55	12.3	240	7	US-11-044-111-9	Sequence 9, Appli
57	55	12.3	519	7	US-11-099-691-10	Sequence 10, Appl
58	55	12.3	828	6	US-10-501-039-2	Sequence 2, Appli
59	55	12.3	1056	7	US-11-044-111-22	Sequence 22, Appl
60	54.5	12.2	356	7	US-11-143-986-8	Sequence 8, Appli
61	54.5	12.2	356	7	US-11-143-986-9	Sequence 9, Appli
62	54	12.1	432	6	US-10-933-115-8	Sequence 8, Appli
63	54	12.1	432	7	US-11-056-354-4	Sequence 4, Appli
64	54	12.1	440	6	US-10-933-115-2	Sequence 2, Appli
65	54	12.1	784	6	US-10-517-939-324	Sequence 324, App
66	53.5	12.0	623	7	US-11-072-512-3378	Sequence 3378, Ap
67	53.5	12.0	662	7	US-11-072-175-184	Sequence 184, App
68	53.5	12.0	951	7	US-11-121-438-14	Sequence 14, Appl
69	53.5	12.0	2630	7	US-11-186-731-2	Sequence 2, Appli
70	53.5	12.0	7968	7	US-11-186-731-5	Sequence 5, Appli
71	53	11.9	104	7	US-11-120-308-74	Sequence 74, Appl
72	53	11.9	216	7	US-11-156-084-244	Sequence 244, App
73	53	11.9	216	7	US-11-156-084-322	Sequence 322, App
74	53	11.9	316	7	US-11-156-084-210	Sequence 210, App
75	53	11.9	316	7	US-11-156-084-280	Sequence 280, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:49:36 ; Search time 74.9339 Seconds
(without alignments)
521.856 Million cell updates/sec

Title: US-09-955-502A-45
Perfect score: 483
Sequence: 1 MORIIFCEYEQRDTEGLDFV.....LNKFLFRRVAKPEGYTPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*
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2: geneseqp1990s:*
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5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
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9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472.5	97.8	90	5	ABB78167 Amino aci
2	246	50.9	87	5	ABB78153 Amino aci
3	238	49.3	107	7	ABO65445 Klebsiell
4	237	49.1	87	5	ABB78151 Amino aci
5	237	49.1	87	5	ABB78152 Amino aci
6	234	48.4	91	5	ABB78150 Amino aci
7	232	48.0	91	5	ABB78161 Amino aci
8	232	48.0	91	5	ABB78159 Amino aci
9	232	48.0	91	5	ABB78162 Amino aci
10	230	47.6	91	5	ABB78163 Amino aci
11	229	47.4	88	5	ABB78160 Amino aci
12	228	47.2	90	5	ABB78155 Amino aci
13	227	47.0	93	7	ADP05158 Bacterial
14	226	46.8	91	5	ABB78158 Amino aci
15	226	46.8	91	5	ABB78157 Amino aci
16	226	46.8	91	5	ABB78156 Amino aci
17	220	45.5	78	5	ABB78164 Amino aci
18	215	44.5	87	5	ABB78176 Amino aci
19	214	44.3	88	5	ABB78178 Amino aci
20	209	43.3	89	9	ABE41576 L. pneumo
21	209	43.3	95	9	ABE38294 L. pneumo
22	205	42.4	87	5	ABB78148 Amino aci
23	205	42.4	87	5	ABB78147 Amino aci
24	203.5	42.1	92	6	ADA34169 Acinetoba

25	203	42.0	90	5	ABB78165	Abb78165 Amino aci
26	201	41.6	87	5	ABB78177	Abb78177 Amino aci
27	201	41.6	88	5	ABB78171	Abb78171 Amino aci
28	201	41.6	88	5	ABB78172	Abb78172 Amino aci
29	201	41.6	88	5	ABB78173	Abb78173 Amino aci
30	201	41.6	88	6	ABP77219	Abp77219 N. gonorr
31	200	41.4	90	5	ABB78168	Abb78168 Amino aci
32	198	41.0	87	5	ABB78169	Abb78169 Amino aci
33	198	41.0	122	7	ABO74609	AbO74609 Pseudomon
34	197	40.8	87	5	ABB78175	Abb78175 Amino aci
35	196	40.6	88	5	ABB78154	Abb78154 Amino aci
36	195	40.4	86	5	ABB78149	Abb78149 Amino aci
37	192	39.8	87	5	ABB78170	Abb78170 Amino aci
38	191	39.5	87	5	ABB78174	Abb78174 Amino aci
39	183	37.9	76	5	ABB78166	Abb78166 Amino aci
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41	71	14.7	582	8	ADY10873	AdY10873 Plant ful
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43	67	13.9	87	3	AAB54259	Aab54259 Human pan
44	67	13.9	302	4	AAU35741	Aau35741 Helicobac
45	67	13.9	302	7	ABU30804	Abu30804 Protein e
46	67	13.9	305	7	ADM25449	Adm25449 Hyperther
47	66	13.7	379	4	AAV97562	Aay97562 Mouse Wnt
48	66	13.7	379	6	ABG71361	Abg71361 Mouse Wnt
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50	66	13.7	379	7	ADD90566	Add90566 Mouse WIF
51	66	13.7	379	7	ADD90583	Add90583 WIF domai
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59	63	13.0	305	7	ADM25966	Adm25966 Hyperther
60	63	13.0	544	3	AAG40947	Aag40947 Zea may
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63	62.5	12.9	363	7	ADE55261	Ades55261 Rat Prote
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65	62.5	12.9	405	6	AAE32119	Aae32119 Human cyt
66	62.5	12.9	439	6	ABU50419	Abu50419 protein e
67	62	12.8	174	2	AAV34740	Aay34740 Chlamydia
68	62	12.8	409	8	ADT58047	Adt58047 Plant pol
69	62	12.8	435	4	ABG08894	Abg08894 Novel hum
70	62	12.8	533	2	AAR39705	Aar39705 Chicken p
71	62	12.8	646	3	AAV57307	Aay57307 P. aerugi
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73	62	12.8	667	3	ADN73801	Adn73801 Thale cre
74	62	12.8	670	8	AAV57314	Aay57314 P. aerugi
75	62	12.8	686	7	ABO80650	AbO80650 Pseudomon

ALIGNMENTS

RESULT 1	ABB78167	standard; protein; 90 AA.
ID	ABB78167;	
AC	ABB78167;	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Xylella fastidiosa.	
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 61	

FT /note= "not specified"
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 90 AA;
SQ
Query Match 97.8%; Score 472.5; DB 5; Length 90;
Best Local Similarity 98.9%; Pred. No. 5.7e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MORIIFCEYEQRDTGGLDFVYPYGBELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60
Db 1 MORIIFCEYEQRDTGGLDFVYPYGBELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60
QY 61 -SHRAFLBEBLNKFLFERRVAKPEGYIEPD 89
Db 61 XSHRAFLBEBLNKFLFERRVAKPEGYIEPD 90
RESULT 2
ABB78153
ID ABB78153 standard; protein; 87 AA.
XX
XX ABB78153;
AC
XX
XX 05-NOV-2002 (first entry)
DT
XX
XX Amino acid sequence of a YggX homologue.
DE
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
XX US2002072118-A1.
PN
XX
XX 13-JUN-2002.
PD
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA

PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX Sequence 87 AA;
SQ
Query Match 50.9%; Score 246; DB 5; Length 87;
Best Local Similarity 51.2%; Pred. No. 4.1e-22;
Matches 44; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY 1 MORIIFCEYEQRDTGGLDFVYPYGBELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60
Db 1 MARWVCEYLKKEAGLDLQLYPGELGKRIFNSISKQAWAEWIKQTMVLVNEKLANMNP 60
QY 61 SHRAFLBEBLNKFLFERRVAKPEGYI 86
Db 61 EHRQLLEAEWVNFLEFGKDVHIDGYV 86
RESULT 3
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
XX ABO65445;
AC
XX
XX 29-JUL-2004 (first entry)
DT
XX
XX *Klebsiella pneumoniae* polypeptide seqid 11962.
DE
XX
XX Recombinant expression vector; transcription regulatory element;
KW *Klebsiella pneumoniae* protein; antibacterial; Vaccine.
XX
XX *Klebsiella pneumoniae*.
OS
XX
XX US6610836-B1.
PN
XX
XX 26-AUG-2003.
PD
XX
XX 27-JAN-2000; 2000US-00489039.
PF
XX
XX 29-JAN-1999; 99US-0117747P.
PR
XX
XX (GENO-) GENOME THERAPEUTICS CORP.
PA
XX
XX Breton GL, Osborne M;
PI
XX
XX WPI; 2003-895346/82.
DR
XX
XX N-PSDB; ACH98996.
DR
XX
XX New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
PT preparing a vaccine composition against *Klebsiella pneumoniae*.
PT
XX
XX Disclosure; SEQ ID NO 11962; 932pp; English.
XX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.9971 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-45

Perfect score: 483

Sequence: 1 MORIFCEYEQRTBGIDFV.....LNKFLFERRVAKPEGYTEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	100.0	105	2	C82624	conserved hypothet
2	243	50.3	90	2	C64013	hypothetical prote
3	232	48.0	91	2	AH0879	conserved hypothet
4	228	47.2	90	2	C82320	conserved hypothet
5	226	46.8	91	2	A85954	hypothetical prote
6	226	46.8	91	2	A65082	hypothetical prote
7	226	46.8	91	2	F91108	hypothetical prote
8	203	42.0	90	2	AI0116	conserved hypothet
9	201	41.6	88	2	H81014	conserved hypothet
10	198	41.0	90	2	H83003	conserved hypothet
11	185	38.3	93	2	B84994	hypothetical prote
12	67.5	14.0	272	2	H87075	probable conserved
13	67	13.9	302	2	B64584	GTP-binding protei
14	63.5	13.1	587	2	S23312	retrovirus-related
15	63.5	13.1	1131	2	T14517	hypothetical prote
16	63	13.0	105	2	E75442	conserved hypothet
17	63	13.0	415	2	S55617	hypothetical prote
18	62.5	12.9	219	2	C96510	hypothetical prote
19	62.5	12.9	439	2	AC0491	xylose isomerase (
20	62	12.8	188	2	C86508	hypothetical prote
21	62	12.8	188	2	H72114	transcription regu
22	62	12.8	305	1	OWPSAA	ornithine carbamoy
23	62	12.8	526	2	S26420	protein-tyrosine k
24	62	12.8	533	1	TVCHS	conserved hypothet
25	62	12.8	670	2	C83540	probable finger pr
26	62	12.8	863	2	S38140	hypothetical prote
27	61.5	12.7	359	2	C84983	hypothetical prote
28	61.5	12.7	445	2	T01591	hypothetical prote
29	61.5	12.7	494	2	S23315	hypothetical prote

30	61.5	12.7	729	2	G97169	protein containing
31	61.5	12.7	869	1	A47257	1-phosphatidylinos
32	61	12.6	143	2	I47053	relaxin B,C and A
33	61	12.6	301	2	G71929	GTP-binding protei
34	61	12.6	332	2	B47017	transcription init
35	61	12.6	332	2	AD2541	Wnt inhibitory fac
36	61	12.6	379	2	A59180	xylose isomerase (
37	60.5	12.5	440	2	AC0980	plexin 1 precursor
38	60.5	12.5	1894	2	JC4980	3-ketoacyl-acyl ca
39	60	12.4	243	2	AF1611	hypothetical prote
40	60	12.4	318	2	C83555	conserved hypothet
41	60	12.4	360	1	F64601	probable endopepti
42	60	12.4	878	2	G71371	alpha-actinin 3 -
43	60	12.4	901	1	FAHUA3	hypothetical prote
44	60	12.4	984	2	T48216	hypothetical prote
45	59.5	12.3	761	2	AC0791	ribonucleoside-dip
46	59.5	12.3	761	2	S32629	glutamate receptor
47	59.5	12.3	997	2	S33754	hypothetical prote
48	59.5	12.3	1017	2	T08553	conserved hypothet
49	59	12.2	231	2	AE0725	hypothetical prote
50	59	12.2	231	2	AF3028	hypothetical prote
51	59	12.2	231	2	E98256	conserved hypothet
52	59	12.2	283	2	D72398	DNA polymerase, ba
53	59	12.2	290	2	AC3417	hypothetical prote
54	59	12.2	360	2	E71910	glutamate-tRNA lig
55	59	12.2	486	2	F98106	conserved hypothet
56	59	12.2	496	2	D83614	surfactin syntheta
57	59	12.2	3587	2	I40486	probable gastrin p
58	58.5	12.1	127	2	B72593	hypothetical prote
59	58.5	12.1	231	2	AF1838	hypothetical prote
60	58.5	12.1	323	2	H71481	cyclin-dependent k
61	58.5	12.1	496	2	JC5110	hypothetical prote
62	58.5	12.1	1327	2	T21268	hypothetical 21.6k
63	58	12.0	194	2	I39526	hypothetical prote
64	58	12.0	247	2	T27205	hypothetical prote
65	58	12.0	251	2	E90428	hypothetical prote
66	58	12.0	457	2	F64095	argininosuccinate
67	58	12.0	526	1	TVFVR	protein-tyrosine k
68	58	12.0	526	2	S15582	chemotactic transd
69	58	12.0	632	2	H83106	hyaluronidase [imp
70	58	12.0	1066	2	B95037	hyaluronate lyase
71	58	12.0	1078	2	F97907	hypothetical prote
72	58	12.0	1107	2	T21280	gramicidin S synth
73	58	12.0	4450	2	JX0340	gramicidin S synth
74	58	12.0	4452	2	YGBSG2	probable citra prot
75	57.5	11.9	373	2	F70781	

ALIGNMENTS

RESULT 1
C82624
conserved hypothetical protein XF1908 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82624
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: AB2515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-105 <SIM>
A/Cross-references: UNIPARC:UPI00000C288F; GB:AE004010; GB:AE003849; NID:g9106992; PIDN:
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Rehnach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincant, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 / Search time 67.2615 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502A-45
Perfect score: 483
Sequence: 1 MQRIFCEYEQRDTEGLDFV.....LNKFLFERRVAKPEGYIEPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	100.0	90	1	FETP_XYLFA	Q9PC73 xylella fas
2	465	96.3	90	1	FETP_XYLFT	Q87D06 xylella fas
3	380	78.7	92	1	FETP_XANCP	Q8P829 xanthomonas
4	380	78.7	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
5	367	76.0	91	1	FETP_XANAC	Q8PJH7 xanthomonas
6	367	76.0	92	1	FETP_XANOR	Q5GY22 xanthomonas
7	247	51.1	90	1	FETP_IDILO	Q5GY58 idiominas
8	246	50.9	94	1	FETP_HAEDU	Q7VKB6 haemophilus
9	244	50.5	90	1	FETP_PHOLL	Q7N711 photorhabdu
10	243	50.3	90	1	FETP_HABIN	P44048 haemophilus
11	243	50.3	90	1	FETP_PASMU	Q9C1B9 pasteurilla
12	243	50.3	90	2	Q4QMD9_HABIB	Q4QMD9 haemophilus
13	236	48.9	91	1	FETP_MANSM	Q65VC7 mannheimia
14	228	47.2	90	1	FETP_VIBCH	Q9KUR4 vibrio chol
15	227	47.0	90	1	FETP_SALCH	Q57K04 salmonella
16	227	47.0	90	1	FETP_SALPA	Q5PMN1 salmonella
17	227	47.0	90	1	FETP_SALTI	P67617 salmonella
18	227	47.0	90	1	FETP_SALTY	Q6D819 erwinia car
19	225	46.6	90	1	FETP_ERWCT	Q87115 vibrio para
20	222	46.0	90	1	FETP_VIBPA	Q8A8P4 escherichia
21	221	45.8	90	1	FETP_BCO57	P0A8P3 escherichia
22	221	45.8	90	1	FETP_BCOI1	P0A8P5 shigella fl
23	221	45.8	90	1	FETP_SHIFL	Q6LHK7 photobacter
24	219	45.3	90	1	FETP_PHOPR	Q8FE19 escherichia
25	217	44.9	90	1	FETP_ECOL6	Q8DCS5 vibrio vuln
26	217	44.9	90	1	FETP_VIBVU	Q7MHI4 vibrio vuln
27	217	44.9	90	1	FETP_VIBVU	Q83D06 coxiella bu
28	214	43.9	90	1	FETP_COXBU	Q8Y010 ralstonia s
29	212	43.7	90	1	FETP_RALSO	Q7W06 bordetella
30	211	43.7	90	1	FETP_BORBR	Q7W3Q2 bordetella
31	211	43.7	90	1	FETP_BORPA	

32	211	43.7	90	1	FETP_BORPE	Q7WVC4 bordetella
33	211	43.7	90	1	FETP_YERPS	Q66M3 yersinia ps
34	209	43.3	89	1	FETP_LEGPA	Q5X3X9 legionella
35	209	43.3	89	1	FETP_LEGPH	Q5ZU80 legionella
36	209	43.3	90	1	FETP_VIBP1	Q5E7C0 vibrio fisc
37	208	43.1	89	1	FETP_LEGPL	Q5WVC4 legionella
38	207	42.9	90	1	FETP_METCA	Q60AJ7 methylococc
39	206	42.7	87	1	FETP_FRATY	Q5NHJ8 francisella
40	204.5	42.3	90	1	FETP_AC1AD	Q6FIB3 acinetobact
41	204	42.2	90	1	FETP_PSEPK	Q88R49 pseudomonas
42	203	42.0	90	1	FETP_YERPE	Q8ZHE7 yersinia pe
43	203	42.0	91	1	FETP_BURMA	Q62IUS burkholderi
44	203	42.0	91	1	FETP_BURPS	Q63SJ4 burkholderi
45	203	42.0	91	2	Q4LS19_9BURK	Q41819 burkholderi
46	201	41.6	88	1	FETP_NEIG1	Q5F553 neisseria g
47	201	41.6	88	1	FETP_NEIMA	P67615 neisseria m
48	201	41.6	88	1	FETP_NEIMB	P67616 neisseria m
49	200	41.4	90	1	FETP_CHRVO	Q7NSR4 chromobacte
50	200	41.4	90	1	FETP_NITBU	Q82XF2 nitrosomona
51	200	41.4	90	1	FETP_PSESM	Q87UF5 pseudomonas
52	200	41.4	90	2	Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
53	198	41.0	90	1	FETP_PSEAB	Q9HU36 pseudomonas
54	197	40.8	90	2	Q4J228_AZOVI	Q4J228 azotobacter
55	196	40.6	92	1	FETP_SHEON	Q8BXK6 shewanella
56	194	40.2	90	2	Q4KJT2_PSEF5	Q4KJT2 pseudomonas
57	191	39.5	78	1	FETP_BUCAP	Q8K925 buchnera ap
58	190	39.3	90	2	Q6T7F6_PSEPL	Q6T7F6 pseudomonas
59	185	38.3	77	1	FETP_BUCAT	P57618 buchnera ap
60	180	37.3	78	1	FETP_WIGBR	Q8D3C5 wiggleswort
61	172	35.6	87	1	FETP_BUCBP	Q89A44 buchnera ap
62	168	34.8	92	2	Q4NWQ4_9DELT	Q4NWQ4 anaeromyxob
63	156	32.3	79	1	FETP_CANBF	Q4FWG9 candidatus
64	154	31.9	96	2	Q4FVU7_9GAMM	Q4FVJ7 psychrobact
65	91.5	18.9	123	2	Q81221_BACCR	Q81221 bacillus ce
66	75.5	15.6	635	2	Q6YBY0_TOXGO	Q6YBY0 toxoplasma
67	74.5	15.4	402	2	Q7NVX6_CHRVO	Q7NVX6 chromobacte
68	73	15.1	174	2	Q68658_HELPY	Q68658 helicobacte
69	70.5	14.6	468	2	Q7UPU4_RHOBA	Q7UPU4 rhodopirell
70	70.5	14.6	764	2	Q8LMT3_ORYSA	Q8LMT3 oryza sativ
71	69.5	14.4	217	2	Q9DQ04_AHSV7	Q9DQ04 african hor
72	68.5	14.2	129	2	Q6BJ04_DEBHA	Q6BJ04 debaryomyce
73	68.5	14.2	1065	2	Q9FJL6_ARATH	Q9FJL6 arabidopsis
74	68	14.1	5141	2	Q7S6D3_NEUCR	Q7S6D3 neurospora
75	67.5	14.0	272	2	Q9ZBD7_MYCLE	Q9ZBD7 mycobacteri

ALIGNMENTS

RESULT 1
FETP_XYLFA
ID FETP_XYLFA STANDARD; PRT; 90 AA.
AC Q9PC73;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=XF1908;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.B., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Britones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrier H.,
RA Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto B., Docena C., El-Dorri H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

```
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitchajima J.P.,
RA Krieger J.B., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.B.S.,
RA Nhani A. Jr., Nobrega P.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terezzi M.F., Truffi D., Tsai S.M., Tsubako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen Xylella fastidiosa.";
RL Nature 406:151-159(2000).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE004010; AAF84714.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 1055 MW; E9BEB3BCA6D104A3 CRC64;

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Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MQRIFCEYEQDTEGLDFVYPYPGELGQKIFACIGKVGAAMLVHQTMLINENRLSPRNP 60

QY 61 SHRAFLBEEINKFLFERRVAKPEGYIEPD 89
Db 61 SHRAFLBEEINKFLFERRVAKPEGYIEPD 89

RESULT 2
FETP_XYLFT STANDARD; PRT; 90 AA.
ID FETP_XYLFT
AC Q87D06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=PD0883;
OS Xylella fastidiosa (strain Temecula / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,
```

```
RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorri H., Tsai S.M.,
RA Carrer H., Carreiro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Harakava R., Kuramae E.B.,
RA Marino C.L., Gaglioti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Cannavan F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Tsukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitchajima J.P.;
RT "Comparative analyses of the complete genome sequences of Pierce's
RT disease and citrus variegated chlorosis strains of Xylella
RT fastidiosa.";
RL J. Bacteriol. 185:1018-1026(2003).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE012556; AA028748.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10430 MW; B5C6936496F4171D CRC64;

Query Match 96.3%; Score 465; DB 1; Length 90;
Best Local Similarity 95.5%; Pred. No. 1.9e-45;
Matches 85; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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QY 61 SHRAFLBEEINKFLFERRVAKPEGYIEPD 89
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RESULT 3
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ID FETP_XANCP
AC Q8P829;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=XCC2419;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.B.A., Camarotte G., Cannavan F., Cardozo J., Chambergo F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorri H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.F., Lemos E.G.M., Lemos M.V.F.,
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:30:02 ; Search time 19.6925 Seconds
(without alignments)
373.651 Million cell updates/sec

Title: US-09-955-502A-45
Perfect score: 483
Sequence: 1 MQRIFCEYEQDTEGLDFV.....LNKFLFRRVAKPEGYTEPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	49.3	107	2	US-09-489-039A-11962
2	227	47.0	93	2	US-09-543-681A-5443
3	203.5	42.1	92	2	US-09-328-352-5456
4	198	41.0	122	2	US-09-252-991A-23355
5	150	31.1	110	2	US-09-540-236-2859
6	62	12.8	174	2	US-09-198-452A-158
7	62	12.8	198	2	US-09-438-185A-141
8	62	12.8	645	2	US-09-328-501-1
9	62	12.8	646	2	US-09-777-710A-1
10	62	12.8	646	5	US-10-191-289A-1
11	62	12.8	670	2	US-09-328-501-15
12	62	12.8	670	2	US-09-777-710A-15
13	62	12.8	670	5	US-10-191-289A-15
14	62	12.8	686	2	US-09-252-991A-29396
15	61	12.6	333	2	US-09-107-532A-4544
16	61	12.6	461	2	US-09-107-433-2847
17	60.5	12.5	251	2	US-09-489-039A-7987
18	60	12.4	286	2	US-09-543-681A-5269
19	59.5	12.3	626	2	US-09-248-796A-27023
20	59.5	12.3	770	2	US-09-543-681A-4291
21	59	12.2	170	2	US-09-489-039A-7536
22	59	12.2	295	2	US-08-952-089A-1
23	59	12.2	295	2	US-09-690-885-1
24	59	12.2	320	2	US-09-248-796A-15469
25	59	12.2	348	1	US-08-844-153-2
26	59	12.2	480	1	US-08-962-203-2
27	59	12.2	480	2	US-09-282-125A-2

28	59	12.2	480	2	US-09-273-142-2	Sequence 2, Appli
29	58.5	12.1	185	2	US-09-270-767-36317	Sequence 36317, A
30	58.5	12.1	185	2	US-09-270-767-51534	Sequence 51534, A
31	58.5	12.1	496	2	US-09-695-795A-8	Sequence 8, Appli
32	58.5	12.1	771	1	US-08-742-753-2	Sequence 2, Appli
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34	58	12.0	640	2	US-09-252-991A-23252	Sequence 23252, A
35	58	12.0	776	2	US-09-284-180A-3	Sequence 3, Appli
36	58	12.0	2353	2	US-08-984-709A-50	Sequence 50, Appli
37	57.5	11.9	278	1	US-08-258-261B-20	Sequence 20, Appli
38	57.5	11.9	278	1	US-08-456-837-20	Sequence 20, Appli
39	57.5	11.9	278	1	US-08-457-342-20	Sequence 20, Appli
40	57.5	11.9	278	1	US-08-457-646A-20	Sequence 20, Appli
41	57.5	11.9	278	1	US-08-458-076A-20	Sequence 20, Appli
42	57.5	11.9	278	1	US-08-457-335A-20	Sequence 20, Appli
43	57.5	11.9	278	1	US-08-729-214-20	Sequence 20, Appli
44	57.5	11.9	278	2	US-09-028-934-20	Sequence 20, Appli
45	57.5	11.9	647	2	US-09-252-991A-32816	Sequence 32816, A
46	57	11.8	184	2	US-09-270-767-46275	Sequence 46275, A
47	57	11.8	293	2	US-09-071-035-496	Sequence 496, App
48	57	11.8	293	2	US-09-206-576-496	Sequence 496, App
49	57	11.8	316	2	US-09-071-035-494	Sequence 494, App
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51	57	11.8	371	2	US-09-543-681A-6429	Sequence 6429, Ap
52	57	11.8	379	2	US-09-907-794A-4	Sequence 4, Appli
53	57	11.8	379	2	US-09-905-125A-4	Sequence 4, Appli
54	57	11.8	379	2	US-09-905-646-4	Sequence 4, Appli
55	57	11.8	379	2	US-09-902-775A-4	Sequence 4, Appli
56	57	11.8	379	2	US-09-906-700-4	Sequence 4, Appli
57	57	11.8	379	2	US-09-903-603A-4	Sequence 4, Appli
58	57	11.8	379	2	US-09-904-920A-4	Sequence 4, Appli
59	57	11.8	379	2	US-09-909-064-4	Sequence 4, Appli
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61	57	11.8	379	2	US-09-906-618-4	Sequence 4, Appli
62	57	11.8	379	2	US-09-906-646-4	Sequence 4, Appli
63	57	11.8	379	2	US-09-904-462-4	Sequence 4, Appli
64	57	11.8	379	2	US-09-902-736A-4	Sequence 4, Appli
65	57	11.8	379	2	US-09-906-722A-4	Sequence 4, Appli
66	57	11.8	380	2	US-09-205-258-441	Sequence 441, App
67	57	11.8	380	2	US-10-004-860-441	Sequence 441, App
68	57	11.8	484	2	US-08-913-578-2	Sequence 2, Appli
69	56.5	11.7	321	2	US-08-785-427-2	Sequence 2, Appli
70	56.5	11.7	357	2	US-09-107-532A-4975	Sequence 4975, Ap
71	56.5	11.7	394	2	US-09-489-039A-13955	Sequence 13955, A
72	56.5	11.7	394	1	US-08-646-590B-40	Sequence 40, Appli
73	56.5	11.7	527	1	US-08-365-486A-26	Sequence 26, Appli
74	56.5	11.7	527	2	US-08-880-342-26	Sequence 26, Appli
75	56.5	11.7	1206	2	US-09-252-991A-19632	Sequence 19632, A

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIORITY FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIORITY FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 49.3%; Score 238; DB 2; Length 107;
Best Local Similarity 51.7%; Pred. No. 1e-23;
Matches 46; Conservative 12; Mismatches 31; Indels 0; Gaps 0;

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DB 17 MSRTIFCTFLQREADGQDFQLYPGELGKRITVNEISKEAWQWQHKTMLINEKLSMMP 76

OY 61 SHRAFLBEELNKFLFERRVAKPEGYIEPD 89
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DB 77 EHRKLEQEMVQFLFEGKDVHIEGYTPPE 105

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETTON

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 47.0%; Score 227; DB 2; Length 93;
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Matches 42; Conservative 14; Mismatches 33; Indels 0; Gaps 0;

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DB 4 MSRTIFCTFLNKREADGLDQLYPGELGKRITVNEISKEAWQWQHKTMLINEKLSMMP 63

OY 61 SHRAFLBEELNKFLFERRVAKPEGYIEPD 89
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DB 64 DDRKLEQEMVQFLFEGKDVHIDGYTPPE 92

RESULT 3
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNIT FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 42.1%; Score 203.5; DB 2; Length 92;
Best Local Similarity 46.5%; Pred. No. 3.2e-19;
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OY 61 SHRAFLBEELNKFL-FERRVAKPEGY 85

DB 64 EAKKFLBEQREKFFNNDSEVEKAEGW 89
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RESULT 4
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity 42.0%; Pred. No. 2.5e-18;
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DB 33 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQHQTMLINERLNMMA 92

OY 61 SHRAFLBEELNKFLFERRVAKPEGYIEP 88
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DB 93 EDRKFLQEMDKFLSGEDYAKADGYVPP 120

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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DB 24 MVFCRKYYQNLPLXLPNPPFNPAKQGEIQTISAKAWNAWLELQTMLINEKLSMIDPOAK 83

OY 64 AFLBEELNKFLFERRVAKPEGY 85
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DB 84 KYLINEQREKFLDNGDYKPAKY 105

RESULT 6
US-09-198-452A-158
; Sequence 158, Application US/09198452A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:44:45 ; Search time 57.7989 Seconds
(without alignments)
643.383 Million cell updates/sec

Title: US-09-955-502A-45
Perfect score: 483
Sequence: 1 MORLFCFEYERDTEGLDFV.....LNKPLFRRVAKPEGYTEPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	237	49.1	87	3	US-09-955-502-7
5	234	48.4	91	3	US-09-955-502-5
6	232	48.0	91	3	US-09-955-502-14
7	232	48.0	91	3	US-09-955-502-16
8	232	48.0	91	3	US-09-955-502-17
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11	228	47.2	90	3	US-09-955-502-10
12	226	46.8	91	3	US-09-955-502-11
13	226	46.8	91	3	US-09-955-502-12
14	226	46.8	91	3	US-09-955-502-13
15	220	45.5	78	3	US-09-955-502-19
16	215	44.5	87	3	US-09-955-502-31
17	214	44.3	88	3	US-09-955-502-33
18	205	42.4	87	3	US-09-955-502-2
19	205	42.4	87	3	US-09-955-502-3
20	203	42.0	90	3	US-09-955-502-20
21	201	41.6	87	3	US-09-955-502-32
22	201	41.6	88	3	US-09-955-502-26
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24	201	41.6	88	3	US-09-955-502-28
25	200	41.4	90	3	US-09-955-502-23
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27	197	40.8	87	3	US-09-955-502-29

28	197	40.8	87	3	US-09-955-502-30	Sequence 30, Appl
29	196	40.6	88	3	US-09-955-502-9	Sequence 9, Appli
30	195	40.4	86	3	US-09-955-502-4	Sequence 4, Appli
31	192	39.8	87	3	US-09-955-502-25	Sequence 25, Appl
32	183	37.9	76	3	US-09-955-502-21	Sequence 21, Appl
33	71	14.7	580	4	US-10-425-115-224020	Sequence 224020,
34	71	14.7	582	4	US-10-425-114-66688	Sequence 66688, A
35	70.5	14.6	764	4	US-10-437-963-104787	Sequence 104787,
36	67.5	14.0	272	4	US-10-080-170-163	Sequence 163, App
37	67.5	14.0	272	4	US-10-080-170-163	Sequence 163, App
38	67.5	14.0	272	4	US-10-468-356-163	Sequence 163, App
39	67	13.9	87	3	US-09-925-297-711	Sequence 711, App
40	67	13.9	115	4	US-10-425-115-337472	Sequence 337472,
41	67	13.9	302	3	US-09-815-242-11334	Sequence 11334, A
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45	66	13.7	379	5	US-10-745-110-2	Sequence 2, Appli
46	66	13.7	379	5	US-10-507-343-2	Sequence 2, Appli
47	66	13.7	379	5	US-10-507-343-15	Sequence 15, Appl
48	66	13.7	379	5	US-10-507-343-17	Sequence 17, Appl
49	66	13.7	379	5	US-10-507-343-19	Sequence 19, Appl
50	66	13.7	379	5	US-10-507-343-21	Sequence 21, Appl
51	66	13.7	593	4	US-10-424-599-213920	Sequence 213920,
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54	64.5	13.4	73	4	US-10-424-599-262025	Sequence 262025,
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56	64.5	13.4	327	3	US-09-727-892-81	Sequence 81, Appl
57	64	13.3	112	4	US-10-437-963-131206	Sequence 131206,
58	64	13.3	365	5	US-10-507-343-6	Sequence 6, Appli
59	64	13.3	658	4	US-10-156-761-14350	Sequence 14350, A
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63	63.5	13.1	288	4	US-10-437-963-163689	Sequence 163689,
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66	62.5	12.9	314	4	US-10-282-122A-72800	Sequence 72800, A
67	62.5	12.9	375	5	US-10-732-923-11589	Sequence 11589, A
68	62.5	12.9	389	4	US-10-108-260A-3014	Sequence 3014, Ap
69	62.5	12.9	405	4	US-10-473-574-17	Sequence 17, Appl
70	62.5	12.9	439	4	US-10-282-122A-78343	Sequence 78343, A
71	62	12.8	174	4	US-10-289-762-158	Sequence 158, App
72	62	12.8	409	5	US-10-739-930-8124	Sequence 8124, Ap
73	62	12.8	435	5	US-10-450-763-39253	Sequence 39253, A
74	62	12.8	453	5	US-10-732-923-13651	Sequence 13651, A
75	62	12.8	478	4	US-10-424-599-260720	Sequence 260720,

ALIGNMENTS

RESULT 1
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; Sequence 22, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Xylella fastidiosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502A-45
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	201	41.6	88	6	US-10-467-657-968 Sequence 968, Appl
2	66	13.7	379	7	US-11-136-619-22 Sequence 22, Appl
3	64	13.3	379	7	US-11-136-619-23 Sequence 23, Appl
4	61	12.6	335	7	US-11-136-619-30 Sequence 30, Appl
5	61	12.6	379	7	US-11-136-619-2 Sequence 2, Appl
6	58	12.0	351	7	US-11-136-619-14 Sequence 14, Appl
7	58	12.0	776	6	US-10-925-970-3 Sequence 3, Appl
8	57	11.8	378	7	US-11-129-143-49 Sequence 49, Appl
9	57	11.8	379	6	US-10-131-826A-308 Sequence 308, Appl
10	56	11.6	372	7	US-11-143-980-37 Sequence 37, Appl
11	56	11.6	533	7	US-11-230-995-3 Sequence 3, Appl
12	56	11.6	536	6	US-10-821-231C-1 Sequence 1, Appl
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14	55.5	11.5	430	7	US-11-126-313-36 Sequence 36, Appl
15	55.5	11.5	496	6	US-10-770-726-72 Sequence 72, Appl
16	55.5	11.5	2080	7	US-11-124-367A-364 Sequence 364, Appl
17	55.5	11.5	2542	7	US-11-124-367A-363 Sequence 363, Appl
18	55	11.4	774	7	US-11-242-730-7 Sequence 7, Appl
19	54.5	11.3	124	7	US-11-072-512-3487 Sequence 3487, Appl
20	54.5	11.3	636	6	US-10-516-587-2 Sequence 12, Appl
21	54	11.2	205	7	US-11-054-281-12 Sequence 70, Appl
22	54	11.2	364	7	US-11-054-281-70 Sequence 68, Appl
23	54	11.2	374	7	US-11-054-281-68 Sequence 66, Appl
24	54	11.2	394	7	US-11-054-281-66 Sequence 67, Appl
25	54	11.2	394	7	US-11-054-281-67 Sequence 67, Appl

26	54	11.2	418	7	US-11-244-219-2	Sequence 2, Appl
27	54	11.2	1225	7	US-11-102-476-2	Sequence 2, Appl
28	54	11.2	1424	7	US-11-102-476-4	Sequence 4, Appl
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31	53.5	11.1	774	7	US-11-242-730-6	Sequence 6, Appl
32	53.5	11.1	787	7	US-11-154-227-110	Sequence 110, Appl
33	53.5	11.1	2504	6	US-10-647-956A-8	Sequence 8, Appl
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36	53	11.0	1207	6	US-10-755-092-7	Sequence 7, Appl
37	52.5	10.9	148	7	US-11-072-512-3547	Sequence 3547, Ap
38	52.5	10.9	200	7	US-11-176-830-710	Sequence 710, App
39	52.5	10.9	296	6	US-10-467-657-3198	Sequence 3198, Ap
40	52.5	10.9	498	6	US-10-510-947-9	Sequence 9, Appl
41	52.5	10.9	528	6	US-10-511-538-255	Sequence 255, App
42	52.5	10.9	685	7	US-11-098-686-10574	Sequence 10574, A
43	52	10.8	181	7	US-11-000-463-890	Sequence 890, App
44	52	10.8	182	7	US-11-000-463-418	Sequence 418, App
45	52	10.8	235	7	US-11-098-686-11270	Sequence 11270, A
46	52	10.8	271	6	US-10-857-780-19	Sequence 19, Appl
47	52	10.8	271	6	US-11-107-028-25	Sequence 25, Appl
48	52	10.8	309	6	US-10-873-528-156	Sequence 156, App
49	52	10.8	486	6	US-10-821-234-1063	Sequence 1063, Ap
50	52	10.8	516	7	US-11-080-991-2	Sequence 2, Appl
51	52	10.8	575	7	US-11-072-512-3622	Sequence 3622, Ap
52	51.5	10.7	417	7	US-11-098-686-10533	Sequence 10533, A
53	51.5	10.7	844	7	US-11-097-463-4	Sequence 4, Appl
54	51.5	10.7	1508	7	US-11-043-889-47	Sequence 47, Appl
55	51	10.6	245	7	US-11-072-512-2600	Sequence 2600, Ap
56	51	10.6	474	6	US-10-986-501-249	Sequence 249, App
57	51	10.6	496	7	US-11-069-642-20	Sequence 20, Appl
58	51	10.6	818	7	US-11-144-985-13	Sequence 13, Appl
59	51	10.6	1020	7	US-11-144-985-3	Sequence 3, Appl
60	51	10.6	1340	7	US-11-070-575-6	Sequence 6, Appl
61	51	10.6	1344	7	US-11-169-041-193	Sequence 20, Appl
62	51	10.6	1822	7	US-11-169-041-193	Sequence 193, App
63	51	10.6	5712	7	US-11-143-980-47	Sequence 47, Appl
64	50.5	10.5	200	7	US-11-176-830-722	Sequence 722, App
65	50.5	10.5	290	6	US-10-793-626-1892	Sequence 1892, Ap
66	50.5	10.5	303	6	US-10-793-626-1140	Sequence 1140, Ap
67	50.5	10.5	304	6	US-10-055-877-173	Sequence 173, App
68	50.5	10.5	359	6	US-10-793-626-2742	Sequence 2742, Ap
69	50.5	10.5	525	6	US-10-763-712A-108	Sequence 108, App
70	50.5	10.5	554	6	US-10-467-657-8240	Sequence 8240, Ap
71	50	10.4	193	6	US-10-467-657-2700	Sequence 2700, Ap
72	50	10.4	200	7	US-11-176-830-726	Sequence 726, App
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ALIGNMENTS

RESULT 1
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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.76888 Seconds
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280.957 Million cell updates/sec

Title: US-09-955-502A-37

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

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Post-processing: Minimum Match 0%

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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	62.5	13.2	259	US-11-179-977-21	Sequence 21, Appl
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6	62	13.1	593	US-11-194-246-317	Sequence 317, App
7	61	12.9	922	US-11-072-512-2694	Sequence 2694, Ap
8	61	12.9	1614	US-10-821-234-903	Sequence 903, App
9	60.5	12.8	548	US-10-467-657-7704	Sequence 7704, Ap
10	60	12.7	571	US-11-072-512-3814	Sequence 3814, Ap
11	58.5	12.4	1432	US-10-510-386-218	Sequence 218, Appl
12	57.5	12.2	980	US-11-052-554A-17	Sequence 17, Appl
13	57	12.1	646	US-10-491-096-190	Sequence 190, App
14	57	12.1	1504	US-11-019-711-98	Sequence 98, Appl
15	56.5	11.9	136	US-10-485-517-261	Sequence 261, Appl
16	56.5	11.9	506	US-11-099-691-5	Sequence 5, Appli
17	56.5	11.9	563	US-11-072-512-3625	Sequence 3625, Ap
18	56.5	11.9	893	US-11-072-512-3504	Sequence 3504, Ap
19	56.5	11.9	1976	US-11-069-834-52	Sequence 52, Appl
20	56.5	11.9	1976	US-11-069-834-54	Sequence 54, Appl
21	56	11.8	1678	US-11-124-367A-340	Sequence 340, Appl
22	56	11.8	1678	US-11-124-367A-341	Sequence 341, Appl
23	55.5	11.7	305	US-11-156-084-178	Sequence 178, App
24	55.5	11.7	381	US-11-072-512-3313	Sequence 3313, Ap
25	55.5	11.7	401	US-10-131-826A-486	Sequence 486, App

26	55	11.6	109	US-11-049-536-504	Sequence 504, App
27	55	11.6	189	US-11-071-262-1	Sequence 1, Appli
28	55	11.6	251	US-11-054-515-1496	Sequence 1496, Ap
29	55	11.6	253	US-11-054-515-1249	Sequence 1249, Ap
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33	54.5	11.5	124	US-11-072-512-2018	Sequence 2018, Ap
34	54.5	11.5	210	US-10-467-657-6318	Sequence 6318, Ap
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36	54.5	11.5	577	US-11-072-175-187	Sequence 187, App
37	54.5	11.5	601	US-10-944-272-3	Sequence 3, Appli
38	54.5	11.5	601	US-11-096-191-720	Sequence 720, Appl
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58	53	11.2	2335	US-10-821-234-1610	Sequence 1610, App
59	52.5	11.1	264	US-10-821-234-1555	Sequence 1555, Ap
60	52.5	11.1	319	US-10-793-626-2760	Sequence 2760, Ap
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66	52	11.0	384	US-11-219-282-19	Sequence 19, Appl
67	52	11.0	395	US-11-009-658-46	Sequence 46, Appl
68	52	11.0	456	US-11-069-642-8	Sequence 8, Appli
69	52	11.0	497	US-10-454-437-410	Sequence 410, App
70	52	11.0	588	US-11-052-554A-339	Sequence 339, App
71	52	11.0	599	US-11-109-157A-3	Sequence 3, Appli
72	52	11.0	600	US-11-072-512-3845	Sequence 3845, Ap
73	52	11.0	1145	US-10-793-626-1432	Sequence 1432, Ap
74	52	11.0	1613	US-11-108-528-84	Sequence 84, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Total number of hits satisfying chosen parameters: 2443163

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	5	ABB78152 Amino aci
2	435	94.4	87	5	ABB78151 Amino aci
3	434	94.1	91	5	ABB78150 Amino aci
4	425	92.2	87	5	ABB78153 Amino aci
5	387	83.9	91	5	ABB78158 Amino aci
6	387	83.9	91	5	ABB78157 Amino aci
7	387	83.9	91	5	ABB78156 Amino aci
8	386	83.7	90	5	ABB78155 Amino aci
9	385	83.5	88	5	ABB78160 Amino aci
10	385	83.5	91	5	ABB78161 Amino aci
11	385	83.5	91	5	ABB78159 Amino aci
12	385	83.5	91	5	ABB78162 Amino aci
13	378	82.0	91	5	ABB78163 Amino aci
14	372	80.7	107	7	ABO65445 Klebsiell
15	371	80.5	93	7	ADF05158 Bacteri
16	363	78.7	90	5	ABB78165 Amino aci
17	356	77.2	88	5	ABB78154 Amino aci
18	325	70.5	78	5	ABB78164 Amino aci
19	256	55.5	76	5	ABB78166 Amino aci
20	256	55.5	87	5	ABB78148 Amino aci
21	256	55.5	87	5	ABB78147 Amino aci
22	241	52.3	87	5	ABB78175 Amino aci
23	238.5	51.7	86	5	ABB78149 Amino aci
24	236	51.2	87	5	ABB78170 Amino aci

25	236	51.2	122	7	ABO74609 Pseudomon
26	235.5	51.1	89	9	AEB41576 L. pneumo
27	235.5	51.1	95	5	AEB38294 L. pneumo
28	235	51.0	87	5	ABB78174 Amino aci
29	230	49.9	90	5	ABB78168 Amino aci
30	229	49.7	87	5	ABB78169 Amino aci
31	227.5	49.3	90	5	ABB78167 Amino aci
32	227	49.2	88	5	ABB78171 Amino aci
33	227	49.2	88	5	ABB78172 Amino aci
34	227	49.2	88	5	ABB78173 Amino aci
35	227	49.2	88	6	ABP77219 N. gonorr
36	224	48.6	87	5	ABB78177 Amino aci
37	224	48.6	88	5	ABB78178 Amino aci
38	214.5	46.5	92	6	ADA34169 Acinetoba
39	202	43.8	87	5	ABB78176 Amino aci
40	144	31.2	110	8	ADL05173 M. catarr
41	76.5	16.6	591	2	AAV41141 Mouse mam
42	76.5	16.6	860	2	AAV41140 Mouse mam
43	76.5	16.6	1755	2	AAV41139 Mouse mam
44	73	15.8	975	5	ABP66068 Bifidobac
45	73	15.8	1144	3	ADS44344 Bacteri
46	72	15.6	506	3	AAV74371 Neisseria
47	71	15.4	503	4	ABG16577 Novel hum
48	71	15.4	883	8	ADN47233 Thermococ
49	70.5	15.3	723	7	ADB85144 Rat calci
50	70.5	15.3	723	8	AD181552 Rat calci
51	70.5	15.3	723	8	AD181556 Rat calci
52	70.5	15.3	949	6	ABU40639 Protein e
53	70.5	15.3	959	7	ADF06594 Bacteri
54	69.5	15.1	227	3	AAG38052 Arabidops
55	69.5	15.1	593	4	ABG19947 Novel hum
56	69	15.0	484	8	ADM90985 Human pha
57	69	15.0	507	6	ABU40210 Protein e
58	68.5	14.9	218	3	AAG45909 Arabidops
59	68.5	14.9	234	3	AAG45908 Arabidops
60	68	14.8	257	3	AAG31203 Arabidops
61	68	14.8	297	3	AAG31202 Arabidops
62	68	14.8	324	3	AAG31201 Arabidops
63	67.5	14.6	283	8	ADY12704 Plant ful
64	67	14.5	474	7	ABO75727 Pseudomon
65	67	14.5	507	3	AAV74372 Neisseria
66	67	14.5	507	3	AAV74373 Neisseria
67	67	14.5	546	6	ABU38097 Protein e
68	67	14.5	1399	8	ADR75314 Bovine ac
69	67	14.5	1401	4	ADR75290 Bovine ac
70	66.5	14.4	330	4	AAU35726 Helicobac
71	66.5	14.4	330	6	ABU30763 Protein e
72	66.5	14.4	487	8	ADN01595 Enterobac
73	66.5	14.4	730	8	AD181550 Rabbit ep
74	66.5	14.4	765	6	ADA20715 Artichoke
75	66.5	14.4	818	6	ADA20725 Artichoke

ALIGNMENTS

RESULT 1
ABB78152 standard; protein; 87 AA.
XX ABB78152;
AC 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Haemophilus influenzae.
OS
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Ygix protein, a
XX protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Ygix protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Ygix reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent Ygix homologues
XX
SQ Sequence 87 AA;

Query Match	100.0%;	Score 461;	DB 5;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 9.8e-47;		
Matches 87;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy      1 MARTVFC EYLKKEAGELDPQLYPGELGRIFDSVS KKAWEWIKKQTM LVNEKKLNMNA    60
        |||||
Db      1 MARTVFCEY LKKEAGELDPQLYPGELGRIFDSVS KKAWEWIKKQTM LVNEKKLNMNA    60
```

QY 61 EHRKLLLEQEMVNFLEFGKDVIHIEGYVP 87
|||||
Db 61 EHRKLLLEQEMVNFLEFGKDVIHIEGYVP 87

RESULT 2
ABB78151

AC ABB878151;

DT 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

Pasteurella multocida.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

XX

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX
SQ Sequence 87 AA;

SQ Sequence 87 AA;

Query Match	94.4%	Score 435;	DB 5;	length 87;
Best Local Similarity	92.0%	Pred. No. 1.2e-43;		
Matches 80; Conservative	6;	Mismatches 1;	Indels 0;	Gaps 0;

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Qy      1 MARTVFCEYLKKEAEGIDFQLYPGELGKRIFPSVSKOAMGEWIKKQITMLVNEKKLNMNNA 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 MARTVFCEYLKQESSEGLDFQLYPGELGKRIFPSISKQAMREWMKKQITMLVNEKKLNMNNA 60

```

Dy 61 EHKRLLEQEMVNFLFEKGDVHIIEGYR 87
:
Db 61 DHRQLLEQEMVNFLFEKGDVHIIEGYR 87

ID ABB78150 standard; protein; 91 AA.

AC ABB78150;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;

KW hydroxyl radical; DNA damage; yggx homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

PI Downs D, Grahnick JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a

CC native amount of yggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-38

Perfect score: 461
Sequence: 1 MARTVPCBYLKKEAGLDFQ.....QEMVNFLEKGVHIEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	461	100.0	90	2	C64013	hypothetical prote
2	387	83.9	91	2	A85954	hypothetical prote
3	387	83.9	91	2	A65082	hypothetical prote
4	387	83.9	91	2	F91108	hypothetical prote
5	386	83.7	90	2	C82320	conserved hypotet
6	385	83.5	91	2	AH0879	conserved hypotet
7	363	78.7	90	2	AI0116	conserved hypotet
8	256	55.5	93	2	E84994	hypothetical prote
9	237	51.4	105	2	C82624	conserved hypotet
10	236	51.2	90	2	H83003	conserved hypotet
11	227	49.2	88	2	H81014	conserved hypotet
12	76.5	16.6	591	1	FOMVMM	gag polyprotein -
13	73	15.8	1024	2	T41415	probable leucine p
14	72.5	15.7	353	1	FOMVGR	gag polyprotein -
15	68.5	14.9	1206	2	E96507	hypothetical prote
16	68	14.8	324	2	T05429	hypothetical prote
17	68	14.8	555	2	C96667	unknown protein, 7
18	68	14.8	583	2	T48365	hypothetical prote
19	68	14.8	593	2	C64097	probable soluble 1
20	67.5	14.6	1119	2	T18491	hypothetical prote
21	67	14.5	328	2	T28363	ORF MSV202 hypotet
22	67	14.5	485	2	A84043	chromosome replica
23	67	14.5	507	2	A83105	probable fumarate
24	67	14.5	546	2	C81063	fumarate hydratase
25	66.5	14.4	330	1	A81807	fumarate hydratase
26	66.5	14.4	330	1	B64561	ketol-acid reducto
27	66.5	14.4	394	2	B70206	hypothetical prote
28	66.5	14.4	487	1	LQBP34	DNA ligase (ATP) (
29	66	14.3	258	2	S58159	hypothetical prote

30	66	14.3	548	2	A54510	63K antigen - nema
31	65.5	14.2	152	2	B70423	transcription regu
32	65.5	14.2	300	2	F84178	hypothetical prote
33	65.5	14.2	348	2	H70337	conserved hypotet
34	65.5	14.2	723	2	JC7795	epithelial calcium
35	65.5	14.2	1787	2	G97222	hypothetical prote
36	65	14.1	166	2	C95944	probable acetyltra
37	65	14.1	182	2	C69416	hypothetical prote
38	65	14.1	330	2	G91204	hypothetical prote
39	65	14.1	367	2	A86051	hypothetical prote
40	65	14.1	392	2	H90174	hypothetical prote
41	65	14.1	548	2	A28209	probable Fe-S oxid
42	65	14.1	548	2	B97026	hypothetical prote
43	65	14.1	558	2	A85296	hypothetical prote
44	65	14.1	559	2	T05786	isomerase fucil (EC
45	65	14.1	604	2	F64081	shikimate kinase (
46	64.5	14.0	165	2	A81382	GLG1 protein - yea
47	64.5	14.0	480	2	S38134	WD-40 repeat prote
48	64.5	14.0	1526	2	AC2239	spectrin beta-H ch
49	64.5	14.0	1645	2	A37792	repeat organellar
50	64.5	14.0	1939	2	T18372	probable sops prot
51	64	13.9	342	2	T13113	ribosomal protein
52	64	13.9	553	2	G70115	methylenetetrahydr
53	64	13.9	641	2	T38659	glycosyltransferas
54	64	13.9	720	1	JC5131	kinesin-related pr
55	64	13.9	742	1	S58691	hypothetical prote
56	64	13.9	946	2	T31488	tetrahydrodipicoli
57	63.5	13.8	236	2	P69866	hypothetical prote
58	63.5	13.8	996	2	A71080	conserved hypotet
59	63.5	13.8	1008	2	H72310	mucin MUC5B, trach
60	63.5	13.8	1321	2	JE0352	protein C05B4.8 [I
61	63	13.7	225	2	C88939	hypothetical prote
62	63	13.7	241	2	T27636	probable WRKY-type
63	63	13.7	271	2	A84643	gene 2 protein - p
64	63	13.7	274	2	S04610	probable RNA nucle
65	63	13.7	372	2	B81350	hypothetical prote
66	63	13.7	501	2	A84784	hypothetical prote
67	63	13.7	1209	2	T46027	hypothetical prote
68	63	13.7	1262	2	T33074	translation activa
69	63	13.7	2672	2	A48126	hypothetical prote
70	62.5	13.6	91	2	H90521	probable proteinas
71	62.5	13.6	308	2	B71697	moesin - human
72	62.5	13.6	577	1	A41289	hypothetical prote
73	62.5	13.6	853	2	S74609	probable ATP-depen
74	62.5	13.6	1101	2	G70951	pyruvate carboxyla
75	62.5	13.6	1150	2	G89881	

ALIGNMENTS

RESULT 1

C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae

C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C/Accession: C64013

R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J

, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, .

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64013

A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:q15

C/Superfamily: fe(II) trafficking protein YxgX

Query Match 100.0%; Score 461; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;

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Matches      87;   Conservative      0;   Mismatches      0;   Indels      0;   Gaps      0;

Oy          1 MARTVFC EYLKKEAEGIDFQLYPGELGKRIFDSVSQAAMGEWIKQTMLVNEKKLMMNA    60
            |||||
Db          1 MARTVFCEYLLKKEAEGIDFQLYPGELGKRIFDSVSQAAMGEWIKQTMLVNEKKLMMNA    60

Oy          61 EHRKLLEQEMVNFLPEGKDVIHIEGYVP    87
            |||||
Db          61 EHRKLLEQEMVNFLPEGKDVIHIEGYVP    87

RESULT 2
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:/Species: Escherichia coli
C:/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:/Accession: A85954
R:/Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;/Reference number: A85480; MUID:21074935; PMID:11206551
A;/Accession: A85954
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <STO>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A;/Experimental source: strain O157:H7, substrain EDL933
C;/Genetics:
A;/Gene: yggX
C;/Superfamily: fe(II) trafficking protein YggX
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```

Query Match      83.9%; Score 387; DB 2; Length 91;
Best Local Similarity 78.2%; Pred. No. 4,6e-32;
Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

Oy      1 MARTVFCBYLKKEAGELDFQLYPGELGKRIFDSVSQAQWGEWIKKQTMLVNEKKLMMNA 60
        |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MSRTTCTFLQREAEAGDPLQLYPGELGKRIYNEISKEAWAQOHKQTMLINEKKLNMINA 60

Oy      61 EHRKLLQEEMVNFLFEGKDVIHIEGYTP 87
        |||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      61 EHRKLLQEEMVNFLFEGKEVHIIEGYTP 87

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YggX

```

Query Match	83.9%	Score 387;	DB 2;	Length 91;
Best Local Similarity	78.2%	Pred. No. 4.6e-32;		
Matches	68;	Conservative 12;	Mismatches 7;	Indels 0; Gaps
OY	1 MARTVFCEYLKKEAGGLDLPOLYPGEIGKRIPDSVSKQAMGWEIKQTMLVNEKKLNMNA	60		
Dd	1 MSRTIFCTFLQREAEQGDFOLYPGEIGKRIRYNISKEAWAQMOHKQTMLINEKKLNMAA	60		
OY	61 EHRKLLQEEMVNFLFEGKDVIIEGYVP	87		

Db 61 EHRKLEQEMVNFLEGEKEVHIEGYTP 87

```

RESULT 4
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RIMD 0509952)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;/Reference number: A99629, MUID:21156231, PMID:11258796
A;/Accession: F91108
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <HAY>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163404; GB:BA000007; PIDN:BAB37261.1;
A;/Experimental source: strain O157:H7, substrain RIMD 0509952
C;/Genetics:
A;/Gene: ECs3838
C;/Superfamily: fe(II) trafficking protein YggX

```

	Query Match	83.9%	Score 387;	DB 2;	length 91;	
	Best Local Similarity	78.2%;	Pred. No. 4.6e-32;			
	Matches	Conservative 12;	Mismatches 7;	Indels	Gaps	0;
Qy	1 MARTVFC EYLKKRAEGDLPEQLYPGELGKRIFDSVS SKOANGEWIKQTMLVN EKKLN MNNA	60				
Dd	1 MSRTIFCTFLQREAE GQDFQLYPGELGKRIYNEISKEA MAQWQH KQTMLINEKKLNNMNA	60				
Qy	61 EHRKLLEQEMWNFLPFGKDVHIEGYVP	87				
Dd	61 EHRKLLEQEMWNFLPFGKEVHIIEGYTP	87				

RESULT 5
C82320
conserved hypothetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serogr
C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82320
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A;Experimental source: serogroup O1, strain N16961, biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein YgX

[illegible]

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-38
Perfect score: 461
Sequence: 1 MARYFCEYLKKEAEGLDFO.....QEMVNFLEGGKVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	461	100.0	90 1	FETP_HAEIN P44048 haemophilus
2	461	100.0	90 2	Q4QMD9_HAEI8 Q4qmd9 haemophilus
3	439	95.2	91 1	FETP_MANSU Q65vt7 manheimia
4	435	94.4	90 1	FETP_PASMU Q9clb9 pasteurella
5	425	92.2	94 1	FETP_HABDU Q7vkb6 haemophilus
6	389	84.4	90 1	FETP_VIBPA Q87li5 vibrio para
7	387	83.9	90 1	FETP_VIBVU Q8dc55 vibrio vuln
8	387	83.9	90 1	FETP_VIBVY Q7mh14 vibrio vuln
9	386	83.7	90 1	FETP_VIBCH Q9kur4 vibrio chol
10	382	82.9	90 1	FETP_ECO57 P0a8p4 escherichia
11	382	82.9	90 1	FETP_ECOLI P0a8p5 escherichia
12	382	82.9	90 1	FETP_SHIEL P0a8p3 shigella fl
13	380	82.4	90 1	FETP_SALCH Q57k04 salmonella
14	380	82.4	90 1	FETP_SALPA Q5pmn1 salmonella
15	380	82.4	90 1	FETP_SALTI P67618 salmonella
16	380	82.4	90 1	FETP_SALTY P67617 salmonella
17	379	82.2	90 1	FETP_PHOPR Q6lmk7 photobacter
18	378	82.0	90 1	FETP_ECOL6 Q8fel9 escherichia
19	371	80.5	90 1	FETP_YERPS Q66m3 yersinia ps
20	363	78.7	90 1	FETP_YERPE Q8zhe7 yersinia pe
21	361	78.3	90 1	FETP_VIBF1 Q5e7t0 vibrio fisc
22	356	77.2	92 1	FETP_SHEON Q8ebx6 shewanella
23	353	76.6	90 1	FETP_ERWCT Q6d8j9 erwinia car
24	348	75.5	90 1	FETP_PHOLU Q7n7i1 photorhabdu
25	330	71.6	90 1	FETP_IDILO Q5qy58 idiomarina
26	256	55.5	77 1	FETP_BUCAI P57618 buchera ap
27	256	55.5	90 1	FETP_BORBR Q7wh06 bordetella
28	256	55.5	90 1	FETP_BORPA Q7w9q2 bordetella
29	256	55.5	90 1	FETP_BORPE Q7wvc4 bordetella
30	244	52.9	91 1	FETP_XANAC Q8pjh7 xanthomonas
31	243	52.7	90 1	FETP_NITEU Q82xf2 nitrosomona

32	241	52.3	90 1	FETP_XYLFT Q87d06 xylella fas
33	241	52.3	91 1	FETP_BURMA Q62iug burkholderi
34	241	52.3	91 1	FETP_BURPS Q63sj4 burkholderi
35	239.5	52.0	89 1	FETP_LEGPL Q5wvc4 legionella
36	239	51.8	92 1	FETP_XANOR Q5gy22 xanthomonas
37	237	51.4	90 1	FETP_XYLFA Q9pc73 xylella fas
38	236	51.2	90 1	FETP_PSEAE Q9hu36 pseudomonas
39	236	51.2	90 2	Q4J2Z8_AZOV1 Q4j228 azotobacter
40	235.5	51.1	89 1	FETP_LEGPA Q5x3x9 legionella
41	235.5	51.1	89 1	FETP_LEGPH Q5zu80 legionella
42	235	51.0	92 1	FETP_XANCP Q8p829 xanthomonas
43	235	51.0	92 1	Q4UW14_XANCP Q4uw14 xanthomonas
44	232	50.3	91 1	FETP_RALSO Q8y010 ralstonia s
45	231	50.1	91 2	Q4LS19_9BURK Q4ls19 burkholderi
46	230	49.9	78 1	FETP_WIGBR Q8d3c5 wigleswort
47	230	49.9	90 1	FETP_PSESM Q87uf5 pseudomonas
48	230	49.9	90 2	Q6T7F6_PSEFL Q6t7f6 pseudomonas
49	230	49.9	90 2	Q4ZLP3_PSESY Q4zlp3 pseudomonas
50	229	49.7	90 1	FETP_PSEPK Q88r49 pseudomonas
51	227	49.2	88 1	FETP_NEIG1 Q5f553 neisseria g
52	227	49.2	88 1	FETP_NEIMA P67615 neisseria m
53	227	49.2	88 1	FETP_NEIMB P67616 neisseria m
54	224	48.6	90 1	FETP_COXBU Q83d06 coxiella bu
55	224	48.6	90 1	FETP_METCA Q60aj7 methylococc
56	224	48.6	90 2	Q4KJT2_PSEF5 Q4kjt2 pseudomonas
57	214	46.4	87 1	FETP_BUCBP Q89a44 buchnera ap
58	214	46.4	90 1	FETP_CHRVO Q7nsr4 chromobacte
59	212	46.0	78 1	FETP_BUCAP Q8k925 buchnera ap
60	211.5	45.9	90 1	FETP_AC1AD Q6f6b3 acinetobact
61	209	45.3	79 1	FETP_CANBF Q7vrg9 candidatus
62	192	41.6	87 1	FETP_FRATF Q5nhj8 francisella
63	154	33.4	92 2	Q4NWQ4_9DELT Q4nwq4 anaeromyxob
64	146	31.7	96 2	Q4FVJ7_9GAMM Q4fvj7 psychrobact
65	77.5	16.8	416 2	Q89KZ1_BRAJA Q89kz1 bradyrhizob
66	76.5	16.6	187 2	Q9HBF7_HUMAN Q9hbf7 homo sapien
67	76.5	16.6	218 2	Q7SPV9_9BETR Q7spv9 human betar
68	76.5	16.6	281 2	Q6PG71_MOUSE Q6pg71 mus musculu
69	76.5	16.6	372 2	Q85648_9BETR Q85648 mouse mamma
70	76.5	16.6	452 2	Q7SPV8_HUMAN Q7spv8 human betar
71	76.5	16.6	590 1	GAG_MMTVB P10258 mouse mamma
72	76.5	16.6	590 1	GAG_MMTVC P11284 mouse mamma
73	76.5	16.6	591 2	Q83391_9BETR Q83391 mouse mamma
74	76.5	16.6	591 2	Q91ZT6_9BETR Q91zt6 exogenous m
75	76.5	16.6	591 2	Q91ZU1_9BETR Q91zu1 endogenous

ALIGNMENTS

RESULT 1
FETP_HAEIN
ID FETP_HAEIN STANDARD; PRT; 90 AA.
AC P44048;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedlocusNames=H10760;
GN Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_Taxid=727;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA Mckenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fritchman J.L., Geoghagen N.S.M.,

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RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "whole-genome random sequencing and assembly of Haemophilus influenzae
RL Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RX DOI=10.1002/(SICI)1522-2683(2000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC
DR EMBL; U32760; AAC22419.1; -; Genomic_DNA.
DR PIR; C64013; C64013.
DR SMR; P44048; 1-87.
DR TIGR; HI0760; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9gX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_Y9gX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;
SQ
Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARTVFCYLLKKEAGGLDFQLYPGLGKRIFDSVSKQAWGEWIKQTM LVNEKLLNMNNA 60
Db 1 MARTVFCYLLKKEAGGLDFQLYPGLGKRIFDSVSKQAWGEWIKQTM LVNEKLLNMNNA 60

Oy 61 EHRKLLQEQMVNPLFEGKDVHIEGYVP 87
Db 61 EHRKLLQEQMVNPLFEGKDVHIEGYVP 87

RESULT 2
O4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
ID O4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
AC O4QMD9;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS OrderedLocuNames=NTHI0920;
GN Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=281310;
OX [1]
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RX Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT d, strain KW20.";
RT J. Bacteriol. 187:4627-4636(2005).
RL EMBL; CP000057; AAX87808.1; -; Genomic DNA.

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DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF737B93B CRC64;

Query Match
Best Local Similarity 100.0%; Score 461; DB 2; Length 90;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCFYLKKEAGLDLFDLPYLGELGKRIFDSVSKQAWGEWIKKQTMVNEKKLNMNNA 60
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DB 1 MARTVFCFYLKKEAGLDLFDLPYLGELGKRIFDSVSKQAWGEWIKKQTMVNEKKLNMNNA 60
   |||||

QY 61 EHRKLLLEQEMVNFLEFGKDVHIEGYVP 87
   |||||
DB 61 EHRKLLLEQEMVNFLEFGKDVHIEGYVP 87
   |||||

RESULT 3
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ID_FETP_MANSM STANDARD; PRT; 91 AA.
AC O65VT7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=MS0316;
OS Mannheimia succiniciproducens (strain MBEL55E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxId=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens."
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE016827; AUA36923.1; -; Genomic_DNA.
DR SMR; O65VT7; 1-88.
DR HAMAP; MF_00686; -, 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AAC CRC64;

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Matches 79; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSRTVFCFYLKKEAGLDLFDLPYLGELGKRIFDNISSKAWGEWIKKQTMVNEKKLNMNNA 60
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QY 61 EHRKLLLEQEMVNFLEFGKDVHIEGYVP 87
   |||||
DB 61 EHRKLLLEQEMVNFLEFGKDVHIEGYVP 87
   |||||

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-38
Perfect score: 461
Sequence: 1 MARTVFCBYLKKEABGLDFQ.....QEMVNFLPEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
6: /cgn2_6/ptodata/1/iaa/backfilest1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	372	80.7	107	2	US-09-489-039A-11962
2	371	80.5	93	2	US-09-543-681A-5443
3	236	51.2	122	2	US-09-252-991A-23355
4	214.5	46.5	92	2	US-09-328-352-5456
5	144	31.2	110	2	US-09-540-236-2859
6	76.5	16.6	591	2	US-09-370-368-8
7	70.5	15.3	959	2	US-09-543-681A-6879
8	67.5	14.6	271	2	US-09-248-796A-19265
9	67	14.5	474	2	US-09-252-991A-24473
10	67	14.5	1401	2	US-09-750-590A-2
11	66	14.3	548	2	US-09-167-299-3
12	65.5	14.2	623	2	US-10-104-047-2547
13	65	14.1	292	2	US-09-328-352-5836
14	65	14.1	482	2	US-09-248-796A-17800
15	64.5	14.0	415	1	US-08-602-010A-10
16	64.5	14.0	415	1	US-08-680-726A-10
17	64.5	14.0	415	2	US-09-092-409-10
18	64.5	14.0	683	2	US-09-270-767-46792
19	64	13.9	217	2	US-09-543-681A-7862
20	64	13.9	633	2	US-09-328-352-6519
21	64	13.9	680	2	US-09-298-924-4
22	64	13.9	720	1	US-08-840-236-1
23	64	13.9	720	1	US-08-505-448A-1
24	63.5	13.8	586	2	US-09-270-767-44373
25	62.5	13.6	177	1	US-08-647-960-6
26	62.5	13.6	2285	2	US-09-308-375-2
27	62.5	13.6	2285	2	US-09-932-183A-2

28	62	13.4	337	2	US-09-270-767-41746	Sequence 41746, A
29	62	13.4	455	2	US-09-270-767-45790	Sequence 45790, A
30	62	13.4	550	2	US-09-107-532A-7201	Sequence 7201, Ap
31	62	13.4	674	2	US-08-961-083-200	Sequence 200, App
32	62	13.4	674	2	US-09-536-784-200	Sequence 200, App
33	62	13.4	674	2	US-09-765-271-200	Sequence 200, App
34	62	13.4	674	2	US-09-765-272A-200	Sequence 200, App
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36	61.5	13.3	734	2	US-09-442-055-2	Sequence 2, Appli
37	61	13.2	191	1	US-08-468-576B-13	Sequence 13, Appl
38	61	13.2	191	1	US-08-468-579B-13	Sequence 13, Appl
39	61	13.2	191	1	US-08-468-577B-13	Sequence 13, Appl
40	61	13.2	359	2	US-09-092-770-6	Sequence 6, Appli
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42	61	13.2	359	2	US-10-265-062-6	Sequence 6, Appli
43	61	13.2	404	1	US-09-092-770-3	Sequence 3, Appli
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45	61	13.2	404	2	US-10-265-062-3	Sequence 3, Appli
46	61	13.2	407	2	US-09-949-016-11184	Sequence 11184, A
47	61	13.2	625	2	US-09-949-016-8485	Sequence 8485, Ap
48	61	13.2	625	2	US-09-949-016-8810	Sequence 8810, Ap
49	60.5	13.1	279	2	US-09-198-452A-221	Sequence 221, App
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51	60.5	13.1	438	2	US-09-198-452A-985	Sequence 985, App
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53	60.5	13.1	547	2	US-09-438-185A-914	Sequence 914, App
54	60.5	13.1	720	2	US-09-583-110-2940	Sequence 2940, App
55	60.5	13.1	720	2	US-09-107-433-4193	Sequence 4193, Ap
56	60.5	13.1	782	2	US-09-710-279-2352	Sequence 2352, Ap
57	60.5	13.1	794	2	US-09-134-001C-4310	Sequence 4310, Ap
58	60	13.0	243	2	US-09-270-767-31727	Sequence 31727, A
59	60	13.0	243	2	US-09-270-767-46944	Sequence 46944, A
60	60	13.0	280	2	US-09-323-998E-37	Sequence 37, Appl
61	60	13.0	319	2	US-09-710-279-2760	Sequence 2760, Ap
62	60	13.0	443	2	US-09-134-001C-3183	Sequence 3183, Ap
63	60	13.0	465	2	US-09-769-787-164	Sequence 164, App
64	60	13.0	1248	1	US-09-080-897-2	Sequence 2, Appli
65	60	13.0	1248	2	US-09-323-735-2	Sequence 2, Appli
66	60	13.0	1315	2	US-08-899-595-3	Sequence 3, Appli
67	60	13.0	2101	1	US-08-466-390-4	Sequence 4, Appli
68	60	13.0	2101	1	US-08-470-950-4	Sequence 4, Appli
69	60	13.0	2101	1	US-08-467-781-4	Sequence 4, Appli
70	60	13.0	2101	1	US-08-195-487-4	Sequence 4, Appli
71	60	13.0	2101	2	US-08-483-924-4	Sequence 4, Appli
72	60	13.0	2101	2	US-09-452-294-1	Sequence 32, Appli
73	60	13.0	2101	4	PCT-US93-06160-4	Sequence 4, Appli
74	60	13.0	2101	4	US-09-949-016-7646	Sequence 7646, Ap
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ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Berton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-38

Perfect score: 461
Sequence: 1 MARTVFCEYLKKEAGLDFQ.....QEMVNFLEGGKVHIEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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Published Applications AA Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	434	94.1	91	3	US-09-955-502-5
4	425	92.2	87	3	US-09-955-502-8
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6	387	83.9	91	3	US-09-955-502-12
7	387	83.9	91	3	US-09-955-502-13
8	386	83.7	90	3	US-09-955-502-10
9	385	83.5	88	3	US-09-955-502-15
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19	256	55.5	87	3	US-09-955-502-3
20	241	52.3	87	3	US-09-955-502-29
21	241	52.3	86	3	US-09-955-502-30
22	238.5	51.7	86	3	US-09-955-502-4
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24	236	51.2	87	3	US-09-955-502-25
25	230	49.9	90	3	US-09-955-502-23
26	229	49.7	87	3	US-09-955-502-24
27	227	49.2	88	3	US-09-955-502-26

28	227	49.2	88	3	US-09-955-502-27	Sequence 27, Appl
29	227	49.2	88	3	US-09-955-502-28	Sequence 28, Appl
30	224	48.6	87	3	US-09-955-502-32	Sequence 32, Appl
31	224	48.6	88	3	US-09-955-502-33	Sequence 33, Appl
32	202	43.8	87	3	US-09-955-502-31	Sequence 31, Appl
33	76.5	16.6	591	3	US-09-827-822-8	Sequence 8, Appl
34	73	15.8	1144	4	US-10-369-493-22774	Sequence 22774, A
35	71	15.4	503	5	US-10-450-763-46936	Sequence 46936, A
36	70.5	15.3	723	4	US-10-205-194-25	Sequence 25, Appl
37	70.5	15.3	723	4	US-10-231-913-139	Sequence 139, App
38	70.5	15.3	723	4	US-10-231-913-140	Sequence 140, App
39	70.5	15.3	723	4	US-10-342-844-22	Sequence 22, Appl
40	70.5	15.3	723	4	US-10-342-844-26	Sequence 26, Appl
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43	70	15.2	1261	4	US-10-437-963-189166	Sequence 189166,
44	69.5	15.1	593	5	US-10-450-763-50306	Sequence 50306, A
45	69	15.0	507	5	US-10-282-122A-68134	Sequence 68134, A
46	68.5	14.9	2724	5	US-10-756-149-5518	Sequence 5518, App
47	67.5	14.6	283	4	US-10-425-114-68519	Sequence 68519, A
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71	64.5	14.0	579	4	US-10-360-849A-24	Sequence 24, Appl
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74	64	13.9	553	4	US-10-282-122A-47026	Sequence 47026, A
75	64	13.9	553	5	US-10-732-923-18350	Sequence 18350, A

ALIGNMENTS

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; Sequence 7, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus influenzae

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-38
Perfect score: 461
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Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	66.5	14.4	818	US-11-120-308-94	Sequence 94, Appl
5	65.5	14.2	623	US-11-072-512-2547	Sequence 2547, Ap
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7	61	13.2	342	US-11-156-084-25	Sequence 25, Appl
8	61	13.2	342	US-11-156-084-44	Sequence 44, Appl
9	61	13.2	359	US-11-087-227-8	Sequence 8, Appli
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11	61	13.2	369	US-11-156-084-45	Sequence 45, Appl
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13	61	13.2	404	US-11-192-450-3	Sequence 3, Appli
14	61	13.2	619	US-11-156-084-24	Sequence 24, Appl
15	60.5	13.1	285	US-10-467-657-222	Sequence 222, App
16	60.5	13.1	285	US-10-467-657-8230	Sequence 8230, Ap
17	60.5	13.1	496	US-11-069-642-20	Sequence 20, Appl
18	60.5	13.1	782	US-10-793-626-2352	Sequence 2352, Ap
19	60	13.0	319	US-10-793-626-2760	Sequence 2760, Ap
20	60	13.0	465	US-10-873-528-164	Sequence 164, App
21	60	13.0	2101	US-10-857-780-23	Sequence 23, Appl
22	59	12.8	834	US-10-453-372-658	Sequence 658, App
23	59	12.8	1734	US-11-192-967-6	Sequence 6, Appli
24	59	12.8	1734	US-11-193-715-6	Sequence 6, Appli
25	58.5	12.7	253	US-10-724-598-28	Sequence 28, Appl

26	58.5	12.7	466	US-10-524-647-114	Sequence 114, App
27	58.5	12.7	466	US-10-524-972-102	Sequence 102, App
28	58.5	12.7	729	US-10-511-538-101	Sequence 101, App
29	58.5	12.7	774	US-11-070-627-7	Sequence 7, Appli
30	58	12.6	296	US-11-087-227-10	Sequence 10, Appl
31	58	12.6	452	US-10-467-962B-14	Sequence 14, Appl
32	57.5	12.5	305	US-11-156-084-178	Sequence 178, App
33	57.5	12.5	635	US-11-098-686-10433	Sequence 10433, A
34	57.5	12.5	650	US-10-467-657-1948	Sequence 1948, Ap
35	57	12.4	336	US-10-453-372-640	Sequence 640, App
36	57	12.4	391	US-11-207-626A-16	Sequence 16, Appl
37	57	12.4	391	US-11-207-626A-27	Sequence 27, Appl
38	57	12.4	695	US-10-453-372-648	Sequence 648, App
39	57	12.4	700	US-10-995-561-922	Sequence 922, App
40	57	12.4	700	US-10-995-561-924	Sequence 924, App
41	57	12.4	775	US-10-453-372-656	Sequence 656, App
42	57	12.4	793	US-10-995-561-925	Sequence 925, App
43	57	12.4	804	US-10-453-372-650	Sequence 650, App
44	57	12.4	847	US-10-453-372-654	Sequence 654, App
45	57	12.4	857	US-10-453-372-652	Sequence 652, App
46	57	12.4	905	US-10-453-372-638	Sequence 638, App
47	57	12.4	905	US-10-453-372-662	Sequence 662, App
48	57	12.4	905	US-10-453-372-664	Sequence 664, App
49	57	12.4	963	US-10-995-561-923	Sequence 923, App
50	57	12.4	963	US-10-995-561-923	Sequence 923, App
51	57	12.4	1012	US-10-453-372-646	Sequence 646, App
52	56.5	12.3	349	US-10-821-234-1387	Sequence 1387, Ap
53	56.5	12.3	411	US-11-072-512-3452	Sequence 3452, Ap
54	56.5	12.3	1766	US-11-075-185-10	Sequence 10, Appl
55	55.5	12.0	250	US-11-098-686-10812	Sequence 10812, A
56	55.5	12.0	268	US-10-995-561-718	Sequence 718, App
57	55.5	12.0	299	US-11-156-084-288	Sequence 288, App
58	55.5	12.0	301	US-11-055-822-1062	Sequence 1062, Ap
59	55.5	12.0	355	US-10-995-561-720	Sequence 720, App
60	55.5	12.0	739	US-10-131-826A-478	Sequence 478, App
61	55	11.9	266	US-09-995-493-6	Sequence 6, Appli
62	55	11.9	279	US-11-098-686-10812	Sequence 10812, A
63	55	11.9	504	US-11-072-512-3467	Sequence 3467, Ap
64	55	11.9	560	US-11-131-479-16	Sequence 16, Appl
65	54.5	11.8	242	US-11-022-562-220	Sequence 220, App
66	54.5	11.8	1299	US-10-821-234-1145	Sequence 1145, Ap
67	54	11.7	139	US-10-793-626-1310	Sequence 1310, Ap
68	54	11.7	175	US-09-978-360A-762	Sequence 762, App
69	54	11.7	175	US-10-821-234-1522	Sequence 1522, Ap
70	54	11.7	175	US-10-072-175-206	Sequence 206, App
71	54	11.7	177	US-10-467-657-1658	Sequence 1658, Ap
72	54	11.7	254	US-11-072-512-3198	Sequence 3198, Ap
73	54	11.7	403	US-11-192-450-4	Sequence 4, Appli
74	54	11.7	603	US-10-770-726-75	Sequence 75, Appl
75	54	11.7	1122	US-10-467-657-6112	Sequence 6112, Ap

ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 : Search time 71.531 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-39
Perfect score: 466
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Scoring table: BLOSUM62
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Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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4	346	74.2	93	7	ADF05158	Adf05158 Bacterial
5	345	74.0	87	5	ABB78151	Abb78151 Amino aci
6	344	73.8	91	5	ABB78150	Abb78150 Amino aci
7	336	72.1	87	5	ABB78153	Abb78153 Amino aci
8	336	72.1	88	5	ABB78160	Abb78160 Amino aci
9	336	72.1	91	5	ABB78161	Abb78161 Amino aci
10	336	72.1	91	5	ABB78159	Abb78159 Amino aci
11	336	72.1	91	5	ABB78162	Abb78162 Amino aci
12	332	71.2	91	5	ABB78158	Abb78158 Amino aci
13	332	71.2	91	5	ABB78157	Abb78157 Amino aci
14	332	71.2	91	5	ABB78156	Abb78156 Amino aci
15	327	70.2	107	7	ABO65445	AbO65445 Klebsiell
16	326	70.0	91	5	ABB78163	Abb78163 Amino aci
17	308	66.1	90	5	ABB78165	Abb78165 Amino aci
18	292	62.7	78	5	ABB78164	Abb78164 Amino aci
19	256	54.9	87	5	ABB78148	Abb78148 Amino aci
20	256	54.9	87	5	ABB78147	Abb78147 Amino aci
21	242.5	52.0	86	5	ABB78149	Abb78149 Amino aci
22	237	50.9	87	5	ABB78169	Abb78169 Amino aci
23	235	50.4	87	5	ABB78170	Abb78170 Amino aci
24	235	50.4	122	7	ABO74609	ABO74609 Pseudomon

25	230	49.4	88	5	ABB78171	Abb78171 Amino aci
26	230	49.4	88	5	ABB78172	Abb78172 Amino aci
27	230	49.4	88	5	ABB78173	Abb78173 Amino aci
28	230	49.4	88	6	ABP77219	Abp77219 N. gonorr
29	228	48.9	90	5	ABB78168	Abb78168 Amino aci
30	226	48.5	87	5	ABB78175	Abb78175 Amino aci
31	220	47.2	87	5	ABB78174	Abb78174 Amino aci
32	216	46.4	76	5	ABB78166	Abb78166 Amino aci
33	215	46.1	87	5	ABB78177	Abb78177 Amino aci
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40	130	27.9	110	8	ADL05173	Adl05173 M. catarr
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42	77.5	16.6	2364	8	ABM80299	Abm80299 Tumour-as
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45	75.5	16.2	1630	7	ADJ70625	Adj70625 Mouse hea
46	75.5	16.2	2154	2	AAW81639	Aaw81639 Mouse elf
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48	75.5	16.2	2154	8	ADQ88363	Adq88363 Mouse elf
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69	68	14.6	737	7	ADF83526	Adf83526 C. reinha
70	66.5	14.3	689	8	ADS28247	Ads28247 Bacterial
71	66.5	14.3	1176	6	ABR53186	AbR53186 Protein s
72	66.5	14.3	1176	7	ADK63224	Adk63224 Disease t
73	66	14.2	261	8	ADP81257	Adp81257 Protein o
74	66	14.2	269	8	ADP81258	Adp81258 Protein o
75	66	14.2	307	5	ABB90271	Abb90271 Human pol

ALIGNMENTS

RESULT 1
ABB78154
ID ABB78154 standard; protein; 88 AA.
XX ABB78154;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16bp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 88 AA;

```

Query Match          100.0%; Score 466; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.8e-49;
Matches      88; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

QY      1 MARTVNCVHLNKEADGLDFOLYPGDLGRIFDNI SKEAWGLWKKQTMLIN EKLNMNV 60
        |||
Db       1 MARTVNCVHLNKEADGLDFOLYPGDLGRIFDNI SKEAWGLWKKQTMLIN EKLNMNV 60
        |||

QY      61 DDRKFLEAQM TSFLFEGK DVEIEGFVPE 88
        |||
Db       61 DDRKFLEAQM TSFLFEGK DVEIEGFVPE 88

RESULT 2
ABB78152 standard; protein; 87 AA.
XX      ABB78152;
AC      ABB78152;
XX      05-NOV-2002 (first entry)
DT      Amino acid sequence of a YggX homologue.
DE      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW      hydroxyl radical; DNA damage; YggX homologue.
XX      Haemophilus influenzae.
OS      US2002072118-A1.
PN      13-JUN-2002.
PD      18-SEP-2001; 2001US-00955502.
PF      22-SEP-2000; 2000US-0234588P.
PR      (DOWN/) DOWNS D.
PA      (GRAL/) GRALNICK J A.
XX      Downs D, Gralnick JA,
XX
```

DR WPI, 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more Yggx protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX

PS Example; Fig 1A; 16pp; English.

XX

CC The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the

CC native amount of Yggx protein (a protein identified from *Salmonella*

CC *enterica* serovar typhimurium) or its homolog, where the cells are

CC rendered more resistant to superoxide damage. Yggx reduces the oxidation

CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from

CC clusters. The resulting decrease in free-iron levels generates fewer

CC hydroxyl radicals and thus reduced DNA damage. The method is useful for

CC reducing superoxide damage in a bacterial, yeast, mammalian or plant

CC cell. ABB78147-78 represent Yggx homologues

XX

SQ Sequence 87 AA;

```

Query Match          76.4%; Score 356; DB 5; Length 87;
Best Local Similarity 74.7%; Pred. No. 1.4e-35;
Matches 65; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

QY      1 MARTVNCVHLNKEADGLDLPQLYPGLGKRIFDNIKSRAWGLWQKQTMLINEKLLNNMNV 60
        ||||| : ||||:|||||||:|||||||:|:|:| |||||:|||||||
Db      1 MARTVFCBYLKKAEGLDLPQLYPGLGKRIFDSVSKAWGEWIKKQTMVLNNEKLLNNMNA 60

QY      61 DDRKFLBAQMTSFLPEGKDVIEIGFVP 87
        : || || : ||||| ||||| |||:|
Db      61 EHRKLLQEMWVNFLEPGKDVHIEGYVP 87

```

CC	The native amount of YggX protein (a protein identified from Salmonella
PS	Example; Fig 1A; 16pp; English.
XX	
XX	
PT	Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT	cell, comprises engineering the cell to produce more YggX protein, a
PT	protein identified from Salmonella enterica Serovar Typhimurium.
XX	
XX	Downs D, Gralnick JA;
DR	WPI, 2002-589476/63.
XX	
PA	(DOWN/) DOWNS D.
PA	(GRAL/) GRALNICK J A.
XX	
PR	22-SEP-2000; 2000US-0234588P.
XX	
PF	18-SEP-2001; 2001US-00955502.
XX	
PD	13-JUN-2002.
XX	
PN	US2002072118-A1.
OS	Vibrio cholerae.
XX	
KM	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	hydroxyl radical; DNA damage; YggX homologue.
DE	Amino acid sequence of a YggX homologue.
DT	05-NOV-2002 (first entry)
AC	ABB78155;
ID	ABB78155 standard; protein; 90 AA.
RESULT 3	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.52424 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-39
Perfect score: 466
Sequence: 1 MARTVNCVHLNKEADGLDFQ.....QMTSFLPEKGKVEIEGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	356	76.4	90	2	C64013	hypothetical prote
2	347	74.5	90	2	C82320	conserved hypotet
3	336	72.1	91	2	AH0879	conserved hypotet
4	332	71.2	91	2	A85954	hypothetical prote
5	332	71.2	91	2	A65082	hypothetical prote
6	332	71.2	91	2	F91108	hypothetical prote
7	308	66.1	90	2	AI0116	conserved hypotet
8	235	50.4	90	2	H83003	conserved hypotet
9	230	49.4	88	2	H81014	conserved hypotet
10	216	46.4	93	2	E84994	hypothetical prote
11	196	42.1	105	2	C82624	conserved hypotet
12	77.5	16.6	2364	1	A44159	spectrin beta-G ch
13	75.5	16.2	1252	2	A47213	beta-fodrin - huma
14	70	15.0	936	2	H71728	2-oxoglutarate deh
15	68.5	14.7	412	2	S62538	hypothetical colle
16	67.5	14.5	568	2	T25859	hypothetical prote
17	67.5	14.5	1111	2	T23047	hypothetical prote
18	67	14.4	928	2	C97728	hypothetical prote
19	66.5	14.3	260	2	H82925	hypothetical prote
20	66.5	14.3	689	2	F83902	beta-galactosidase
21	66.5	14.3	1123	2	T30880	dynein heavy chain
22	66.5	14.3	1176	2	S40899	VPS8 protein - yea
23	66	14.2	384	2	F64438	hypothetical prote
24	65.5	14.1	1021	2	AC2202	hypothetical prote
25	65	13.9	300	2	T15690	hypothetical prote
26	65	13.9	380	2	T18509	hypothetical prote
27	65	13.9	651	2	G69177	methionine-tRNA 11
28	64.5	13.8	577	1	S39804	moesin - pig
29	64.5	13.8	1119	2	T18491	hypothetical prote

30	64	13.7	365	2	C83885	hypothetical prote
31	64	13.7	578	2	T11659	hypothetical prote
32	64	13.7	964	2	T32482	hypothetical prote
33	63.5	13.6	310	2	C64370	modification methy
34	63.5	13.6	1333	2	S65812	RNA-directed DNA p
35	63.5	13.6	1492	2	T14652	protein J - Yersin
36	63.5	13.6	1545	2	T14966	phage lambda-relat
37	63	13.5	151	2	S72243	dynein heavy chain
38	63	13.5	151	2	S72245	dynein heavy chain
39	63	13.5	408	2	H64513	hypothetical prote
40	63	13.5	507	2	C81063	fumarate hydratase
41	63	13.5	546	2	A81807	fumarate hydratase
42	63	13.5	793	2	C72219	DNA mismatch repai
43	63	13.5	1638	2	D87749	protein unc-73b [1
44	63	13.5	2488	2	T42739	guanine nucleotide
45	62.5	13.4	432	2	G71961	hypothetical prote
46	62.5	13.4	432	2	C97258	sugar-binding peri
47	62.5	13.4	481	2	T14300	hypothetical prote
48	62.5	13.4	516	2	A96753	probable threonine
49	62	13.3	150	2	S72244	dynein heavy chain
50	62	13.3	169	2	PN0560	phytochrome - long
51	62	13.3	171	2	PN0558	phytochrome - wild
52	62	13.3	179	2	B71274	probable translati
53	62	13.3	486	2	B46341	helper component p
54	62	13.3	593	2	C64097	probable soluble 1
55	62	13.3	679	2	E90560	hypothetical prote
56	62	13.3	972	2	S35521	DNA topoisomerase
57	62	13.3	1006	2	T00050	hypothetical prote
58	61.5	13.2	118	2	I55515	dynein-like protei
59	61.5	13.2	237	2	A71082	hypothetical prote
60	61.5	13.2	265	2	T46013	hypothetical prote
61	61.5	13.2	423	2	H84566	probable RING zinc
62	61.5	13.2	504	2	C64398	hypothetical prote
63	61.5	13.2	583	1	A41129	radixin - mouse
64	61.5	13.2	583	1	A46127	radixin - human
65	61.5	13.2	583	1	S39805	hypothetical prote
66	61.5	13.2	813	2	D64527	nucleotide diphosp
67	61.5	13.2	905	1	A27410	vsaa-like (mycopla
68	61.5	13.2	1017	2	D90550	hypothetical prote
69	61.5	13.2	1922	2	T00637	dynein heavy chain
70	61	13.1	151	2	S72239	dynein-like protei
71	61	13.1	188	2	I70176	beta-glucosidase h
72	61	13.1	477	2	G69760	helper component p
73	61	13.1	486	2	A46341	hypothetical prote
74	61	13.1	583	2	T48365	conserved hypotet
75	61	13.1	847	2	G95843	

ALIGNMENTS

RESULT 1

C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kiehlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:q15
C/Superfamily: fe(II) trafficking protein YggX
Query Match 76.4%; Score 356; DB 2; Length 90;
Best Local Similarity 74.7%; Pred. No. 1.9e-30;

Matches	65; Conservative	11; Mismatches	11; Indels	0; Gaps	0;
OY	1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV	60			
Db	1 MARTVFCEYLKKEAEGLDLFQLYPGBELKRIFDSVSKQAWGSEWIKKQTMVLNEKKLNMMNA	60			
OY	61 DDRKFLFAQMTSFLFEGKDVIEGFPV	87			
Db	61 EHRKLIEQEMVNFLEFGKDVHIEGYVP	87			

RESULT 2
 C82320
 conserved hypothetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C/Species: *Vibrio cholerae*
 C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
 C/Accession: C82320
 R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.;
 chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B.
 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A/Reference number: A82035; MUID:20406833; PMID:10952301
 A/Accession: C82320
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-90 <HEI>
 A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN
 A/Experimental source: serogroup O1, strain N16961, biotype El Tor
 C/Genetics:
 A/Gene: VC0451
 A/Map position: 1
 C/Superfamily: fe(II) trafficking protein YggX

Query Match	74.5%;	Score 347;	DB 2;	Length 90;
Best Local Similarity	74.7%;	Pred. No. 1.7e-29;		
Matches	65;	Conservative	7;	Mismatches 15; Indels 0; Gaps 0;
QY	1	MARTVNCVHLNKEADGLDPOLYPEDGKRIFDNISKEAWGLQKQOTMLINEKLLNMNV	60	
		: :		
Db	1	MARTVFCTRLQKEADGLDPOLYPEDGKRIFDNICKEAWAQWOTKOTMLINEKLLNMNDP	60	
QY	61	DDRKFLEAQMTSFLFEGKOVEIEGFVP	87	
		: : : : :		
Db	61	EHRKLLQEOMVNFLEFGKEVHIIEGYTP	87	

RESULT 3
AH0879
conserved hypothetical protein STY3266 [imported] - *Salmonella enterica* subsp. *enterica*
C;Species: *Salmonella enterica* subsp. *enterica* serovar Typh1
A;Note: this species has also been called *Salmonella typhi*
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A;Title: Complete genome sequence of a multiple drug resistant *Salmonella enterica* sero
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <PAR>
A;Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189;
C;Genetics:
A;Gene: STY3266
C;Superfamily: fe(II) trafficking protein YggX

Query Match	72.1%;	Score 336;	DB 2;	Length 91;
Best Local Similarity	68.2%;	Pred. No. 2.4e-28;		
Matches 60;	Conservative 13;	Mismatches 15;	Indels 0;	Gaps 0;

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QY      1 MARTVNCVHLNKEADGLDFOLYPBGDLGKRIFDNISKEAWGLWOKKOTMLINEKKLNMNV   60
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      1 MSRTICTTYLRDAEAGODFOLYPGELGKRITNEIISKDAAWQHKKOTMLINEKKLNMAVA   60
        |||::||::||::||::||::||::||::||::||::||::||::||::||::||
QY      61 DDRKFLEAOMTSFLPEGKDVEIEGFVPE   88
        :||::|||||||::||
Db      61 EHRKLLEQEMWSFLPEGKDVAHIEGYTPE   88
```

RESULT 4
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;/Species: Escherichia coli
C;/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;/Accession: A85954
R;/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Hiller, L.; Grotbeck, E.U.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousts, K.; Apodaca,
Nature 409, 529-533, 2001
A;/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;/Reference number: A85480; MUID:21074935; PMID:11206551
A;/Accession: A85954
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <STO>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A;/Experimental source: strain O157:H7, substrain EDL933
C;/Genetics:
A;/Gene: yggX
C;/Superfamily: fe(II) trafficking protein YggX

```
Query Match          71.2%; Score 332; DB 2; Length 91;
Best Local Similarity 68.2%; Pred. No. 6.3e-28;
Matches 60; Conservative 12; Mismatches 16; Indels 0; Gaps
```

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNIISKEAWGLWQKQTMLINEKLNMMNV 60
 |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 1 MSRTICTFLQREAEQGDFQLYPGELGKRIYNEISKEAWAQWHKQTMLINEKLNMMNA 60

QY 61 DDRKFLEAQMTSFLEEGKDVEIEGFVPE 88
 :|||::|||::|||::|||::|||::|||:
Db 61 EHRKLLEQEMWNFLFEKGKVHIEGYTPS 88

RESULT 5
A65082
hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C.Species: *Escherichia coli*
C.Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C.Accession: A65082
R.Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A.Title: The complete genome sequence of *Escherichia coli* K-12.
A.Reference number: A64720; MUID:97426617; PMID:9278503
A.Accession: A65082
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: DNA
A.Residues: 1-91 <BLAT>
A.Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A.Experimental source: strain K-12, substrain MGI655
C.Superfamily: fe(ii) trafficking protein YggX

	Query Match	71.2%;	Score 332;	DB 2;	Length 91;
	Best Local Similarity	68.2%;	Pred. No. 6.3e-28;		
	Matches 60;	Conservative 12;	Mismatches 16;	Indels 0;	Gaps
QY	1 MARTVNCVHLINKEADGLDFOLYPBGLGKRIFDNIISKEAWGLMOKQTMLINEKLTMMNTV	:	:	:	:
Db	1 MSRTI FCTFLQREAEGQDFLYRGELGRIRYNEISKEAQAQHQKQTMLINEKLTMMNTNA	:	:	:	:
QY	61 DDRKFLEAQMTSFLFEGKDVEIEGFVPE	:	:	:	:

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.991 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-39

Perfect score: 466

Sequence: 1 MARTVNCVHINKKADGLDFQ.....QMTSFLFEGKQVEIRGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	466	100.0	92	1	FETP_SHEON	Q8bxb6 shevanelia
2	362	77.7	90	1	FETP_VIBVU	Q8dccc vibrio vuln
3	362	77.7	90	1	FETP_VIBVY	Q7mbi4 vibrio vuln
4	361	77.5	91	1	FETP_MANSN	Q65vt7 manheimia
5	360	77.3	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
6	359	77.0	90	1	FETP_PHOPR	Q6lmk7 photobacter
7	356	76.4	90	1	FETP_HAE18	P44048 haemophilus
8	356	76.4	90	2	Q4QMD9_HAE18	Q4qmd9 haemophilus
9	347	74.5	90	1	FETP_VIBCH	Q9kxur4 vibrio chol
10	346	74.2	90	1	FETP_VIBPA	Q87li5 vibrio para
11	345	74.0	90	1	FETP_PASMU	Q9cib9 pasteurella
12	341	73.2	90	1	FETP_IDILO	Q5qy58 idiomarina
13	338	72.5	90	1	FETP_ERWCT	Q6d8j9 erwinia car
14	336	72.1	94	1	FETP_HAEDU	Q7vkb6 haemophilus
15	331	71.0	90	1	FETP_SALCH	Q57k04 salmonella
16	331	71.0	90	1	FETP_SALPA	Q5pmn1 salmonella
17	331	71.0	90	1	FETP_SALTI	P67618 salmonella
18	331	71.0	90	1	FETP_SALTY	P67617 salmonella
19	330	70.8	90	1	FETP_ECOL6	Q8fel9 escherichia
20	327	70.2	90	1	FETP_ECOL7	P0a8p4 escherichia
21	327	70.2	90	1	FETP_ECOLI	P0a8p3 escherichia
22	327	70.2	90	1	FETP_SHIFL	P0a8p5 shigella fl
23	322	69.1	90	1	FETP_PHOUL	Q7n7i1 photorhabdu
24	316	67.8	90	1	FETP_YERPS	Q66m3 yersinia ps
25	308	66.1	90	1	FETP_YERPS	Q8zhe7 yersinia pe
26	257	55.2	90	1	FETP_NITBU	Q82xf2 nitrosomona
27	256	54.9	90	1	FETP_BORBR	Q7wh06 bordetella
28	256	54.9	90	1	FETP_BORPA	Q7w9q2 bordetella
29	256	54.9	90	1	FETP_BORPE	Q7wvc4 bordetella
30	240	51.5	90	2	Q4J228_AZOVI	Q4j228 azotobacter
31	237	50.9	90	1	FETP_PSEPK	Q88r49 pseudomonas

ALIGNMENTS

32	236	50.6	91	1	FETP_RALSO	Q8y010 ralstonia s
33	235	50.4	90	1	FETP_PSEAR	Q9hu36 pseudomonas
34	230	49.4	88	1	FETP_NEIG1	Q5f553 neisseria g
35	230	49.4	88	1	FETP_NEIMA	P67615 neisseria m
36	230	49.4	88	1	FETP_NEIMB	P67616 neisseria m
37	229	49.1	90	2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
38	228	48.9	90	1	FETP_PSESM	Q87uf5 pseudomonas
39	228	48.9	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
40	227	48.7	91	2	Q4LS19_9BURK	Q4ls19 pseudomonas
41	226	48.5	91	1	FETP_BURMA	Q62iur burkholderi
42	226	48.5	91	1	FETP_BURPS	Q63sj4 burkholderi
43	224	48.1	90	1	FETP_CHRVO	Q7nsr4 chromobacte
44	224	48.1	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
45	216	46.4	77	1	FETP_BUCAI	P57618 buchnera ap
46	215.5	46.2	89	1	FETP_LEGPI	Q5wvc4 legionella
47	215	46.1	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
48	215	46.1	90	1	FETP_METCA	Q60aj7 methylococc
49	213	45.7	90	1	FETP_XANAC	Q8pjh7 xanthomonas
50	211.5	45.4	89	1	FETP_LEGPA	Q5x3x9 legionella
51	211.5	45.4	89	1	FETP_LEGPH	Q5zu80 legionella
52	208	44.6	79	1	FETP_CANBF	Q5y729 candidatus
53	206	44.2	92	1	FETP_XANOR	Q5y722 xanthomonas
54	205	44.0	90	1	FETP_COXBU	Q83d06 coxiella bu
55	203	43.6	92	1	FETP_XANCP	Q8p829 xanthomonas
56	203	43.6	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
57	199	42.7	78	1	FETP_BUCAP	Q8k925 buchnera ap
58	197.5	42.4	90	1	FETP_AC1AD	Q6f6d3 acinetobact
59	196	42.1	90	1	FETP_XYLFA	Q9pc73 xyliella fas
60	196	42.1	90	1	FETP_XYLFT	Q87d06 xyliella fas
61	185	39.7	87	1	FETP_FRATT	Q5nh18 francisella
62	181	38.8	87	1	FETP_BUCBP	Q89a44 buchnera ap
63	148.5	31.9	92	2	Q4NMQ4_9DELT	Q4nwq4 anaeromyxob
64	131	28.1	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	92	19.7	507	2	Q4YI97_PLABE	Q4y197 plasmodium
66	92	19.7	1132	2	Q4Z7L5_PLABR	Q4z7l5 plasmodium
67	81	17.4	1096	2	Q7RTB1_PLAYO	Q7rtel plasmodium
68	77.5	16.6	2155	2	Q8IX99_HUMAN	Q8ix99 homo sapien
69	77.5	16.6	2364	1	SPTB2_HUMAN	Q01082 homo sapien
70	76.5	16.4	546	2	Q4MPZ8_BACCE	Q4mpz8 bacillus ce
71	75.5	16.2	2154	2	Q9QWJ7_MOUSE	Q9qwj7 mus musculu
72	75.5	16.2	2154	2	Q5SQL9_MOUSE	Q5sq19 mus musculu
73	75.5	16.2	2314	2	Q53R99_HUMAN	Q53r99 homo sapien
74	75.5	16.2	2363	2	Q5SQL8_MOUSE	Q5sq18 mus musculu
75	75.5	16.2	2377	2	Q59ER3_HUMAN	Q59er3 homo sapien

RESULT 1

ID	FETP_SHEON	STANDARD;	PRT;	92 AA.
AC	Q8EBX6;			
DT	10-OCT-2003 (Rel. 42, Created)			
DT	10-OCT-2003 (Rel. 42, Last sequence update)			
DT	13-SEP-2005 (Rel. 48, Last annotation update)			
DE	Probable Fe(2+) trafficking protein.			
GN	OrderedLocusNames=SO33369;			
OS	Shewanella oneidensis.			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;			
OC	Shewanellaceae; Shewanella.			
OX	NCBI_TaxID=70863;			
RN	[1]			
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].			
RC	STRAIN=MR-1;			
RX	MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;			
RA	Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,			
RA	Read T.D., Eissen J.A., Seshadri R., Ward N.L., Methe B.A.,			
RA	Clayton R.A., Meyer T., Tsapin A., Scott J., Beanan M.J.,			
RA	Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,			
RA	Hatt D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,			
RA	White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,			
RA	Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,			

RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT *Shewanella oneidensis*.";
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; AE015774; AAN56367.1; -; Genomic_DNA.
DR TIGR; SO3369; -;
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 92 AA; 10742 MW; 3116B2E995289B86.CRC64;

Query Match 100.0%; Score 466; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60

QY 61 DDRKFLAQMSTSLFEGKDVEIEGFVP 88
Db 61 DDRKFLAQMSTSLFEGKDVEIEGFVP 88

RESULT 2
FETP_VIBVU STANDARD; PRT; 90 AA.
ID FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DCG5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=V11514;
OS *Vibrio vulnificus*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.E.;
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.

CC EMBL; AE016801; AA009940.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.

DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C.CRC64;

Query Match 77.7%; Score 362; DB 1; Length 90;
Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGDLGKRIFDNISKEAWGQWQKQTMLINEKLNMMNP 60

QY 61 DDRKFLAQMSTSLFEGKDVEIEGFVP 87
Db 61 EHRKLETEMVNFLFEGKEVHIEGYTP 87

RESULT 3
FETP_VIBVU STANDARD; PRT; 90 AA.
ID FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q7MH14;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=V2885;
OS *Vibrio vulnificus* (strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of *Vibrio vulnificus*, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

CC EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C.CRC64;

Query Match 77.7%; Score 362; DB 1; Length 90;
Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGDLGKRIFDNISKEAWGQWQKQTMLINEKLNMMNP 60

QY 61 DDRKFLAQMSTSLFEGKDVEIEGFVP 87
Db 61 EHRKLETEMVNFLFEGKEVHIEGYTP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.6595 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-39
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLRKGKDVIRIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	346	74.2	93	2	US-09-543-681A-5443
2	327	70.2	107	2	US-09-489-039A-11962
3	235	50.4	122	2	US-09-252-991A-23355
4	200.5	43.0	92	2	US-09-328-352-5456
5	130	27.9	110	2	US-09-540-236-2859
6	77.5	16.6	2364	2	US-09-538-092-1243
7	75.5	16.2	2154	1	US-08-841-349-4
8	75.5	16.2	2154	2	US-09-431-184A-4
9	68	14.6	359	1	US-09-092-770-6
10	68	14.6	359	2	US-09-222-851-6
11	68	14.6	359	2	US-10-265-062-6
12	68	14.6	404	1	US-09-092-770-3
13	68	14.6	404	2	US-09-222-851-3
14	68	14.6	404	2	US-10-265-062-3
15	68	14.6	407	2	US-09-949-016-11184
16	64	13.7	373	2	US-09-071-035-116
17	64	13.7	373	2	US-10-206-576-116
18	64	13.7	406	2	US-09-071-035-114
19	64	13.7	406	2	US-10-206-576-114
20	64	13.7	557	2	US-09-134-000C-4354
21	63	13.5	369	2	US-09-096-779-5
22	62.5	13.4	182	2	US-09-248-796A-17806
23	62.5	13.4	278	2	US-09-567-003C-23
24	62	13.3	309	2	US-09-248-796A-14939
25	62	13.3	525	2	US-09-540-236-2250
26	62	13.3	911	2	US-09-949-002-425
27	62	13.3	1006	2	US-09-023-905A-12

28	62	13.3	1006	2	US-09-949-002-361	Sequence 361, App
29	61.5	13.2	583	2	US-09-538-092-1071	Sequence 1071, Ap
30	61.5	13.2	688	2	US-09-113-750A-3	Sequence 3, Appli
31	61.5	13.2	1143	2	US-09-949-016-6137	Sequence 6137, Ap
32	61.5	13.2	3878	2	US-09-914-259-11	Sequence 11, Appli
33	61	13.1	139	2	US-09-710-279-1310	Sequence 1310, Ap
34	61	13.1	168	2	US-09-134-001C-5599	Sequence 5599, Ap
35	61	13.1	184	2	US-09-325-932A-66	Sequence 66, Appli
36	61	13.1	403	1	US-09-092-770-4	Sequence 4, Appli
37	61	13.1	403	2	US-09-222-851-4	Sequence 4, Appli
38	61	13.1	403	2	US-10-265-062-4	Sequence 5351, Ap
39	61	13.1	901	2	US-09-134-001C-5351	Sequence 4036, Ap
40	61	13.1	1078	2	US-09-583-110-4036	Sequence 4843, Ap
41	61	13.1	1080	2	US-09-107-433-4843	Sequence 6045, Ap
42	61	13.1	1295	2	US-09-328-352-6045	Sequence 84, Appli
43	60.5	13.0	526	2	US-09-071-035-84	Sequence 84, Appli
44	60.5	13.0	526	2	US-10-206-576-84	Sequence 82, Appli
45	60.5	13.0	546	2	US-09-071-035-82	Sequence 82, Appli
46	60.5	13.0	546	2	US-10-206-576-82	Sequence 82, Appli
47	60.5	13.0	586	2	US-09-040-725A-1	Sequence 1, Appli
48	60	12.9	301	2	US-09-107-532A-4953	Sequence 4953, Ap
49	59.5	12.8	92	2	US-09-513-999C-5393	Sequence 5393, Ap
50	59.5	12.8	191	2	US-09-270-767-33624	Sequence 33624, A
51	59.5	12.8	191	2	US-09-270-767-48841	Sequence 48841, A
52	59.5	12.8	305	2	US-09-248-796A-18731	Sequence 18731, A
53	59.5	12.8	380	2	US-09-902-540-15247	Sequence 15247, A
54	59.5	12.8	1078	2	US-09-949-016-11185	Sequence 11185, A
55	59.5	12.8	1085	1	US-08-431-080-28	Sequence 28, Appli
56	59.5	12.8	1085	1	US-08-938-534-28	Sequence 28, Appli
57	59.5	12.8	1085	1	US-08-938-534-28	Sequence 28, Appli
58	59.5	12.7	66	2	US-09-107-532A-4003	Sequence 4003, Ap
59	59	12.7	336	2	US-09-252-991A-28882	Sequence 28882, A
60	59	12.7	376	2	US-09-248-796A-14887	Sequence 14887, A
61	59	12.7	579	2	US-09-949-016-10483	Sequence 10483, A
62	59	12.7	580	2	US-09-248-796A-25118	Sequence 25118, A
63	59	12.7	750	2	US-10-104-047-2432	Sequence 2432, Ap
64	59	12.7	793	1	US-08-468-558-5	Sequence 5, Appli
65	59	12.7	793	2	US-08-676-444-5	Sequence 5, Appli
66	59	12.7	982	2	US-09-023-905A-7	Sequence 7, Appli
67	58.5	12.6	301	2	US-09-543-681A-8264	Sequence 8264, Ap
68	58.5	12.6	342	2	US-09-107-532A-5496	Sequence 5496, Ap
69	58.5	12.6	548	2	US-09-167-299-3	Sequence 3, Appli
70	58.5	12.6	867	2	US-10-104-047-3052	Sequence 3052, Ap
71	58	12.4	170	2	US-10-101-464A-617	Sequence 617, App
72	58	12.4	228	2	US-09-328-352-7306	Sequence 7306, Ap
73	58	12.4	245	2	US-09-902-540-11576	Sequence 11576, A
74	58	12.4	296	2	US-09-100-804-12	Sequence 12, Appli
75	58	12.4	336	2	US-09-848-294-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 74.2%; Score 346; DB 2; Length 93;
Best Local Similarity 73.6%; Pred. No. 2.4e-38;
Matches 64; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 4 MSRTIFCTFLNKEADGLDFQLYPGBELGKRIFNEISKEAWGQMAKQTMLINEKLTNTMP 63

QY 61 DDRKFLAQMSTFLFEGKDVIEIGFVP 87
Db 64 DDRKLEQEMVRFLFEGHDVHIDGYTP 90

RESULT 2
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 70.2%; Score 327; DB 2; Length 107;
Best Local Similarity 69.0%; Pred. No. 1e-35;
Matches 60; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 17 MSRTIFCTFLQREADGQDFQLYPGBELGKRITNEISKEAWAQWQHQTMLINEKLSMNP 76

QY 61 DDRKFLAQMSTFLFEGKDVIEIGFVP 87
Db 77 EHRKLEQEMVQFLFEGKDVHIEGYTP 103

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 50.4%; Score 235; DB 2; Length 122;
Best Local Similarity 52.3%; Pred. No. 2.1e-23;
Matches 46; Conservative 18; Mismatches 22; Indels 2; Gaps 2;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60

Db 33 MSRTVMCRKTHEELPGDLRPPYPGAAGEDIYNNVSRKAWDEWQKHQTMLINEKRLNMMNA 92

QY 61 DDRKFLAQMSTFLFEGKD-VEIEGFVP 87
Db 93 EDRKFLQEMDKFL-SGEDYAKADGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 43.0%; Score 200.5; DB 2; Length 92;
Best Local Similarity 46.1%; Pred. No. 5.7e-19;
Matches 41; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
Db 4 MSRQVFCRKYQKEMEGLDFAFPFGAKGQEFBNVSKQAWQEWLQHQTMLINEKRLNVFEP 63

QY 61 DDRKFLAQMSTFLFEGKDV-IEGFVPE 88
Db 64 EAKKFLBQREKFPNNDSEVEKAEGWKPE 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540, 236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

Query Match 27.9%; Score 130; DB 2; Length 110;
Best Local Similarity 40.9%; Pred. No. 1.8e-09;
Matches 27; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 22 YPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNVDRKFLAQMSTFLFEGKDV 81
Db 42 FPNAGQEIQDTISAKAWNAWLELQTMLINEKLSMIDPQAKYLINEQREKFLNDGYEK 101

QY 82 IEGFVP 87
Db 102 PAGYKP 107

RESULT 6
US-09-538-092-1243
; Sequence 1243, Application US/09538092

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:34:35 ; Search time 55.062 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-39
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFEKDVIEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA_Main:
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	356	76.4	87 3 US-09-955-502-7	Sequence 7, Appli
3	347	74.5	90 3 US-09-955-502-10	Sequence 10, Appli
4	345	74.0	87 3 US-09-955-502-6	Sequence 6, Appli
5	344	73.8	91 3 US-09-955-502-5	Sequence 5, Appli
6	336	72.1	87 3 US-09-955-502-8	Sequence 8, Appli
7	336	72.1	88 3 US-09-955-502-15	Sequence 15, Appli
8	336	72.1	91 3 US-09-955-502-14	Sequence 14, Appli
9	336	72.1	91 3 US-09-955-502-17	Sequence 16, Appli
10	336	72.1	91 3 US-09-955-502-11	Sequence 17, Appli
11	332	71.2	91 3 US-09-955-502-12	Sequence 11, Appli
12	332	71.2	91 3 US-09-955-502-13	Sequence 12, Appli
13	332	71.2	91 3 US-09-955-502-18	Sequence 13, Appli
14	326	70.0	91 3 US-09-955-502-20	Sequence 18, Appli
15	308	66.1	90 3 US-09-955-502-19	Sequence 20, Appli
16	292	62.7	78 3 US-09-955-502-2	Sequence 19, Appli
17	256	54.9	87 3 US-09-955-502-3	Sequence 2, Appli
18	256	54.9	87 3 US-09-955-502-4	Sequence 3, Appli
19	242.5	52.0	86 3 US-09-955-502-24	Sequence 4, Appli
20	237	50.9	87 3 US-09-955-502-25	Sequence 25, Appli
21	235	50.4	87 3 US-09-955-502-26	Sequence 24, Appli
22	230	49.4	88 3 US-09-955-502-27	Sequence 26, Appli
23	230	49.4	88 3 US-09-955-502-28	Sequence 27, Appli
24	230	49.4	88 3 US-09-955-502-29	Sequence 28, Appli
25	228	48.9	90 3 US-09-955-502-23	Sequence 23, Appli
26	226	48.5	87 3 US-09-955-502-29	Sequence 29, Appli
27	226	48.5	87 3 US-09-955-502-30	Sequence 30, Appli

28	216	46.4	76	3	US-09-955-502-21	Sequence 21, Appli
29	215	46.1	87	3	US-09-955-502-32	Sequence 32, Appli
30	213	45.7	87	3	US-09-955-502-31	Sequence 31, Appli
31	205	44.0	88	3	US-09-955-502-33	Sequence 33, Appli
32	196	42.1	89	3	US-09-955-502-22	Sequence 22, Appli
33	177.5	16.6	2364	4	US-10-170-385-15	Sequence 15, Appli
34	75.5	16.2	1630	4	US-10-408-765A-2431	Sequence 2431, Ap
35	75.5	16.2	2154	4	US-10-695-994-4	Sequence 4, Appli
36	75.5	16.2	2154	5	US-10-805-684-150	Sequence 150, App
37	69	14.8	921	5	US-10-732-923-3305	Sequence 3305, Ap
38	68	14.6	315	5	US-10-510-628-4	Sequence 4, Appli
39	68	14.6	359	4	US-10-265-062-6	Sequence 6, Appli
40	68	14.6	359	4	US-10-755-889-324	Sequence 324, App
41	68	14.6	374	5	US-10-732-923-2938	Sequence 2938, Ap
42	68	14.6	404	4	US-10-265-062-3	Sequence 3, Appli
43	68	14.6	404	5	US-10-732-923-2939	Sequence 2939, Ap
44	68	14.6	737	5	US-10-510-628-2	Sequence 2, Appli
45	66.5	14.3	689	4	US-10-369-493-17280	Sequence 17280, A
46	66	14.2	307	4	US-10-264-237-2647	Sequence 2647, Ap
47	66	14.2	316	4	US-10-094-749-2195	Sequence 2195, Ap
48	66	14.2	321	4	US-10-308-279-58	Sequence 58, Appli
49	66	14.2	321	4	US-10-126-103-126	Sequence 126, App
50	66	14.2	321	4	US-10-431-096-126	Sequence 126, App
51	66	14.2	321	5	US-10-719-993-655	Sequence 655, App
52	66	14.2	321	5	US-10-719-993-656	Sequence 656, App
53	66	14.2	321	5	US-10-974-440-57	Sequence 57, Appli
54	66	14.2	344	4	US-10-050-704-281	Sequence 281, App
55	66	14.2	344	4	US-10-798-512-281	Sequence 281, App
56	66	14.2	348	4	US-10-050-704-129	Sequence 129, App
57	66	14.2	348	4	US-10-798-512-129	Sequence 129, App
58	66	14.2	355	4	US-10-424-599-264222	Sequence 264222, A
59	66	14.2	395	5	US-10-501-282-5848	Sequence 5848, Ap
60	65.5	14.1	85	4	US-10-425-115-325713	Sequence 325713, A
61	65.5	14.1	364	4	US-10-282-122A-63394	Sequence 2841, Ap
62	65.5	14.1	806	4	US-10-264-049-2841	Sequence 1407, Ap
63	65	13.9	305	4	US-10-296-115-1407	Sequence 8852, Ap
64	65	13.9	477	4	US-10-369-493-8852	Sequence 19695, A
65	65	13.9	483	5	US-10-732-923-19695	Sequence 5, Appli
66	65	13.9	505	4	US-10-250-613-5	Sequence 538, App
67	65	13.9	687	5	US-10-370-715B-538	Sequence 153968, A
68	64.5	13.8	357	4	US-10-424-599-153968	Sequence 153969, A
69	64.5	13.8	357	4	US-10-424-599-153969	Sequence 48667, A
70	64.5	13.8	393	4	US-10-282-122A-48667	Sequence 50306, A
71	64.5	13.8	593	5	US-10-450-763-50306	Sequence 173299, App
72	64.5	13.8	946	4	US-10-437-963-173299	Sequence 278, App
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ALIGNMENTS

RESULT 1
US-09-955-502-9
; Sequence 9, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 9
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Shewanella putrefaciens

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.66291 Seconds
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280.957 Million cell updates/sec

Title: US-09-955-502A-39

Perfect score: 466

Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFEGRDVEIEGFVPE 88

Scoring table:

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Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	68	14.6	359	7	US-11-087-227-8
3	68	14.6	359	7	US-11-192-450-6
4	68	14.6	404	7	US-11-087-227-6
5	68	14.6	404	7	US-11-192-450-3
6	62	13.3	593	7	US-11-194-246-317
7	61	13.1	139	6	US-10-793-626-1310
8	61	13.1	403	7	US-11-192-450-4
9	60	12.9	296	7	US-11-087-227-10
10	59.5	12.8	577	7	US-11-072-175-187
11	59	12.7	750	7	US-11-072-512-2432
12	58.5	12.6	867	7	US-11-072-512-3052
13	57.5	12.3	468	7	US-11-167-273-1
14	56	12.0	539	6	US-10-793-626-888
15	55.5	11.9	312	6	US-10-793-626-1210
16	55	11.8	266	5	US-09-995-493-6
17	55	11.8	731	6	US-10-613-744-10
18	54.5	11.7	588	6	US-10-793-626-3328
19	54.5	11.7	1432	6	US-10-510-386-218
20	54	11.6	125	7	US-11-098-686-10739
21	54	11.6	205	6	US-10-498-026-83
22	54	11.6	304	7	US-11-156-084-274
23	54	11.6	354	7	US-11-019-711-198
24	54	11.6	391	6	US-10-623-155-110
25	54	11.6	391	7	US-11-019-711-63

26	54	11.6	400	6	US-10-623-155-112	Sequence 112, App
27	54	11.6	400	7	US-11-019-711-12	Sequence 12, Appl
28	54	11.6	400	7	US-11-019-711-14	Sequence 14, Appl
29	54	11.6	466	6	US-10-524-647-114	Sequence 114, App
30	54	11.6	466	6	US-10-524-972-102	Sequence 102, App
31	54	11.6	508	7	US-11-072-512-2186	Sequence 2186, Ap
32	54	11.6	648	6	US-10-467-657-2802	Sequence 2802, Ap
33	54	11.6	829	6	US-10-909-769-26	Sequence 26, Appl
34	53.5	11.5	267	7	US-11-052-554A-219	Sequence 219, App
35	53.5	11.5	326	6	US-10-485-517-306	Sequence 306, App
36	53.5	11.5	340	7	US-11-165-226-128	Sequence 128, App
37	53.5	11.5	734	6	US-10-995-561-770	Sequence 770, App
38	53.5	11.5	756	7	US-11-074-176-202	Sequence 202, App
39	53.5	11.5	765	7	US-11-120-308-84	Sequence 84, Appl
40	53.5	11.5	782	6	US-10-793-626-2352	Sequence 2352, Ap
41	53.5	11.5	818	7	US-11-120-308-94	Sequence 94, Appl
42	53	11.4	177	6	US-10-467-657-1658	Sequence 1658, Ap
43	53	11.4	259	7	US-11-180-418-4	Sequence 4, Appli
44	53	11.4	269	7	US-11-180-418-3	Sequence 3, Appli
45	53	11.4	308	7	US-11-180-418-2	Sequence 2, Appli
46	53	11.4	391	7	US-11-019-711-61	Sequence 61, Appl
47	53	11.4	400	7	US-11-019-711-10	Sequence 10, Appl
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53	53	11.4	2721	7	US-11-096-051-10	Sequence 10, Appl
54	53	11.4	2725	7	US-11-096-051-8	Sequence 8, Appli
55	52.5	11.3	1122	6	US-10-467-657-6112	Sequence 6112, Ap
56	52	11.2	325	7	US-11-074-176-368	Sequence 368, App
57	52	11.2	359	6	US-10-055-877-265	Sequence 265, App
58	52	11.2	359	7	US-11-080-091-1	Sequence 1, Appli
59	52	11.2	359	7	US-11-116-939-15	Sequence 15, Appl
60	52	11.2	359	7	US-11-087-177-23	Sequence 23, Appl
61	52	11.2	359	7	US-11-087-177-25	Sequence 25, Appl
62	52	11.2	359	7	US-11-087-177-29	Sequence 29, Appl
63	52	11.2	364	7	US-11-087-177-31	Sequence 31, Appl
64	52	11.2	364	7	US-11-087-177-33	Sequence 33, Appl
65	52	11.2	365	7	US-11-087-177-27	Sequence 27, Appl
66	52	11.2	386	7	US-11-072-512-2777	Sequence 2777, Ap
67	52	11.2	405	7	US-11-072-512-3581	Sequence 3581, Ap
68	52	11.2	588	7	US-11-052-554A-339	Sequence 339, App
69	52	11.2	640	6	US-10-467-657-4930	Sequence 4930, Ap
70	52	11.2	694	7	US-11-072-512-2469	Sequence 2469, Ap
71	52	11.2	717	6	US-10-793-626-3022	Sequence 3022, Ap
72	52	11.2	842	6	US-10-909-769-22	Sequence 22, Appl
73	52	11.2	893	7	US-11-072-512-3504	Sequence 3504, Ap
74	51.5	11.1	206	7	US-11-124-367A-316	Sequence 316, App
75	51.5	11.1	319	7	US-11-055-822-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.4%; Score 230; DB 6; length 88;
Best Local Similarity 49.4%; Pred. No. 9.2e-20;
Matches 44; Conservative 19; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLMOKQOTMLINEKKLNMNV 60
Db 1 MARMVFCVKLNKEAEGMKPPLPNELGKRIFENVSGEAWAATRHQOTMLINENRSLADP 60

QY 61 DDRKFLQAQMTSFLF-EGKVEIEGFVPE 88
Db 61 RAREYLAQOMEQYFFGDGADA-VQGYVPQ 88

RESULT 2

US-11-087-227-8
; Sequence 8, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:

; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 8
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-8

Query Match 14.6%; Score 68; DB 7; length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKEAWGLMOKQOTMLINEKKLNMNV 60
Db 76 HKEIGTSDFSRFTNYRFKNLFINPSPPLDLSWGCSKEVWLNLMLKKESRYVHDKHFVLAHS 135

QY 61 DDRKFLQAQMTSFLFE 76
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RESULT 3

US-11-192-450-6
; Sequence 6, Application US/11192450
; Publication No. US20050282150A1
; GENERAL INFORMATION:

; APPLICANT: Coats, Steven R.
; APPLICANT: Baas, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: Novel Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/11/192,450
; CURRENT FILING DATE: 2005-07-28
; PRIOR APPLICATION NUMBER: US/10/265,062
; PRIOR FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US/09/442,919
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 09/222,851

; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/092,770
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
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; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Human
US-11-192-450-6

Query Match 14.6%; Score 68; DB 7; length 359;
Best Local Similarity 27.6%; Pred. No. 1.8;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKEAWGLMOKQOTMLINEKKLNMNV 60
Db 76 HKEIGTSDFSRFTNYRFKNLFINPSPPLDLSWGCSKEVWLNLMLKKESRYVHDKHFVLAHS 135

QY 61 DDRKFLQAQMTSFLFE 76
Db 136 D-----LEPQMRSLILD 147

RESULT 4

US-11-087-227-6
; Sequence 6, Application US/11087227
; Publication No. US20050260566A1
; GENERAL INFORMATION:

; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adriann J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 6
; LENGTH: 404
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-087-227-6

Query Match 14.6%; Score 68; DB 7; length 404;
Best Local Similarity 27.6%; Pred. No. 2.1;
Matches 21; Conservative 12; Mismatches 29; Indels 14; Gaps 2;

QY 11 NKEADGLDFQLYPGDLGKRIFDN-----ISKEAWGLMOKQOTMLINEKKLNMNV 60
Db 76 HKEIGTSDFSRFTNYRFKNLFINPSPPLDLSWGCSKEVWLNLMLKKESRYVHDKHFVLAHS 135

QY 61 DDRKFLQAQMTSFLFE 76
Db 136 D-----LEPQMRSLILD 147

RESULT 5

US-11-192-450-3
; Sequence 3, Application US/11192450
; Publication No. US20050282150A1
; GENERAL INFORMATION:

; APPLICANT: Coats, Steven R.
; APPLICANT: Baas, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: Novel Cyclin E Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/11/192,450
; CURRENT FILING DATE: 2005-07-28

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 70.7181 Seconds

(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477
Sequence: 1 MSRTVMCRKYHEELPGIDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21:*

- 1: geneseqp19808:*
- 2: geneseqp19908:*
- 3: geneseqp20008:*
- 4: geneseqp20018:*
- 5: geneseqp20028:*
- 6: geneseqp20038:*
- 7: geneseqp20048:*
- 8: geneseqp20058:*
- 9: geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	87	5	ABB78170 Amino aci
2	477	100.0	122	7	ABO74609 Pseudomon
3	408	85.5	90	5	ABB78168 Amino aci
4	400	83.9	87	5	ABB78169 Amino aci
5	262.5	55.0	92	6	ADA34169 Acinetoba
6	242	50.7	87	5	ABB78176 Amino aci
7	241	50.5	89	9	AEB41576 L. pneumo
8	241	50.5	95	9	AEB38294 L. pneumo
9	240	50.3	87	5	ABB78148 Amino aci
10	240	50.3	87	5	ABB78147 Amino aci
11	236	49.5	87	5	ABB78152 Amino aci
12	235	49.3	87	5	ABB78177 Amino aci
13	235	49.3	88	5	ABB78154 Amino aci
14	235	49.3	110	8	ADL05173 M. catarr
15	233	48.8	91	5	ABB78150 Amino aci
16	231	48.4	91	5	ABB78158 Amino aci
17	231	48.4	91	5	ABB78157 Amino aci
18	231	48.4	91	5	ABB78156 Amino aci
19	230	48.2	87	5	ABB78151 Amino aci
20	230	48.2	93	7	ADF05158 Bacterial
21	228	47.8	88	5	ABB78160 Amino aci
22	228	47.8	91	5	ABB78161 Amino aci
23	228	47.8	91	5	ABB78159 Amino aci
24	228	47.8	91	5	ABB78162 Amino aci

25	227	47.6	87	5	ABB78175 Amino aci
26	223	46.8	90	5	ABB78155 Amino aci
27	223	46.8	107	7	ABO65445 Klebsiell
28	222.5	46.6	86	5	ABB78149 Amino aci
29	222	46.5	87	5	ABB78153 Amino aci
30	221	46.3	87	5	ABB78174 Amino aci
31	221	46.3	91	5	ABB78163 Amino aci
32	220	46.1	88	5	ABB78178 Amino aci
33	211	44.2	78	5	ABB78164 Amino aci
34	210	44.0	90	5	ABB78165 Amino aci
35	207	43.4	88	5	ABB78171 Amino aci
36	207	43.4	88	5	ABB78172 Amino aci
37	207	43.4	88	5	ABB78173 Amino aci
38	207	43.4	88	6	ABP77219 N. gonorr
39	182.5	38.3	90	5	ABB78167 Amino aci
40	175	36.7	76	5	ABB78166 Amino aci
41	75	15.7	681	8	ADN73327 Thale cre
42	73	15.3	158	3	AAQ10836 Arabidops
43	73	15.3	487	8	ADN74065 Thale cre
44	73	15.3	500	5	AAE27877 Arabidops
45	72.5	15.2	333	4	ABB63075 Pseudomon
46	72	15.1	314	7	AAO23396 Plant ful
47	72	15.1	732	8	ADX92564 Polypepti
48	72	15.1	1043	8	ADM48031 Helicobac
49	71.5	15.0	506	2	AAQ97281 Protein s
50	71.5	15.0	2000	6	ABR52698 Disease t
51	71.5	15.0	2000	7	ADK61900 Protein e
52	70.5	14.8	401	6	ABU24966 Human end
53	70	14.7	148	2	AAQ60188 Human onc
54	70	14.7	171	8	ADP64626 Human onc
55	70	14.7	185	8	ADP64627 Human onc
56	70	14.7	381	7	ADB65159 Human pro
57	70	14.7	400	3	AAE24352 Human pro
58	70	14.7	400	6	ABR47475 Breast ca
59	70	14.7	400	7	ADB75332 Prostata
60	70	14.7	400	9	ADY72549 Human GP7
61	70	14.7	401	3	AAQ91526 Human sec
62	70	14.7	401	3	AAQ99368 Human PRO
63	70	14.7	401	4	AAB66117 Protein O
64	70	14.7	401	4	AAU12414 Human PRO
65	70	14.7	401	4	AAE49770 Amyloid-b
66	70	14.7	401	4	AAE93295 Human pro
67	70	14.7	401	4	AAE88480 Human mem
68	70	14.7	401	5	ABP65020 Human pro
69	70	14.7	401	6	ABO17858 Novel hum
70	70	14.7	401	6	ABU81112 Human PRO
71	70	14.7	401	6	ABU66812 Human PRO
72	70	14.7	401	6	ABU59893 Novel sec
73	70	14.7	401	6	ABO25083 Human sec
74	70	14.7	401	6	ABU67088 Human sec
75	70	14.7	401	6	ADA46005 Novel hum

ALIGNMENTS

RESULT 1
ABB78170
ID ABB78170 standard; protein; 87 AA.
AC ABB78170;
XX 05-NOV-2002 (first entry)
DT Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
XX PN
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English:
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 477; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60
|||
Db 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60

QY 61 EDRKFLOQEMDKFLSGEDYAKADGYVP 87
|||
Db 61 EDRKFLOQEMDKFLSGEDYAKADGYVP 87

RESULT 2
ABO74609
ID ABO74609 standard; protein; 122 AA.
XX
AC ABO74609;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #6784.
XX
KM Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX WPI; 2003-615309/58.
DR

DR N-PSDB; ABD08180.
XX
XX Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
XX
PS Disclosure; SEQ ID NO 23355; 455pp; English.
XX

CC The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

SQ Sequence 122 AA;

Query Match 100.0%; Score 477; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60
|||
Db 33 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 92

QY 61 EDRKFLOQEMDKFLSGEDYAKADGYVP 87
|||
Db 93 EDRKFLOQEMDKFLSGEDYAKADGYVP 119

RESULT 3
ABB78168
ID ABB78168 standard; protein; 90 AA.
XX
AC ABB78168;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KM Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Pseudomonas syringae.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PT

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477

Sequence: 1 MSRTVMCRKYHBEPLGLDRP.....QEMDKPLSGEDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	477	100.0	90	2	H83003	conserved hypothet
2	236	49.5	90	2	C64013	hypothetical prote
3	231	48.4	91	2	A85954	hypothetical prote
4	231	48.4	91	2	A65082	hypothetical prote
5	231	48.4	91	2	F91108	hypothetical prote
6	228	47.8	91	2	AH0879	conserved hypothet
7	223	46.8	90	2	C82320	conserved hypothet
8	210	44.0	90	2	AI0116	conserved hypothet
9	207	43.4	88	2	H81014	conserved hypothet
10	192	40.3	105	2	C82624	conserved hypothet
11	175	36.7	93	2	E84994	hypothetical prote
12	80.5	16.9	314	2	JC5534	catechol 2,3-dioxy
13	73	15.3	500	2	E96739	hypothetical prote
14	72	15.1	435	2	D82905	hypothetical prote
15	71.5	15.0	314	2	S31402	catechol 2,3-dioxy
16	71.5	15.0	2748	2	S57976	nuclear migration
17	69	14.5	926	2	T24923	hypothetical prote
18	68.5	14.4	506	2	H64618	sigma-54 interacti
19	68	14.3	1083	1	S53048	alpha-mannosidase
20	68	14.3	1148	2	D85360	hypothetical prote
21	67	14.0	532	2	D97138	DNA replication pr
22	66.5	13.9	532	2	H72730	probable acyl-CoA
23	66	13.8	1638	2	D87749	protein unc-73b [i
24	66	13.8	2488	2	T42739	guanine nucleotide
25	65.5	13.7	314	2	JB0127	catechol 2,3-dioxy
26	65.5	13.7	342	2	T19021	probable inositol
27	65.5	13.7	2485	1	H71621	serine/threonine-S
28	65	13.6	468	2	T33857	hypothetical prote
29	64.5	13.5	523	2	S23384	protein kinase (EC

30	64.5	13.5	766	2	T48463	hypothetical prote
31	64	13.4	283	2	H86839	hypothetical prote
32	64	13.4	642	2	D96777	hypothetical prote
33	64	13.4	670	2	T29898	kinesin protein OS
34	64	13.4	1553	2	S67483	adenosinetriphosph
35	63.5	13.3	613	2	AH2398	hypothetical prote
36	63	13.2	331	2	G84646	hypothetical prote
37	63	13.2	506	2	F71895	hypothetical prote
38	63	13.2	900	2	T33734	spectrin beta-H ch
39	63	13.2	1645	2	A37792	hypothetical prote
40	62.5	13.1	316	2	T50027	annexin-like prote
41	62.5	13.1	433	2	G70345	hypothetical prote
42	62.5	13.1	637	2	S66236	acetylcholinestera
43	62.5	13.1	985	2	T10339	DNA-directed DNA p
44	62	13.0	244	2	C90580	DNA processing pro
45	62	13.0	442	2	B81418	adenylosuccinate 1
46	62	13.0	830	2	S56940	factor arrest prot
47	62	13.0	921	2	A83968	isoleucyl-tRNA sym
48	62	13.0	1290	1	DVBYS6	mating pheromone a
49	62	13.0	4063	2	T42993	probable spectrin
50	62	13.0	4101	2	T23630	hypothetical prote
51	61.5	12.9	218	2	C70536	hypothetical prote
52	61.5	12.9	455	2	D75043	seryl-tRNA synthet
53	61.5	12.9	509	2	T21512	hypothetical prote
54	61.5	12.9	767	2	T31558	hypothetical prote
55	61.5	12.9	1090	2	AG1749	glycosidase homolo
56	61.5	12.9	1091	2	AF1380	glycosidase homolo
57	61.5	12.9	1111	2	A86922	probable arabinosy
58	61.5	12.9	1120	2	H88449	protein F54D8.1 [i
59	61	12.8	284	2	G72662	hypothetical prote
60	61	12.8	367	2	E81379	probable membrane
61	61	12.8	378	2	H95045	mannitol-1-phospha
62	61	12.8	389	2	T14751	hypothetical prote
63	61	12.8	552	2	C83965	transposase (12) B
64	61	12.8	583	2	A70380	arginine-tRNA liga
65	61	12.8	964	2	T01860	reverse transcript
66	61	12.8	1203	2	A39607	DNA-directed RNA p
67	61	12.8	1232	2	D64413	cobalamin biosynth
68	61	12.8	1822	2	S44849	K12H4.8 protein -
69	60.5	12.7	71	2	H97137	hypothetical prote
70	60.5	12.7	299	2	T29546	protein SPE-11 - C
71	60.5	12.7	303	2	A64423	modification methy
72	60.5	12.7	460	2	G71117	serine-tRNA ligase
73	60.5	12.7	1067	2	D96545	probable DNA polym
74	60.5	12.7	1142	2	E96519	probable reverse t
75	60	12.6	150	2	F90212	hypothetical prote

ALIGNMENTS

RESULT 1

H83003 conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)

C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004

C/Accession: H83003
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lattig, K.; Llm,
.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A/Reference number: AB2950; MUID:20437337; PMID:10984043

A/Accession: H83003

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-90 <STO>

A/Cross-references: UNIPARC:UPI00000C5F26; GB:AB004927; GB:AE004091; NID:G9951437; PIDN:J

A/Experimental source: strain PA01

C/Genetics:

A/Gene: PA5148

C/Superfamily: fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477
Sequence: 1 MSRTVMCRKTHBELPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	477	100.0	90	1	FETP_PSEAE
2	420	88.1	90	2	Q4J228_AZOVI
3	408	85.5	90	1	FETP_PSESM
4	408	85.5	90	2	Q4ZLP3_PSESY
5	401	84.1	90	2	Q4KJ72_PSEFS
6	400	83.9	90	1	FETP_PSEPK
7	383	80.3	90	2	Q6T7F6_PSEFL
8	258.5	54.2	90	1	FETP_ACIAI
9	250	52.4	96	2	Q4FVJ7_9GAMM
10	245	51.4	90	1	FETP_IDILO
11	244	51.2	91	1	FETP_MANSN
12	241	50.5	89	1	FETP_LEGPA
13	241	50.5	89	1	FETP_LEGPH
14	240	50.3	89	1	FETP_LEGPI
15	240	50.3	90	1	FETP_BORPA
16	240	50.3	90	1	FETP_BORBR
17	240	50.3	90	1	FETP_BORPE
18	236	49.5	90	1	FETP_HABIN
19	236	49.5	90	2	Q4QMD9_HABE18
20	235	49.3	90	1	FETP_METCA
21	235	49.3	92	1	FETP_SHEON
22	233	48.8	90	1	FETP_VIBFI
23	230	48.2	90	1	FETP_PASMU
24	230	48.2	90	1	FETP_PHOHL
25	229	48.0	90	1	FETP_ERMCT
26	228	47.8	90	1	FETP_PHOPR
27	228	47.8	91	1	FETP_RALSO
28	227	47.6	90	1	FETP_NITEU
29	227	47.6	90	1	FETP_VIBVU
30	227	47.6	90	1	FETP_VIBVY
31	227	47.6	91	1	FETP_BURMA

32	227	47.6	91	1	FETP_BURPS	Q638j4 burkholderi
33	226	47.4	90	1	FETP_ECOS7	P0A8P4 escherichia
34	226	47.4	90	1	FETP_ECOT1	P0A8P5 shigella fl
35	226	47.4	90	1	FETP_SHIFL	Q418i9 burkholderi
36	224	47.0	91	2	Q4LS19_9BURK	Q57K04 salmonella
37	223	46.8	90	1	FETP_SALCH	Q57K04 salmonella
38	223	46.8	90	1	FETP_SALPA	Q57K04 salmonella
39	223	46.8	90	1	FETP_SALTI	Q57K04 salmonella
40	223	46.8	90	1	FETP_SALTI	Q57K04 salmonella
41	223	46.8	90	1	FETP_VIBGH	Q57K04 salmonella
42	222	46.5	90	1	FETP_ECOT6	Q57K04 salmonella
43	222	46.5	90	1	FETP_VIBPA	Q57K04 salmonella
44	222	46.5	94	1	FETP_HABDU	Q57K04 salmonella
45	220	46.1	90	1	FETP_COXBU	Q57K04 salmonella
46	218	45.7	90	1	FETP_YERPS	Q57K04 salmonella
47	215	45.1	78	1	FETP_WIGBR	Q57K04 salmonella
48	210	44.0	90	1	FETP_CHRVO	Q57K04 salmonella
49	210	44.0	90	1	FETP_YERPE	Q57K04 salmonella
50	208	43.6	92	1	FETP_XANOR	Q57K04 salmonella
51	207	43.4	88	1	FETP_NEIG1	Q57K04 salmonella
52	207	43.4	88	1	FETP_NEIMA	Q57K04 salmonella
53	207	43.4	88	1	FETP_NEIMA	Q57K04 salmonella
54	204	42.8	91	1	FETP_XANAC	Q57K04 salmonella
55	202	42.3	87	1	FETP_PRAIT	Q57K04 salmonella
56	197	41.3	92	1	FETP_XANCP	Q57K04 salmonella
57	197	41.3	92	2	Q4UW14_XANCP	Q57K04 salmonella
58	195	40.9	78	1	FETP_BUCAP	Q57K04 salmonella
59	193	40.5	90	1	FETP_XYLFT	Q57K04 salmonella
60	192	40.3	90	1	FETP_XYLFA	Q57K04 salmonella
61	190	39.8	79	1	FETP_CANBF	Q57K04 salmonella
62	175	36.7	77	1	FETP_BUCAI	Q57K04 salmonella
63	174	36.5	87	1	FETP_BUCBP	Q57K04 salmonella
64	171	35.8	92	2	Q4NWQ4_9DELT	Q57K04 salmonella
65	81.5	17.1	326	2	Q55GT4_DICDI	Q57K04 salmonella
66	80.5	16.9	314	2	Q7MOR6_BURCE	Q57K04 salmonella
67	79	16.6	703	2	Q4WPT2_ASPFU	Q57K04 salmonella
68	78.5	16.5	1097	1	KIFID_RAT	Q57K04 salmonella
69	78	16.4	410	2	Q8SRF4_ENCCU	Q57K04 salmonella
70	76.5	16.0	314	2	Q9RB85_9BURK	Q57K04 salmonella
71	75.5	15.8	280	2	Q81BK9_BACCR	Q57K04 salmonella
72	75	15.7	681	2	Q9LV16_ARATH	Q57K04 salmonella
73	74	15.5	525	2	Q6BNV8_DEBHA	Q57K04 salmonella
74	73.5	15.4	307	2	Q6BFB3_PARTE	Q57K04 salmonella
75	73.5	15.4	549	2	Q6BKE2_DEBHA	Q57K04 salmonella

ALIGNMENTS

RESULT 1
FETP_PSEAE
ID FETP_PSEAE STANDARD; PRT: 90 AA.
AC Q9HU36;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PA5148;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.,
RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an


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RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE004927; AAG08533.1; -; Genomic_DNA.
DR PDB; 1T07; X-ray; A=1-90.
DR SMR; Q9HU36; 1-79.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR 3D-structure; Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10625 MW; 02BB6CEBF7AEF39 CRC64;

Query Match 100.0%; Score 477; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.6e-42;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHBEPLGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60
DB 1 MSRTVMCRKYHBEPLGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYV 87
DB 61 EDRKFLQOEMDKFLSGEDYAKADGYV 87

RESULT 2
Q4J228_AZOVI
ID Q4J228_AZOVI PRELIMINARY; PRT; 90 AA.
AC Q4J228;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AvindRAFT_6916;
OS Azotobacter vinelandii AvOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AvOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AvOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laximer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AvOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AvOP;
RA DOE Joint Genome Institute;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR [4]

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RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AvOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pitluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAU0300001; EAM08363.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10777 MW; F6FE766143D3E5E1 CRC64;

Query Match 88.1%; Score 420; DB 2; Length 90;
Best Local Similarity 88.4%; Pred. No. 5.7e-36;
Matches 76; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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DB 1 MSRTVMCRKYHBEPLGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYV 86
DB 61 EDRKFLQOEMDKFLSGEDYAKADGYV 86

RESULT 3
FETP_PSESM
ID FETP_PSESM STANDARD; PRT; 90 AA.
AC Q87UF5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PSPT05343;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut U., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC removed.
CC -----
DR EMBL; AE016853; AAO58769.1; -; Genomic_DNA.
DR SMR; Q87UF5; 1-79.
DR TIGR; PSPT05343; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477

Sequence: 1 MSRTVMCRKRYHEBLPGLDLP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	477	100.0	122	2	US-09-252-991A-23355
2	262.5	55.0	92	2	US-09-328-352-5456
3	235	49.3	110	2	US-09-540-236-2859
4	230	48.2	93	2	US-09-543-681A-5443
5	223	46.8	107	2	US-09-489-039A-11962
6	72	15.1	314	2	US-09-716-865-4
7	71.5	15.0	506	1	US-08-849-480A-5
8	70	14.7	148	2	US-09-673-395A-389
9	70	14.7	381	2	US-10-104-047-3313
10	70	14.7	401	2	US-09-489-847-202
11	70	14.7	401	2	US-10-012-231A-100
12	70	14.7	401	2	US-10-015-389A-100
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16	70	14.7	401	2	US-10-011-833A-100
17	70	14.7	401	2	US-10-006-041A-100
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19	70	14.7	401	2	US-10-030-269A-8
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21	68	14.3	443	2	US-09-248-796A-16816
22	67.5	14.2	505	2	US-09-543-681A-7151
23	67	14.0	563	2	US-09-902-540-14552
24	66	13.8	361	2	US-09-134-001C-3862
25	65.5	13.7	375	2	US-09-583-110-4950
26	65.5	13.7	382	2	US-09-107-433-3837
27	65	13.6	163	2	US-09-270-767-33714

28	65	13.6	420	2	US-09-248-796A-15323	Sequence 15323, A
29	65	13.6	1042	2	US-09-792-024-106	Sequence 106, App
30	64.5	13.5	327	2	US-09-902-540-10864	Sequence 10864, A
31	64.5	13.5	343	2	US-09-270-767-41701	Sequence 41701, A
32	64.5	13.5	839	2	US-09-758-282B-232	Sequence 232, App
33	64.5	13.5	839	2	US-09-577-304A-232	Sequence 232, App
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38	63.5	13.3	1967	2	US-09-849-602-16	Sequence 16, Appl
39	63	13.2	254	2	US-09-586-106D-111	Sequence 111, App
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41	62.5	13.1	3542	2	US-10-087-013-2	Sequence 2, Appli
42	62	13.0	595	2	US-09-902-540-16334	Sequence 16334, A
43	61	12.8	193	2	US-09-252-991A-17828	Sequence 17828, A
44	61	12.8	378	2	US-09-583-110-3941	Sequence 3941, Ap
45	61	12.8	378	2	US-09-107-433-5197	Sequence 5197, Ap
46	61	12.8	381	2	US-09-949-016-9788	Sequence 9788, Ap
47	61	12.8	381	2	US-09-964-899-13	Sequence 13, Appl
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56	60	12.6	338	2	US-09-328-352-7427	Sequence 7427, Ap
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61	60	12.6	344	2	US-09-765-272A-192	Sequence 192, App
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64	60	12.6	375	2	US-09-107-433-4121	Sequence 4121, App
65	60	12.6	454	2	US-09-771-161A-95	Sequence 95, Appl
66	60	12.6	504	2	US-09-538-092-1170	Sequence 1170, Ap
67	60	12.6	505	2	US-09-949-016-6117	Sequence 6117, Ap
68	60	12.6	505	2	US-09-949-016-1186	Sequence 186, App
69	60	12.6	513	2	US-09-949-016-11517	Sequence 11517, A
70	60	12.6	531	2	US-09-540-236-2072	Sequence 2072, Ap
71	60	12.6	1122	2	US-10-146-704-2	Sequence 2, Appli
72	59.5	12.5	488	2	US-08-911-824-95	Sequence 95, Appl
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ALIGNMENTS

RESULT 1
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-40

Perfect score: 477
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Published Applications_AA_Main:*

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- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	477	100.0	87	3	US-09-955-502-25 Sequence 25, Appl
2	408	85.5	90	3	US-09-955-502-23 Sequence 23, Appl
3	400	83.9	87	3	US-09-955-502-24 Sequence 24, Appl
4	242	50.7	87	3	US-09-955-502-31 Sequence 31, Appl
5	240	50.3	87	3	US-09-955-502-2 Sequence 2, Appli
6	240	50.3	87	3	US-09-955-502-3 Sequence 3, Appli
7	236	49.5	87	3	US-09-955-502-7 Sequence 7, Appli
8	235	49.3	87	3	US-09-955-502-32 Sequence 32, Appli
9	235	49.3	88	3	US-09-955-502-9 Sequence 9, Appli
10	233	48.8	91	3	US-09-955-502-5 Sequence 5, Appli
11	231	48.4	91	3	US-09-955-502-11 Sequence 11, Appl
12	231	48.4	91	3	US-09-955-502-12 Sequence 12, Appl
13	231	48.4	91	3	US-09-955-502-13 Sequence 13, Appl
14	230	48.2	87	3	US-09-955-502-6 Sequence 6, Appli
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18	228	47.8	91	3	US-09-955-502-17 Sequence 17, Appl
19	227	47.6	87	3	US-09-955-502-29 Sequence 29, Appl
20	227	47.6	87	3	US-09-955-502-30 Sequence 30, Appl
21	223	46.8	90	3	US-09-955-502-10 Sequence 10, Appl
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23	222	46.5	87	3	US-09-955-502-8 Sequence 8, Appli
24	221	46.3	91	3	US-09-955-502-18 Sequence 18, Appl
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28	207	43.4	88	3	US-09-955-502-26 Sequence 26, Appl
29	207	43.4	88	3	US-09-955-502-27 Sequence 27, Appl
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32	175	36.7	76	3	US-09-955-502-21 Sequence 21, Appl
33	72.5	15.2	333	6	US-11-097-143-16017 Sequence 16017, A
34	72	15.1	732	4	US-10-425-114-55228 Sequence 55228, A
35	72	15.1	1043	4	US-10-310-154-449 Sequence 449, App
36	72	15.1	1043	5	US-10-732-923-535 Sequence 535, App
37	71	14.9	372	4	US-10-424-599-239645 Sequence 239645,
38	70.5	14.8	401	4	US-10-282-122A-52890 Sequence 52890, A
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42	70	14.7	400	5	US-10-759-803-2 Sequence 2, Appli
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44	70	14.7	400	6	US-11-051-454-156 Sequence 100, App
45	70	14.7	401	3	US-09-946-374-100 Sequence 486, App
46	70	14.7	401	4	US-10-028-072-486 Sequence 486, App
47	70	14.7	401	4	US-10-140-808-486 Sequence 486, App
48	70	14.7	401	4	US-10-121-049-486 Sequence 486, App
49	70	14.7	401	4	US-10-123-904-486 Sequence 486, App
50	70	14.7	401	4	US-10-140-470-486 Sequence 486, App
51	70	14.7	401	4	US-10-175-746-486 Sequence 486, App
52	70	14.7	401	4	US-10-176-918-486 Sequence 486, App
53	70	14.7	401	4	US-10-176-921-486 Sequence 486, App
54	70	14.7	401	4	US-10-137-865-486 Sequence 486, App
55	70	14.7	401	4	US-10-140-474-486 Sequence 486, App
56	70	14.7	401	4	US-10-142-431-486 Sequence 486, App
57	70	14.7	401	4	US-10-143-114-486 Sequence 486, App
58	70	14.7	401	4	US-10-006-856A-100 Sequence 100, App
59	70	14.7	401	4	US-10-142-419-486 Sequence 486, App
60	70	14.7	401	4	US-10-123-262-486 Sequence 486, App
61	70	14.7	401	4	US-10-142-423-486 Sequence 486, App
62	70	14.7	401	4	US-10-006-818A-100 Sequence 100, App
63	70	14.7	401	4	US-10-121-050-486 Sequence 486, App
64	70	14.7	401	4	US-10-141-755-486 Sequence 486, App
65	70	14.7	401	4	US-10-143-032-486 Sequence 486, App
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72	70	14.7	401	4	US-10-140-921-486 Sequence 486, App
73	70	14.7	401	4	US-10-140-928-486 Sequence 100, App
74	70	14.7	401	4	US-10-015-393A-100 Sequence 100, App
75	70	14.7	401	4	US-10-015-869A-100 Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-955-502-25
; Sequence 25, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234, 588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-40
Perfect score: 477
Sequence: 1 MSRTVMCRKYHEELPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	207	43.4	88	US-10-467-657-968	Sequence 968, App
2	70	14.7	381	US-11-072-512-3313	Sequence 3313, Ap
3	70	14.7	401	US-10-131-826A-486	Sequence 486, App
4	65	13.6	353	US-11-098-686-10774	Sequence 10774, A
5	64.5	13.5	1560	US-11-059-982-1	Sequence 1, Appli
6	60	12.6	370	US-10-873-528-160	Sequence 160, App
7	58.5	12.3	310	US-11-198-746-88	Sequence 88, Appl
8	58.5	12.3	310	US-11-198-794-88	Sequence 88, Appl
9	58.5	12.3	315	US-11-198-746-91	Sequence 91, Appl
10	58.5	12.3	315	US-11-198-794-91	Sequence 91, Appl
11	58.5	12.3	322	US-11-198-746-89	Sequence 89, Appl
12	58.5	12.3	322	US-11-198-794-89	Sequence 89, Appl
13	58.5	12.3	528	US-11-198-746-90	Sequence 90, Appl
14	58.5	12.3	528	US-11-198-794-90	Sequence 90, Appl
15	58.5	12.3	548	US-11-198-746-86	Sequence 86, Appl
16	58.5	12.3	548	US-11-198-794-86	Sequence 86, Appl
17	58.5	12.3	695	US-11-198-746-87	Sequence 87, Appl
18	58.5	12.3	695	US-11-198-794-87	Sequence 87, Appl
19	58.5	12.3	832	US-11-065-943-100	Sequence 100, App
20	58.5	12.3	832	US-11-007-797A-11	Sequence 11, Appl
21	58.5	12.3	832	US-11-007-642B-11	Sequence 11, Appl
22	58.5	12.3	832	US-11-198-746-4	Sequence 4, Appli
23	58.5	12.3	832	US-11-198-794-4	Sequence 4, Appli
24	58.5	12.3	832	US-11-242-730-1	Sequence 1, Appli
25	58.5	12.3	833	US-11-198-746-85	Sequence 85, Appl

26	58.5	12.3	833	7	US-11-198-794-85	Sequence 85, Appl
27	58	12.2	589	7	US-11-072-512-2914	Sequence 2914, Ap
28	58	12.2	1206	6	US-10-467-657-72	Sequence 72, Appl
29	58	12.2	1206	6	US-10-467-657-3892	Sequence 3892, Ap
30	57.5	12.1	383	6	US-10-793-626-2426	Sequence 2426, Ap
31	57.5	12.1	1077	7	US-11-054-281-110	Sequence 110, App
32	57	11.9	426	6	US-10-858-730-81	Sequence 81, Appl
33	57	11.9	456	7	US-11-069-642-8	Sequence 8, Appli
34	57	11.9	600	7	US-11-072-512-3845	Sequence 3845, Ap
35	57	11.9	645	6	US-10-510-386-32	Sequence 32, Appl
36	57	11.9	3748	7	US-11-132-686-8	Sequence 8, Appli
37	57	11.9	3749	7	US-11-132-686-6	Sequence 6, Appli
38	57	11.9	3749	7	US-11-132-686-12	Sequence 12, Appl
39	57	11.9	3912	7	US-11-132-686-7	Sequence 7, Appli
40	57	11.9	3913	7	US-11-132-686-5	Sequence 5, Appli
41	57	11.9	3913	7	US-11-132-686-9	Sequence 9, Appli
42	56.5	11.8	2871	7	US-11-124-367A-264	Sequence 264, App
43	56	11.7	315	6	US-10-878-556A-178	Sequence 178, App
44	56	11.7	333	6	US-10-821-234-1036	Sequence 1036, Ap
45	56	11.7	647	7	US-11-000-463-722	Sequence 722, App
46	56	11.7	1897	6	US-10-821-234-1635	Sequence 1635, Ap
47	56	11.7	1907	7	US-11-000-463-250	Sequence 250, App
48	55.5	11.6	357	7	US-11-053-100-33	Sequence 33, Appl
49	55.5	11.6	400	7	US-11-202-566-27	Sequence 27, Appl
50	55.5	11.6	526	7	US-11-055-822-124	Sequence 124, App
51	55.5	11.6	657	7	US-11-053-100-35	Sequence 35, Appl
52	55	11.5	211	7	US-11-124-368A-175	Sequence 175, App
53	55	11.5	211	7	US-11-124-368A-176	Sequence 176, App
54	55	11.5	395	6	US-10-793-626-656	Sequence 656, App
55	55	11.5	701	6	US-10-467-657-7872	Sequence 7872, Ap
56	55	11.5	805	6	US-10-485-517-198	Sequence 198, App
57	55	11.5	1386	7	US-11-091-643-6	Sequence 6, Appli
58	54.5	11.4	39	6	US-10-841-956A-3	Sequence 3, Appli
59	54.5	11.4	39	7	US-11-029-003-3	Sequence 3, Appli
60	54.5	11.4	40	7	US-11-112-277-34	Sequence 34, Appl
61	54.5	11.4	203	6	US-10-454-437-326	Sequence 326, App
62	54.5	11.4	415	6	US-10-763-712A-25	Sequence 25, Appl
63	54.5	11.4	436	6	US-10-763-712A-5	Sequence 5, Appli
64	54.5	11.4	746	7	US-11-072-175-169	Sequence 169, App
65	54	11.3	426	6	US-10-858-730-80	Sequence 80, Appl
66	54	11.3	3433	6	US-10-714-781A-67	Sequence 67, Appl
67	53.5	11.2	612	6	US-10-467-657-3988	Sequence 3988, Ap
68	53.5	11.2	1717	7	US-11-182-016-20	Sequence 20, Appl
69	53	11.1	120	6	US-10-793-626-958	Sequence 958, App
70	53	11.1	120	6	US-10-793-626-1444	Sequence 1444, Ap
71	53	11.1	383	7	US-11-072-512-3140	Sequence 3140, Ap
72	53	11.1	532	6	US-10-793-626-546	Sequence 546, App
73	53	11.1	618	7	US-11-110-082-25	Sequence 25, Appl
74	53	11.1	744	7	US-11-186-284-37	Sequence 37, Appl
75	53	11.1	744	7	US-11-186-284-39	Sequence 39, Appl

ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 : Search time 70.7181 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-41
Perfect score: 472
Sequence: 1 MTRVTMCRRYQSEELPGLERP.....AEMDKFPAGEEYQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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5: geneseqp2002s: *
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9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	400	84.7	122	7	ABO74609 Pseudomon
5	265.5	56.2	92	6	ADA34169 Acinetoba
6	239	50.6	87	5	ABB78177 Amino aci
7	237	50.2	87	5	ABB78176 Amino aci
8	237	50.2	88	5	ABB78154 Amino aci
9	232	49.2	89	9	ABB41576 Amino aci
10	232	49.2	95	9	ABB38294 L. pneumo
11	229	48.5	87	5	ABB78175 Amino aci
12	229	48.5	87	5	ABB78152 Amino aci
13	228	48.3	90	5	ABB78155 Amino aci
14	228	48.3	91	5	ABB78150 Amino aci
15	225	47.7	87	5	ABB78151 Amino aci
16	225	47.7	91	5	ABB78158 Amino aci
17	225	47.7	91	5	ABB78157 Amino aci
18	225	47.7	91	5	ABB78156 Amino aci
19	224	47.5	110	8	ADL05173 M. catarr
20	223	47.2	87	5	ABB78174 Amino aci
21	222	47.0	87	5	ABB78148 Amino aci
22	222	47.0	87	5	ABB78147 Amino aci
23	219	46.4	87	5	ABB78153 Amino aci
24	219	46.4	88	5	ABB78171 Amino aci

25	219	46.4	88	5	ABB78172 Amino aci
26	219	46.4	88	5	ABB78173 Amino aci
27	219	46.4	88	5	ABP77219 N. gonorr
28	218	46.2	88	5	ABB78160 Amino aci
29	218	46.2	91	5	ABB78161 Amino aci
30	218	46.2	91	5	ABB78159 Amino aci
31	218	46.2	91	5	ABB78162 Amino aci
32	213	45.1	107	7	ABO65445 Klebsiell
33	211	44.7	91	5	ABB78163 Amino aci
34	209	44.3	93	7	ADF05158 Bacterial
35	204.5	43.3	86	5	ABB78149 Amino aci
36	204	43.2	88	5	ABB78178 Amino aci
37	197.5	41.8	78	5	ABB78164 Amino aci
38	188.5	39.9	90	5	ABB78167 Amino aci
39	188	39.8	90	5	ABB78165 Amino aci
40	159	33.7	76	5	ABB78166 Amino aci
41	73	15.5	451	7	ADF07116 Bacterial
42	72	15.3	259	3	AAG43535 Arabidops
43	72	15.3	307	3	AAG43534 Arabidops
44	72	15.3	795	4	ABG07025 Novel hum
45	72	15.3	844	8	ADH71956 Human pro
46	72	15.3	844	8	ADH71960 Human pro
47	72	15.3	847	8	ADO54839 Rat prick
48	72	15.3	901	8	ADT49817 Murine lO
49	70	14.8	670	5	ADN23314 Bacteria
50	69.5	14.7	1091	5	ABBA48258 Listeria
51	69	14.6	247	6	ABU33468 Protein e
52	69	14.6	251	4	AAM93928 Human pol
53	69	14.6	251	8	ADL32064 Human pro
54	67.5	14.3	689	5	ABB49714 Listeria
55	67.5	14.3	689	5	ABU33095 Protein e
56	67	14.2	559	8	ADN21954 Bacterial
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58	66	14.0	140	5	ABB47391 Listeria
59	66	14.0	250	8	ADN47605 Thermococ
60	66	14.0	967	8	ADBS2670 Human pro
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62	66	14.0	1651	4	ABG14648 Novel hum
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66	65.5	13.9	484	9	ABB40396 L. pneumo
67	65.5	13.9	926	8	ADN24302 Bacterial
68	65	13.8	36946	9	ADV97835 Murine pr
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ALIGNMENTS

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AC	ABB78169;	
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DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Pseudomonas putida.	
XX		
PN	US2002072118-A1.	
XX		

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
XX (GERAL/) GRALNICK J A.
PI
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
SQ Sequence 87 AA;

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Query Match      100.0%; Score 472; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.8e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB       1 MTRITVCMCRYQEELPGLERPPYPGAKGQDIFEHISQKAWADWQKHQTMLIN EKRLNMNNA 60
        |||

QY      61 EDRKFLOAEMDKFPAGEEYAQAEGYVP 87
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DB       61 EDRKFLOAEMDKFPAGEEYAQAEGYVP 87

RESULT 2
ABB78168
ID      ABB78168 standard; protein; 90 AA.
XX
AC      ABB78168;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Amino acid sequence of a YggX homologue.
XX
KW      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM      hydroxyl radical; DNA damage; YggX homologue.
XX
OS      Pseudomonas syringae.
XX
PN      US2002072118-A1.
XX
PD      13-JUN-2002.
XX
PF      18-SEP-2001; 2001US-00955502.
XX
PR      22-SEP-2000; 2000US-0234588P.
XX
PA      (DOWN/) DOWNS D.
PA      (GRAL/) GRALNICK J A.
XX
PI      Downs D, Gralnick JA;
XX
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DR WPI, 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;

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Query Match.          91.5%; Score 432; DB 5; Length 90;
Best Local Similarity 88.5%; Pred. No. 2.2e-46;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Db      61 EDRKFLQTEMDKFLSGEEYQAQEGYVP 87

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RESULT 3
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ID ABB78170 standard; protein; 87 AA.
XX
AC ABB78170;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-41

Perfect score: 472
Sequence: 1 MTRIVMCRKYGELPGLERP.....AEMDKFFAGBRYAQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	400	84.7	90	2 H83003	conserved hypothet
2	229	48.5	90	2 C64013	hypothetical prote
3	228	48.3	90	2 C82320	conserved hypothet
4	225	47.7	91	2 A85954	hypothetical prote
5	225	47.7	91	2 A65082	hypothetical prote
6	225	47.7	91	2 F91108	hypothetical prote
7	219	46.4	88	2 H81014	conserved hypothet
8	218	46.2	91	2 AH0879	conserved hypothet
9	198	41.9	105	2 C82624	conserved hypothet
10	188	39.8	90	2 A10116	conserved hypothet
11	159	33.7	93	2 E84994	hypothetical prote
12	70	14.8	670	2 T29898	kinesin protein OS
13	69.5	14.7	1091	2 AF1380	glycosidase homolo
14	69	14.6	165	2 C75419	hypothetical prote
15	68.5	14.5	1090	2 AG1749	glycosidase homolo
16	68	14.4	388	1 QOYV	transforming prote
17	67.5	14.3	689	2 AC1408	transcription anti
18	66.5	14.1	1124	2 T30340	dsRNA adenosine de
19	66	14.0	140	2 AB1428	transcription regu
20	66	14.0	1553	2 S67483	adenosinetriphosph
21	65.5	13.9	926	2 T24923	hypothetical prote
22	65.5	13.9	959	2 H69344	hypothetical prote
23	65	13.8	528	2 T24730	hypothetical prote
24	64.5	13.7	767	2 T31558	hypothetical prote
25	64	13.6	140	2 A11801	transcription regu
26	64	13.6	732	2 S23001	transcription regu
27	63.5	13.5	288	2 T45715	trial protein - Bsc
28	63.5	13.5	397	2 C87470	hypothetical prote
29	63.5	13.5	689	2 AC1784	hypothetical prote

30	63	13.3	150	2 F90212	hypothetical prote
31	63	13.3	555	2 C87515	ABC transporter, A
32	63	13.3	559	2 T12680	peroxisomal target
33	63	13.3	561	2 T06628	hypothetical prote
34	63	13.3	568	2 G84455	hypothetical prote
35	62.5	13.2	352	2 F84799	hypothetical prote
36	62.5	13.2	677	2 G69895	formate dehydrogen
37	62.5	13.2	985	2 S15965	hypothetical prote
38	62	13.1	242	2 S67270	CCAAT-binding fact
39	62	13.1	1175	2 D35815	myosin heavy chain
40	62	13.1	1175	2 C35815	myosin heavy chain
41	62	13.1	1201	2 A35815	myosin heavy chain
42	62	13.1	1201	2 B35815	myosin heavy chain
43	62	13.1	2385	2 A32491	myosin heavy chain
44	62	13.1	2411	2 B32491	myosin heavy chain
45	61.5	13.0	284	2 D82486	probable lipase ac
46	61.5	13.0	339	2 AG2041	queine tRNA-ribos
47	61.5	13.0	430	2 I48755	MSAP1a - mouse
48	61.5	13.0	470	2 D84614	hypothetical prote
49	61.5	13.0	709	2 D86307	elongation factor
50	61.5	13.0	863	2 JC7537	beta-N-acetylgluco
51	61	12.9	213	2 B27898	luxp protein - Vib
52	61	12.9	245	2 S49045	arabinose operon r
53	61	12.9	310	2 A25027	hypothetical prote
54	61	12.9	389	2 T14751	cytochrome P450 10
55	61	12.9	410	1 O4BS6M	B1 protein - human
56	61	12.9	474	2 S16250	exodeoxyribonuclea
57	61	12.9	604	2 S36493	IS3 family transpo
58	61	12.9	1212	2 B82809	insertion element
59	60.5	12.8	88	2 A13122	hypothetical prote
60	60.5	12.8	88	2 F98164	conserved hypothet
61	60.5	12.8	142	2 F81296	hypothetical prote
62	60.5	12.8	323	2 B83215	hypothetical prote
63	60.5	12.8	335	2 T33483	hypothetical prote
64	60.5	12.8	458	2 F84275	neopullulanase - S
65	60.5	12.8	508	2 S74848	major vault protei
66	60.5	12.8	843	2 A47132	alpha-mannosidase
67	60.5	12.8	1083	1 S53048	hypothetical prote
68	60	12.7	177	2 D70862	DNA replication pr
69	60	12.7	282	2 D97138	H+/K+-exchanging A
70	60	12.7	290	2 JN0904	arabinose operon r
71	60	12.7	310	2 AB0275	protein F3P9.6 (lm
72	60	12.7	326	2 G96812	phe-tRNA synthetas
73	60	12.7	352	2 F89884	probable N6-adenin
74	60	12.7	373	2 A96927	serine hydroxymeth
75	60	12.7	426	2 D87153	

ALIGNMENTS

RESULT 1
H83003
Conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C:Accession: H83003
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Llm,
. ; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: H83003
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <STO>
A:Cross-references: UNIPARC:UPI00000C5F26; GB:AE004927; GB:AE004091; NID:G9951437; PIDN:
A:Experimental source: Strain PA01
C:Genetics:
A:Gene: PA5148
C:Superfamily: fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502a-41

Perfect score: 472
Sequence: 1 MTRVTMCRKYGELPGLERP.....AEMDKFPAGREYAQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	472	100.0	90	1	FETP_PSEPK
2	439	93.0	90	2	Q4KJT2_PSEF5
3	432	91.5	90	1	FETP_PSESM
4	432	91.5	90	2	Q4ZLP3_PSESY
5	411	87.1	90	2	Q6T7F6_PSEFL
6	400	84.7	90	1	FETP_PSEAB
7	393	83.3	90	2	Q4J228_AZOV1
8	261.5	55.4	90	1	FETP_AC1AD
9	250	53.0	90	1	FETP_ID1LO
10	244	51.7	96	2	Q4FVJ7_9GAMM
11	239	50.6	90	1	FETP_METCA
12	237	50.2	92	1	FETP_SHEON
13	234	49.6	91	1	FETP_MANSN
14	233	49.4	91	1	FETP_RALSO
15	232	49.2	89	1	FETP_LEGPA
16	232	49.2	89	1	FETP_LEGPH
17	232	49.2	90	1	FETP_NITEU
18	231	48.9	89	1	FETP_LEGPL
19	229	48.5	90	1	FETP_HAEIN
20	229	48.5	90	1	FETP_PHOPR
21	229	48.5	90	2	Q4QMD9_HAE18
22	229	48.5	91	1	FETP_BURMA
23	229	48.5	91	1	FETP_BURPS
24	228	48.3	90	1	FETP_VIBCH
25	226	47.9	90	1	FETP_VIBVU
26	226	47.9	90	1	FETP_VIBVY
27	225	47.7	90	1	FETP_PASMU
28	225	47.7	90	1	FETP_VIBPA
29	223	47.2	91	2	Q4LS19_9BURK
30	222	47.0	90	1	FETP_BORBR
31	222	47.0	90	1	FETP_BORPA

32	222	47.0	90	1	FETP_BORPE	Q7WVC4 bordetella
33	220	46.6	90	1	FETP_ECO57	P0A8P4 escherichia
34	220	46.6	90	1	FETP_ECOLI	P0A8P3 escherichia
35	220	46.6	90	1	FETP_PHOHL	Q7N711 photorhabdu
36	220	46.6	90	1	FETP_SHIFL	P0A8P5 shigella fl
37	219	46.4	88	1	FETP_NEIG1	O5F553 neisseria g
38	219	46.4	88	1	FETP_NEIMA	P67615 neisseria m
39	219	46.4	88	1	FETP_NEIMB	P67616 neisseria m
40	219	46.4	90	1	FETP_ERWCT	Q6D8J9 erwinia car
41	219	46.4	90	1	FETP_VIBF1	Q5E7T0 vibrio fisc
42	219	46.4	94	1	FETP_HABDU	Q7VKB6 haemophilus
43	216	45.8	90	1	FETP_ECOL6	Q8FE19 escherichia
44	213	45.1	90	1	FETP_SALCH	Q57K04 salmonella
45	213	45.1	90	1	FETP_SALPA	Q5PMN1 salmonella
46	213	45.1	90	1	FETP_SALTI	P67618 salmonella
47	213	45.1	90	1	FETP_SALTY	P67617 salmonella
48	207	43.9	90	1	FETP_CHRVO	Q7NSR4 chromobacte
49	206	43.6	91	1	FETP_XANAC	Q8PJH7 xanthomonas
50	206	43.6	92	1	FETP_XANOR	Q5GY22 xanthomonas
51	204	43.2	90	1	FETP_COXBU	Q83D06 coxiella bu
52	199	42.2	92	1	FETP_XANCP	Q8P829 xanthomonas
53	199	42.2	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
54	198	41.9	90	1	FETP_XYLFA	Q9PC73 xylella fas
55	196	41.5	90	1	FETP_YERPS	Q666M3 yersinia ps
56	194	41.1	90	1	FETP_XYLFT	Q87D06 xylella fas
57	193	40.9	78	1	FETP_WIGBR	Q8D3C5 wigleswort
58	188	39.8	90	1	FETP_YERPE	Q8ZHE7 yersinia pe
59	185	39.2	87	1	FETP_FRATT	O5N1J8 francisella
60	180	38.1	79	1	FETP_CANBF	Q7VRG9 candidatus
61	177	37.5	78	1	FETP_BUCAP	Q8K925 buchnera ap
62	172	36.4	92	2	Q4NMQ4_9DELT	Q4NMQ4 anaeromyxob
63	159	33.7	77	1	FETP_BUCAI	P57618 buchnera ap
64	157	33.3	87	1	FETP_BUCBP	Q89444 buchnera ap
65	84	17.8	703	2	Q4WPT2_ASFPU	Q4WPT2 aspergillus
66	79.5	16.8	280	2	Q81BK9_BACCR	Q81BK9 bacillus ce
67	78.5	16.6	603	2	Q6EPW5_ORYSA	Q6EPW5 oryza sativ
68	74	15.7	220	2	Q5WAF4_BACSK	Q5WAF4 bacillus cl
69	74	15.7	1141	2	Q5B318_EMENT	Q5B318 aspergillus
70	72	15.3	307	2	Q9FJU6_ARATH	Q9FJU6 arabidopsis
71	72	15.3	844	1	PRIC2_HUMAN	Q7Z3G6 homo sapien
72	72	15.3	845	1	PRIC2_MOUSE	Q80Y24 mus musculu
73	71	15.0	437	2	Q60EH0_ORYSA	Q60EH0 oryza sativ
74	70.5	14.9	259	2	Q52J13_BRARE	Q52J13 brachydanio
75	70.5	14.9	353	2	Q6NN67_DROME	Q6NN67 drosophila

ALIGNMENTS

RESULT 1
FETP_PSEPK
ID FETP_PSEPK STANDARD; PRT; 90 AA.
AC Q8BR49;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=PP0285;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCHI_TaxID=160488;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
Hance I., Chris Lee P., Holtzaple B.K., Scanlan D., Tran K.,
Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
Wedler H., Lauber J., Stjepandic D., Hohnselt J., Straetz M., Helm S.,

RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
 RA Fraser C.M.,
 RT "Complete genome sequence and comparative analysis of the
 RT metabolically versatile *Pseudomonas putida* KT2440.";
 RL Environ. Microbiol. 4:799-808(2002).
 CC -1- FUNCTION: Could be a mediator in iron transactions between iron
 CC acquisition and iron-requiring processes, such as synthesis and/or
 CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
 CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC -----
 DR EMBL; AE016775; AAN65916.1; -; Genomic_DNA.
 DR SMR; Q88R49; 1-79.
 DR TIGR; PP0285; -.

DR HAMAP; MF_00686; -; 1.
 DR InterPro; IPR007457; YggX.
 DR Pfam; PF04362; DUF495; 1.

DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
 DR ProDom; PD029191; DUF495; 1.
 KW Complete proteome; Iron.

SQ SEQUENCE 90 AA; 10596 MW; 0C802FD7163B75A2 CRC64;

Query Match 100.0%; Score 472; DB 1; Length 90;
 Best Local Similarity 100.0%; Pred. No. 9.6e-44;
 Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRTVMCRKYQBELPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINEKRLNMNA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MTRTVMCRKYQBELPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINEKRLNMNA 60

QY 61 EDRKFLQAEEMDKFFPAGEEYQAQAEGYVP 87
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 61 EDRKFLQAEEMDKFFPAGEEYQAQAEGYVP 87

RESULT 2

Q4KJT2_PSEFS
 ID Q4KJT2_PSEFS PRELIMINARY; PRT; 90 AA.

AC Q4KJT2;
 DT 13-SEP-2005 (TReMBLrel. 31, Created)

DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)

DE Hypothetical protein.

GN ORFNames=PFL_0357;

OS *Pseudomonas fluorescens* (strain Pf-5).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=220664;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=PF-5;

RX PubMed=15980861; DOI=10.1038/nbt1110;

RA Paulsen I.T., Press C., Ravel J., Kobayashi D., Myers G.S.,

RA Mavrodi D., DeBoy R.T., Seshadri R., Ren Q., Madupu R., Dodson R.J.,

RA Durkin S., Brinkac L.M., Daugherty S.C., Sullivan S.A., Rosovitz M.,

RA Gwinn M.L., Zhou L., Nelson W.C., Weidman J., Watkins K., Tran K.,

RA Khouri H.M., Pierson E., Pierson L. III, Thomasow L., Loper J.;

RT "Complete genome sequence of the plant commensal *Pseudomonas*

RT *fluorescens* Pf-5."

RL Nat. Biotechnol. 23:873-878(2005).

DR EMBL; CP000076; AAY95766.1; -; Genomic_DNA.

KW Hypothetical protein.

SQ SEQUENCE 90 AA; 10483 MW; 816D3C774C2B7C12 CRC64;

Query Match 93.0%; Score 439; DB 2; Length 90;
 Best Local Similarity 88.5%; Pred. No. 3.9e-40;
 Matches 77; Conservative 8; Mismatches 2; Indels 0; Gaps 0;

QY 1 MTRTVMCRKYQBELPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINEKRLNMNA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 1 MTRTVMCRKYQBELPGLERPPYPGAKGODIFDHVSQKAWADWQKHQTMLINEKRLNMNA 60

QY 61 EDRKFLQAEEMDKFFPAGEEYQAQAEGYVP 87
 :||:|||||:|||||:|||||:|||||
 Db 61 DDRKYLQEMDKFFSGEYAKADGYVP 87

RESULT 3

FETP_PSESM
 ID FETP_PSESM STANDARD; PRT; 90 AA.

AC Q87UF5;

DT 10-OCT-2003 (Rel. 42, Created)

DT 10-OCT-2003 (Rel. 42, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Probable Fe(2+) trafficking protein.

GN OrderedLocusNames=PSPT05343;

OS *Pseudomonas syringae* (pv. tomato).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=323;

RN [1]

RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].

RC STRAIN=DC3000;

RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;

RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,

RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,

RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,

RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,

RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,

RA Uterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,

RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,

RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,

RA Bender C.L., White O., Fraser C.M., Collier A.;

RT "The complete genome sequence of the Arabidopsis and tomato pathogen

RT *Pseudomonas syringae* pv. tomato DC3000.";

RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).

CC -1- FUNCTION: Could be a mediator in iron transactions between iron

CC acquisition and iron-requiring processes, such as synthesis and/or

CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC -----

CC EMBL; AE016853; AAO58769.1; -; Genomic_DNA.

DR SMR; Q87UF5; 1-79.

DR TIGR; PSPT05343; -.

DR HAMAP; MF_00686; -; 1.

DR InterPro; IPR007457; YggX.

DR Pfam; PF04362; DUF495; 1.

DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.

DR ProDom; PD029191; DUF495; 1.

KW Complete proteome; Iron.

SQ SEQUENCE 90 AA; 10621 MW; 1086288DF6532973 CRC64;

Query Match 91.5%; Score 432; DB 1; Length 90;
 Best Local Similarity 88.5%; Pred. No. 2.3e-39;

Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRTVMCRKYQBELPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINEKRLNMNA 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 1 MTRTVMCRKYQBELPGLERAPPYPGAKGODIFNHVSQKAWADWQKHQTMLINEKRLNMNA 60

QY 61 EDRKFLQAEEMDKFFPAGEEYQAQAEGYVP 87
 |||||||||||||||:|||||||||||||

Db 61 EDRKFLQTEMDFKFLSGEYQAQAEGYVP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-41

Perfect score: 472
Sequence: 1 MTRITVCKRYQELPLGERP.....AEMDKFFAGEBYAQAEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	84.7	122	2	US-09-252-991A-23355
2	265.5	56.2	92	2	US-09-328-352-5456
3	224	47.5	110	2	US-09-540-236-2859
4	213	45.1	107	2	US-09-489-039A-11962
5	209	44.3	93	2	US-09-543-681A-5443
6	73	15.5	451	2	US-09-543-681A-7401
7	69	14.6	443	2	US-09-248-796A-16816
8	64.5	13.7	163	2	US-09-270-767-33714
9	64	13.6	317	2	US-09-107-532A-4653
10	64	13.6	420	2	US-09-248-796A-15323
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12	63	13.3	314	2	US-09-716-865-4
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17	62	13.1	448	2	US-09-107-532A-4482
18	62	13.1	1156	2	US-08-996-083-1
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25	60.5	12.8	205	2	US-09-919-039-258
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28	60	12.7	569	2	US-09-252-991A-32290	Sequence 32290, A
29	60	12.7	689	2	US-09-489-039A-7677	Sequence 7677, Ap
30	59.5	12.6	468	2	US-09-976-594-462	Sequence 462, App
31	59.5	12.6	468	2	US-09-999-833A-337	Sequence 337, App
32	59.5	12.6	468	2	US-10-020-445A-337	Sequence 337, App
33	59	12.5	184	2	US-09-040-229B-9	Sequence 9, Appli
34	59	12.5	212	1	US-08-531-525-18	Sequence 18, Appl
35	59	12.5	212	1	US-08-718-270A-18	Sequence 18, Appl
36	59	12.5	212	2	US-09-399-913-67	Sequence 67, Appl
37	59	12.5	212	2	US-09-350-614-67	Sequence 67, Appl
38	59	12.5	216	2	US-09-949-016-10750	Sequence 10750, A
39	59	12.5	298	2	US-09-328-352-7544	Sequence 7544, Ap
40	59	12.5	278	2	US-09-543-681A-8107	Sequence 8107, Ap
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43	59	12.5	504	2	US-09-538-092-1170	Sequence 1170, Ap
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45	59	12.5	505	2	US-09-949-016-186	Sequence 186, App
46	59	12.5	513	2	US-09-949-016-11517	Sequence 11517, A
47	59	12.5	1242	2	US-09-583-110-5051	Sequence 5051, Ap
48	59	12.5	1243	2	US-09-107-433-3942	Sequence 3942, Ap
49	58.5	12.4	205	2	US-09-216-393B-124	Sequence 124, App
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67	58	12.3	903	2	US-08-720-229-22	Sequence 22, Appl
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71	57.5	12.2	324	2	US-09-252-991A-26001	Sequence 26001, A
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ALIGNMENTS

RESULT 1
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
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667.774 Million cell updates/sec

Title: US-09-955-502A-41

Perfect score: 472

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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7	229	48.5	87	3	US-09-955-502-7
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9	229	48.5	87	3	US-09-955-502-30
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29	198	41.9	89	3	US-09-955-502-22	Sequence 22, Appl
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34	73	15.5	766	4	US-10-437-963-146099	Sequence 146099,
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38	70	14.8	670	4	US-10-369-493-5967	Sequence 5967, Ap
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43	69	14.6	981	4	US-10-437-963-165498	Sequence 165498,
44	68.5	14.5	526	4	US-10-437-963-156176	Sequence 156176,
45	68	14.4	794	4	US-10-437-963-173233	Sequence 173233,
46	68	14.4	900	4	US-10-437-963-126879	Sequence 126879,
47	67.5	14.3	689	4	US-10-282-122A-61019	Sequence 61019, A
48	67.5	14.3	818	4	US-10-437-963-156121	Sequence 156121,
49	67.5	14.3	890	4	US-10-437-963-156221	Sequence 156221,
50	67	14.2	365	4	US-10-437-963-107715	Sequence 107715,
51	67	14.2	559	4	US-10-369-493-4607	Sequence 4607, Ap
52	67	14.2	560	5	US-10-732-923-13914	Sequence 13914, A
53	67	14.2	561	5	US-10-732-923-13915	Sequence 13915, A
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63	66	14.0	1553	5	US-10-732-923-22705	Sequence 22705, A
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ALIGNMENTS

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; Sequence 24, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas putida

GenCore version 5.1.7
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Title: US-09-955-502A-41
Perfect score: 472
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Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

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Post-processing: Minimum Match 0%
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SUMMARIES

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5	61.5	13.0	689	US-11-121-438-2	Sequence 2, Appli
6	61	12.9	3433	US-10-714-781A-67	Sequence 67, Appl
7	60.5	12.8	645	US-10-510-386-32	Sequence 32, Appl
8	60	12.7	426	US-10-858-730-81	Sequence 81, Appl
9	59.5	12.6	690	US-10-467-657-4758	Sequence 4758, Ap
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14	56	11.9	211	US-11-124-368A-175	Sequence 175, App
15	56	11.9	211	US-11-124-368A-176	Sequence 176, App
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17	55.5	11.8	1432	US-10-510-386-218	Sequence 218, App
18	55	11.7	106	US-11-072-512-2218	Sequence 2218, Ap
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22	54.5	11.5	310	US-11-198-794-88	Sequence 88, Appl
23	54.5	11.5	315	US-11-198-746-91	Sequence 91, Appl
24	54.5	11.5	315	US-11-198-794-91	Sequence 91, Appl
25	54.5	11.5	320	US-10-467-657-3254	Sequence 3254, Ap

26	54.5	11.5	322	7	US-11-198-746-89	Sequence 89, Appl
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33	54.5	11.5	648	6	US-10-467-657-2802	Sequence 2802, Ap
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61	52.5	11.1	215	6	US-10-131-826A-488	Sequence 488, App
62	52.5	11.1	215	7	US-11-080-991-112	Sequence 112, App
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66	52	11.0	370	6	US-10-873-528-160	Sequence 160, App
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72	52	11.0	505	6	US-10-514-878A-13	Sequence 13, Appl
73	52	11.0	505	7	US-11-179-478-2	Sequence 2, Appli
74	52	11.0	593	7	US-11-194-246-317	Sequence 317, App
75	52	11.0	924	6	US-10-467-657-4290	Sequence 4290, Ap

ALIGNMENTS

RESULT 1
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Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON Spa
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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Title: US-09-955-502A-42
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*
1: Geneseqp1980s:*
2: Geneseqp1990s:*
3: Geneseqp2000s:*
4: Geneseqp2001s:*
5: Geneseqp2002s:*
6: Geneseqp2003as:*
7: Geneseqp2003bs:*
8: Geneseqp2004s:*
9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	88	5	ABB781171 Amino aci
2	467	100.0	88	5	ABB781172 Amino aci
3	467	100.0	88	5	ABB781173 Amino aci
4	467	100.0	88	6	ABP77219 N. gonorr
5	339	72.6	87	5	ABB781175 Amino aci
6	333	71.3	87	5	ABB781174 Amino aci
7	294	63.0	87	5	ABB781176 Amino aci
8	290	62.1	87	5	ABB781148 Amino aci
9	290	62.1	87	5	ABB781147 Amino aci
10	272.5	58.4	86	5	ABB781149 Amino aci
11	271	58.0	89	9	ABE41576 L. pneumo
12	271	58.0	95	9	ABE38294 L. pneumo
13	258	55.2	88	5	ABB781178 Amino aci
14	243	52.0	87	5	ABB781177 Amino aci
15	240	51.4	90	5	ABB781155 Amino aci
16	235	50.3	87	5	ABB781153 Amino aci
17	230	49.3	88	5	ABB781154 Amino aci
18	228	48.8	91	5	ABB781150 Amino aci
19	227	48.6	87	5	ABB781152 Amino aci
20	227	48.6	107	7	ABO65445 Klebsiell
21	225.5	48.3	92	6	ADA34169 Acinetoba
22	221	47.3	93	7	ADF05158 Bacteri
23	219	46.9	87	5	ABB781169 Amino aci
24	217	46.5	87	5	ABB781151 Amino aci

25	213	45.6	91	5	ABB781158	Abb78158 Amino aci
26	213	45.6	91	5	ABB781157	Abb78157 Amino aci
27	213	45.6	91	5	ABB781156	Abb78156 Amino aci
28	211	45.2	88	5	ABB781160	Abb78160 Amino aci
29	211	45.2	91	5	ABB781161	Abb78161 Amino aci
30	211	45.2	91	5	ABB781159	Abb78159 Amino aci
31	211	45.2	91	5	ABB781162	Abb78162 Amino aci
32	210	45.0	78	5	ABB781164	Abb78164 Amino aci
33	207	44.3	87	5	ABB781170	Abb78170 Amino aci
34	207	44.3	122	7	ABO74609	ABO74609 Pseudomon
35	202	43.3	91	5	ABB781163	Abb78163 Amino aci
36	198	42.4	90	5	ABB781165	Abb78165 Amino aci
37	198	42.4	90	5	ABB781168	Abb78168 Amino aci
38	193.5	41.4	90	5	ABB781167	Abb78167 Amino aci
39	182	39.0	110	8	ADL05173	Adl05173 M. catar
40	158	33.8	76	5	ABB781166	Abb78166 Amino aci
41	74	15.8	1122	6	ABU22044	Abu22044 Protein e
42	70	15.0	202	7	ABM90380	Abm90380 Rice abio
43	70	15.0	1079	8	ADN19463	Adn19463 Bacterial
44	69	14.8	774	4	ABG29304	Abg29304 Novel hum
45	68.5	14.7	361	7	ABO76259	ABO76259 Pseudomon
46	68	14.6	189	9	ADM18357	Adw18357 Pinus rad
47	67.5	14.5	466	7	ABO84015	ABO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221	Abu19221 Protein e
49	66	14.1	418	7	ABO66638	ABO66638 Klebsiell
50	65.5	14.0	649	7	ADC94671	Adc94671 E. faeciu
51	65.5	14.0	1443	7	ADJ68530	Adj68530 Human hea
52	65.5	14.0	1935	7	ADJ70260	Adj70260 Human hea
53	65.5	14.0	3830	5	ABB81168	Abb81168 TRRAP pro
54	65.5	14.0	3830	8	ADJ78499	Adj78499 PAF/TRRAP
55	65.5	14.0	3830	8	ADQ19749	Adq19749 Human sof
56	65.5	14.0	3830	8	ADQ89826	Adq89826 Antagonis
57	65.5	14.0	3859	7	ADJ68548	Adj68548 Human hea
58	65.5	14.0	3859	8	ADS88242	Ads88242 Human pro
59	65	13.9	255	7	ADM27073	Adm27073 Hyperther
60	65	13.9	296	4	AAU35611	Aau35611 Haemophil
61	65	13.9	296	6	ABU30521	Abu30521 Protein e
62	65	13.9	438	2	AAV11015	Aav11015 H. pylori
63	65	13.9	442	2	AAW20830	Aaw20830 H. pylori
64	65	13.9	465	2	AAW20303	Aaw20303 H. pylori
65	64.5	13.8	207	6	ABM73508	Abm73508 Staphyloc
66	64.5	13.8	207	9	ADV16859	Adv16859 Staphyloc
67	64.5	13.8	207	9	ADM94758	Adw94758 Prolifera
68	64.5	13.8	362	7	ADF89476	Adf89476 Human ery
69	64.5	13.8	362	8	ADK48858	Adk48858 Human tra
70	64.5	13.8	362	8	ADP12457	Adp12457 Protein e
71	64	13.7	260	4	AAM38702	Aam38702 Human pol
72	64	13.7	378	4	AAM40488	Aam40488 Human pol
73	64	13.7	656	4	ABU53239	Abu53239 Human tes
74	64	13.7	656	8	ADL28417	Adl28417 Human nuc
75	64	13.7	2426	2	ADH11285	Adh11285 Vertebrat

ALIGNMENTS

RESULT 1
ABB781171 standard; protein; 88 AA.
XX
AC ABB781171;
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
OS Neisseria gonorrhoeae.
XX
PN US2002072118-A1.

XX 13-JUN-2002.
PD
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
DR
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVKLNKEAGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADP 60

QY 61 RAREVYLAQQMEQYFFGDDGADAVOGYVPQ 88
DB 61 RAREVYLAQQMEQYFFGDDGADAVOGYVPQ 88

RESULT 2
ABB78172
ID ABB78172 standard; protein; 88 AA.
XX
AC ABB78172;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Neisseria meningitidis.
OS
XX
PN US2002072118-A1.
PN
XX
PD 13-JUN-2002.
PD
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX

PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADP 60
DB 1 MARMVFCVKLNKEAGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADP 60

QY 61 RAREVYLAQQMEQYFFGDDGADAVOGYVPQ 88
DB 61 RAREVYLAQQMEQYFFGDDGADAVOGYVPQ 88

RESULT 3
ABB78173
ID ABB78173 standard; protein; 88 AA.
XX
AC ABB78173;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Neisseria meningitidis.
OS
XX
PN US2002072118-A1.
PN
XX
PD 13-JUN-2002.
PD
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
DR
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:27:00 ; Search time 10.8736 Seconds
(without alignments)
778.685 Million cell updates/sec

Title: US-09-955-502a-42

Perfect score: 467
Sequence: 1 MARWVFCVKLNKEAEGRFP.....QMEQYFPGDGADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	467	100.0	88	2	H81014	conserved hypothet
2	240	51.4	90	2	C82320	conserved hypothet
3	227	48.6	90	2	C64013	hypothetical prote
4	213	45.6	91	2	A85954	hypothetical prote
5	213	45.6	91	2	A65082	hypothetical prote
6	213	45.6	91	2	F91108	hypothetical prote
7	211	45.2	91	2	AH0879	conserved hypothet
8	207	44.3	90	2	H83003	conserved hypothet
9	201	43.0	105	2	C82624	conserved hypothet
10	198	42.4	90	2	A10116	conserved hypothet
11	158	33.8	93	2	E84994	hypothetical prote
12	72	15.4	1041	2	A81960	probable DNA helic
13	70	15.0	1079	2	T38913	translation initia
14	68.5	14.7	338	2	A83389	probable permease
15	68.5	14.7	549	2	A11457	ABC transporter ol
16	68	14.6	195	2	S74714	hypothetical prote
17	67.5	14.5	899	2	A83019	conserved hypothet
18	66.5	14.2	401	2	C70159	translation elonga
19	66	14.1	598	1	RGEENX	nitrate/nitrite se
20	66	14.1	598	2	F85702	nitrate/nitrite se
21	66	14.1	598	2	G90844	nitrate/nitrite se
22	65	13.9	296	2	A64110	cell division inhi
23	65	13.9	465	2	C71870	hypothetical prote
24	65	13.9	590	2	E85057	probable transposo
25	64.5	13.8	207	2	E89952	conserved hypothet
26	64.5	13.8	362	2	T45072	erythroid Kruppel-
27	64.5	13.8	400	2	A39254	inositol-1,4-bisph
28	64.5	13.8	1553	2	S67483	adenosinetriphosph
29	64	13.7	676	2	A45984	sperm-binding glyc

30	64	13.7	677	2	S33664	flagella-associate
31	63.5	13.6	288	2	H95018	transcription regu
32	63.5	13.6	301	2	F82446	transcription regu
33	63	13.5	282	2	D97138	DNA replication pr
34	63	13.5	388	1	JC5461	cellulase (EC 3.2.
35	63	13.5	388	1	S43920	cellulase (EC 3.2.
36	62	13.3	120	2	G97833	hypothetical prote
37	62	13.3	200	2	E82203	transcription regu
38	62	13.3	259	2	S55033	transcription init
39	62	13.3	570	2	D83177	probable phosphotr
40	62	13.3	2314	2	T28698	hypothetical prote
41	61.5	13.2	211	2	T38645	transcriptional regu
42	61.5	13.2	288	2	B95122	probable acyl-acyl
43	61.5	13.2	374	2	A96502	tyrosyl tRNA synth
44	61.5	13.2	412	2	G81581	tyrosyl tRNA synth
45	61.5	13.2	422	2	G86535	tyrosine tRNA liga
46	61.5	13.2	422	2	D72088	flagellar biosynth
47	61.5	13.2	589	2	AE3530	mammalian swi/snf
48	61	13.1	425	2	T50184	arginyl-tRNA synth
49	61	13.1	563	2	F97028	hypothetical prote
50	61	13.1	969	2	T33156	probable sensory t
51	61	13.1	1639	2	T50119	19k globulin precu
52	60.5	13.0	186	1	WMKR219	alpha-globulin pre
53	60.5	13.0	186	2	JC4784	dnak-type molecula
54	60.5	13.0	261	2	S14875	heat-inducible tra
55	60.5	13.0	357	2	F82892	heat-inducible tra
56	60.5	13.0	448	2	T45145	glutamate-ammonia
57	60.5	13.0	1888	2	T39009	hypothetical prote
58	60	12.8	292	2	A10422	conserved hypothet
59	60	12.8	306	2	A97249	Zn-binding lipopro
60	60	12.8	309	2	D95843	probable amnopept
61	60	12.8	323	2	T35734	hypothetical prote
62	60	12.8	335	2	D83142	hypothetical prote
63	60	12.8	397	2	A75503	hypothetical prote
64	60	12.8	410	2	T39115	formamidase-like p
65	60	12.8	508	2	T02486	hypothetical prote
66	60	12.8	615	2	E81451	1-deoxyxylulose-5-
67	60	12.8	655	2	E75206	alpha-amylase (or
68	60	12.8	859	2	T29630	hypothetical prote
69	60	12.8	1006	2	A59384	oxytocinase/insuli
70	60	12.8	1021	2	AC2202	oxytocinase/insuli
71	60	12.8	1025	2	A59383	lysosomal traffick
72	60	12.8	3788	2	T30851	heat shock protein
73	59.5	12.7	157	1	HHPM17	sfp homolog gsp -
74	59.5	12.7	237	2	A55218	probable RNA polym
75	59.5	12.7	295	2	T35330	

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.B.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; MID:g7227279; PIDN:
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

```

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: F81958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <PAR>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: NMB2021; NMA0419
C/Superfamily: fe(II) trafficking protein YggX

Query Match      100.0%; Score 467; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.7e-46;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIPENVSGEAWAATRHQTMLINENRLSLADP 60

QY      61 RAREYLAQOMEQYFFGCGADAVQGYVPQ 88
      |||||
Db      61 RAREYLAQOMEQYFFGCGADAVQGYVPQ 88

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serog
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heidelberg, J.F.; Risen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragoi, I.; Sellers, B
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein YggX

Query Match      51.4%; Score 240; DB 2; Length 90;
Best Local Similarity 50.6%; Pred. No. 2.5e-20;
Matches 44; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

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Db      1 MARTVFCSTRLOKEADGLDFQLYPGELGKRIFDNICKAEAWAOWOTKOTMLINEKLNMDP 60

QY      61 RAREYLAQOMEQYFFGCGADAVQGYVP 87
      |||||
Db      61 EHRKLLQEEMVNFLEGEKVHIEGYTP 87

RESULT 3
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
, D.M.; Brandon, R.C.; FINE, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

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A;/Reference number: A64000; MUID:95350630; PMID:7542800
A;/Accession: C64013
A;/Status: nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-90 <TIGR>
A;/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C;/Superfamily: fe(II) trafficking protein YggX

Query Match      48.6%; Score 227; DB 2; Length 90;
Best Local Similarity 50.0%; Pred. No. 7.8e-19;
Matches 44; Conservative 17; Mismatches 25; Indels 2; Gaps 2;

QY      1 MARMVFCVNLNKEABGMKFPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
        ||||| | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db       1 MARTVFCEYLKKEAEGLDFQLYPGELGRIFDSVSQAWEWTIKQTMLVNEKKLNWNNA 60
        ||||| | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :

QY      61 RAREYLAQQMEQYFFGDGADA-VGGYVP 87
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db       61 EHRKLLEQEMVNFLF-EGKDVIHEGYVP 87
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 4
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;/Species: Escherichia coli
C;/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;/Accession: A85954
R;/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, B.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoustis, K.; Apodaca,
Nature 409, 529-533, 2001
A;/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;/Reference number: A85480; MUID:21074935; PMID:11206551
A;/Accession: A85954
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <STO>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A;/Experimental source: strain O157:H7, substrain EDL933
C;/Genetics:
A;/Gene: yggX
C;/Superfamily: fe(II) trafficking protein YggX

Query Match      45.6%; Score 213; DB 2; Length 91;
Best Local Similarity 44.3%; Pred. No. 3.1e-17;
Matches 39; Conservative 16; Mismatches 33; Indels 0; Gaps 0;

QY      1 MARMVFCVNLNKEABGMKFPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db       1 MSRTIFCTFLQREAEAGODFQLYPGELGRIRIYNBSISKEAWAQWHQTMLINEKKLNWNNA 60
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

QY      61 RAREYLAQQMEQYFFGDGADVGGYVPQ 88
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~
Db       61 EHRKLLEQEMVNFLFEGKEVHIIEGYTP 88
        |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:~

RESULT 5
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;/Species: Escherichia coli
C;/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;/Accession: A65082
R;/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;/Title: The complete genome sequence of Escherichia coli K-12.
A;/Reference number: A64720; MUID:97426617; PMID:9278503
A;/Accession: A65082
A;/Status: preliminary; nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-91 <BLAT>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g
A;/Experimental source: strain K-12, substrain MG1655
C;/Superfamily: fe(II) trafficking protein YggX

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:00:23 ; Search time 66.5057 Seconds
(without alignments)
933.551 Million cell updates/sec

Title: US-09-955-502a-42

Perfect score: 467
Sequence: 1 MARMVFCTKLKKAEGMKFP.....QMEGYFFGDGADAVGGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	1	FETP_NEIG1 Q5F553 neisseria g
2	467	100.0	88	1	FETP_NEIMA P67616 neisseria m
3	467	100.0	88	1	FETP_NEIMB P67616 neisseria m
4	354	75.8	91	1	FETP_RALSO Q8Y010 raietonia s
5	348	74.5	91	2	Q4LS19 9BURK Q4LS19 burkholderi
6	339	72.6	91	1	FETP_BURMA Q621u9 burkholderi
7	339	72.6	91	1	FETP_BURPA Q63gj4 burkholderi
8	335	71.7	90	1	FETP_CHRVO Q7nsr4 chromobacte
9	319	68.3	90	1	FETP_NITEU Q82xf2 nitrosomona
10	290	62.1	90	1	FETP_BORBR Q7wh06 bordetella
11	290	62.1	90	1	FETP_BORPA Q7w9q2 bordetella
12	290	62.1	90	1	FETP_BORPE Q7wvc4 bordetella
13	275	58.9	89	1	FETP_LEGPL Q5wvc4 legionella
14	271	58.0	89	1	FETP_LEGPA Q5x3x9 legionella
15	271	58.0	89	1	FETP_LEGPH Q5zu80 legionella
16	258	55.2	90	1	FETP_COXBU Q83d06 coxiella bu
17	254	54.4	90	1	FETP_VIBF1 Q5e7c0 vibrio fisc
18	252	54.0	92	2	Q4NWQ4 9DELT Q4NWQ4 anaeromyxob
19	243	52.0	90	1	FETP_METCA Q60aj7 methylococc
20	242	51.8	90	1	FETP_IDILO Q5gy58 idiomarina
21	240	51.4	90	1	FETP_VIBCH Q9kur4 vibrio chol
22	239	51.2	90	1	FETP_VIBPA Q87115 vibrio para
23	239	51.2	90	1	FETP_VIBVU Q8dcs5 vibrio vuln
24	239	51.2	90	1	FETP_VIBVY Q7mh14 vibrio vuln
25	235	50.3	91	1	FETP_XANAV Q8bjh7 xanthomonas
26	235	50.3	94	1	FETP_XANBU Q7vkb6 haemophilus
27	233	49.9	92	1	FETP_XANOR Q5gy22 xanthomonas
28	230	49.3	92	1	FETP_SHEON Q8ebx6 shewanella
29	227	48.6	90	1	FETP_HAEIN P44048 haemophilus
30	227	48.6	90	2	Q4QMD9 HAE18 Q4QMD9 haemophilus
31	225	48.2	92	1	FETP_XANCP Q8p829 xanthomonas

ALIGNMENTS

32	225	48.2	92	2	Q4UW14_XANCP Q4uw14 xanthomonas
33	224	48.0	91	1	FETP_MANSM Q65vt7 mannheimia
34	220.5	47.2	90	1	FETP_ACTAD Q6fEb3 acinetobact
35	220	47.1	90	1	FETP_PHOPR Q6lmk7 photobacter
36	219	46.9	90	1	FETP_PSEPK Q88r49 pseudomonas
37	217	46.5	90	1	FETP_PASMU Q9clb9 pasteurella
38	217	46.5	90	1	FETP_PHOL Q7n711 photorhabdu
39	211	45.2	90	2	Q6T7F6_PSEFL Q6t7f6 pseudomonas
40	209	44.8	90	1	FETP_XYLFT Q87d06 xylella fas
41	208	44.5	87	1	FETP_FRATT Q5nhj8 francisella
42	208	44.5	90	1	FETP_ECO57 P0a8p4 escherichia
43	208	44.5	90	1	FETP_ECOLI P0a8p3 escherichia
44	208	44.5	90	1	FETP_ERWCT Q6d8j9 erwina car
45	208	44.5	90	1	FETP_SHIFL P0a8p5 shigella fl
46	207	44.3	90	1	FETP_PSEAB Q9hu36 pseudomonas
47	207	44.3	90	2	Q4KJT2_PSEF5 Q4kj22 pseudomonas
48	206	44.1	90	1	FETP_SALCH Q57k04 salmonella
49	206	44.1	90	1	FETP_SALPA Q5pmn1 salmonella
50	206	44.1	90	1	FETP_SALTI P67618 salmonella
51	206	44.1	90	1	FETP_SALTY P67617 salmonella
52	206	44.1	90	1	FETP_YERPS Q66m3 yersinia ps
53	206	44.1	96	2	Q4FVJ7_9GAMM Q4fvj7 psychrobact
54	204	43.7	90	1	FETP_ECOL6 Q8fe19 escherichia
55	201	43.0	90	1	FETP_XYLFPA Q9pc73 xylella fas
56	198	42.4	90	1	FETP_PSESM Q87uf5 pseudomonas
57	198	42.4	90	1	FETP_YERPE Q8zhe7 yersinia pe
58	198	42.4	90	2	Q4ZLP3_PSESY Q4zlp3 pseudomonas
59	196	42.0	90	2	Q4J228_AZQVI Q4j228 azotobacter
60	186	39.8	79	1	FETP_CANBF Q7vrg9 candidatus
61	167	35.8	78	1	FETP_BUCAP Q8k925 buchnera ap
62	167	35.8	78	1	FETP_WIGBR Q8d3c5 wiggleswort
63	158	33.8	77	1	FETP_BUCAI P57618 buchnera ap
64	127	27.2	87	1	FETP_BUCBP Q89a44 buchnera ap
65	75	16.1	359	2	Q7VKN4_HAEDU Q7vkn4 haemophilus
66	74	15.8	453	2	Q4PBL1_USITWA Q4pbl1 uscilago ma
67	74	15.8	1598	2	Q62CB0_BURMA Q62cb0 burkholderi
68	74	15.8	1599	2	Q63KS1_BURPS Q63ks1 burkholderi
69	73	15.6	820	2	Q521A7_MAGGR Q521a7 magnaporthe
70	72.5	15.5	301	2	Q6LNI9_PHOPR Q6lni9 photobacter
71	72	15.4	203	2	Q568W6_BRARE Q568w6 brachydanio
72	72	15.4	1041	2	Q9JWD5_NEIMA Q9jwd5 neisseria m
73	71	15.2	346	2	Q8BF42_SHEON Q8bf42 shewanella
74	70.5	15.1	320	2	Q6PKY5_XENILA Q6pkys xenopus lae
75	70	15.0	1079	1	IP2P_SCHPO Q10251 schizosach

RESULT 1
FETP_NEIG1
ID FETP_NEIG1 STANDARD; PRT; 88 AA.

AC Q5F553;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=NGO2083;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaespy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC


```
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE004969; AAW90684.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_trafftc_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
SQ Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60
    |||
Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQQOMEQYFFFGDADAVQGYVPQ 88
    |||
Db 61 RAREYLAQQOMEQYFFFGDADAVQGYVPQ 88

RESULT 2
FETP_NEIMA STANDARD; PRT; 88 AA.
ID FETP_NEIMA
AC P67615; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=NMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL162753; CAB83718.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_trafftc_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
```

```
KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60
    |||
Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60

Qy 61 RAREYLAQQOMEQYFFFGDADAVQGYVPQ 88
    |||
Db 61 RAREYLAQQOMEQYFFFGDADAVQGYVPQ 88

RESULT 3
FETP_NEIMB STANDARD; PRT; 88 AA.
ID FETP_NEIMB
AC P67616; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Winn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzo M.,
RA Grandl G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB002098; AAF42344.1; -; Genomic_DNA.
DR TIGR; NMB2021; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60
    |||
Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60
```

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.81093 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502a-28

Perfect score: 467
Sequence: 1 MARMVFCVKLNKGAEGMKFP.....QMEQYFFGDGADVQGYVFPQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Published Applications_AA_New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	US-10-467-657-968	Sequence 968, App
2	60	12.8	1092	US-10-821-234-999	Sequence 999, App
3	58	12.4	380	US-10-525-674-28	Sequence 28, Appl
4	58	12.4	614	US-11-165-576-2	Sequence 2, Appl
5	58	12.4	614	US-11-165-576-4	Sequence 4, Appl
6	57.5	12.3	200	US-10-793-626-1186	Sequence 1186, App
7	57.5	12.3	200	US-10-793-626-2390	Sequence 2390, App
8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, A
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, A
10	57	12.2	384	US-11-219-282-19	Sequence 19, Appl
11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
12	56.5	12.1	575	US-11-098-686-10635	Sequence 10635, A
13	56.5	12.1	688	US-11-165-226-124	Sequence 124, App
14	56	12.0	1124	US-11-090-617-688	Sequence 688, App
15	56	12.0	1375	US-10-995-561-809	Sequence 809, App
16	56	12.0	1376	US-11-100-640-32	Sequence 32, Appl
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, Appl
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, App
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, A
20	55	11.8	258	US-11-090-439-38	Sequence 38, Appl
21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, Appl
23	55	11.8	633	US-11-193-561-13	Sequence 13, Appl
24	55	11.8	633	US-11-193-771-13	Sequence 13, Appl
25	55	11.8	633	US-11-193-789-13	Sequence 13, Appl

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, Appl
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, Appl
28	55	11.8	925	6	US-10-454-437-50	Sequence 50, Appl
29	55	11.8	967	7	US-11-202-268-6	Sequence 6, Appl
30	55	11.8	1011	7	US-11-202-268-2	Sequence 2, Appl
31	54.5	11.7	719	7	US-11-087-227-14	Sequence 14, Appl
32	54	11.6	307	6	US-10-793-626-522	Sequence 522, App
33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, A
34	54	11.6	738	7	US-11-140-625-11	Sequence 11, Appl
35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
36	53.5	11.5	310	7	US-11-055-163-7	Sequence 7, Appl
37	53.5	11.5	344	7	US-11-055-163-6	Sequence 6, Appl
38	53.5	11.5	432	6	US-10-933-115-8	Sequence 8, Appl
39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, Appl
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, Appl
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	710	7	US-11-124-367A-359	Sequence 359, App
46	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
47	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, App
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, Appl
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, App
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, Appl
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appl
56	52.5	11.2	4128	6	US-10-770-726-77	Sequence 77, Appl
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, Appl
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, Appl
61	52	11.1	1022	7	US-11-156-084-118	Sequence 118, App
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 94, Appl
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 2, Appl
64	51.5	11.0	403	7	US-11-074-176-354	Sequence 354, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 186, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 286, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 871, App
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 2343, App
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 12, Appl
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 9, Appl
71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, A
72	51	10.9	387	7	US-11-219-282-20	Sequence 20, Appl
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 10, Appl
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-29
Perfect score: 465
Sequence: 1 MARMHCNKLGKEAEGIDFP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*

2: geneseqp1990s:*

3: geneseqp2000s:*

4: geneseqp2001s:*

5: geneseqp2002s:*

6: geneseqp2003as:*

7: geneseqp2003bs:*

8: geneseqp2004s:*

9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	87	5	ABB781175
2	459	98.7	87	5	ABB781174
3	339	72.9	88	5	ABB781171
4	339	72.9	88	5	ABB781172
5	339	72.9	88	5	ABB781173
6	339	72.9	88	6	ABP77219
7	310	66.7	87	5	ABB781176
8	300	64.5	87	5	ABB781148
9	300	64.5	87	5	ABB781147
10	282.5	60.8	86	5	ABB781149
11	278	59.8	89	9	AEBA1576
12	278	59.8	95	9	AEBA38294
13	276	59.4	87	5	ABB781177
14	263	56.6	88	5	ABB781178
15	255	54.8	87	5	ABB781153
16	245.5	52.8	92	6	ADA34169
17	242	52.0	91	5	ABB781150
18	241	51.8	87	5	ABB781152
19	238	51.2	87	5	ABB781151
20	229	49.2	87	5	ABB781169
21	227	48.8	87	5	ABB781170
22	227	48.8	122	7	ABO74609
23	226	48.6	88	5	ABB781154
24	226	48.6	90	5	ABB781155

25	218	46.9	93	7	ADF05158	Adf05158 Bacterial
26	211	45.4	107	7	ABO65445	AbO65445 Klebsiell
27	208	44.7	90	5	ABB78168	Abb78168 Amino aci
28	206	44.3	88	5	ABB78160	Abb78160 Amino aci
29	206	44.3	91	5	ABB78161	Abb78161 Amino aci
30	206	44.3	91	5	ABB78158	Abb78158 Amino aci
31	206	44.3	91	5	ABB78159	Abb78159 Amino aci
32	206	44.3	91	5	ABB78162	Abb78162 Amino aci
33	206	44.3	91	5	ABB78157	Abb78157 Amino aci
34	206	44.3	91	5	ABB78156	Abb78156 Amino aci
35	199	42.8	90	5	ABB78165	Abb78165 Amino aci
36	199	42.8	91	5	ABB78163	Abb78163 Amino aci
37	197.5	42.5	78	5	ABB78164	Abb78164 Amino aci
38	189.5	40.8	90	5	ABB78167	Abb78167 Amino aci
39	181	38.9	76	5	ABB78166	Abb78166 Amino aci
40	181	38.9	110	8	ADL05173	AdL05173 M. catarr
41	71.5	15.4	206	7	ADS92530	AdS92530 B. lichen
42	71.5	15.4	5458	6	ABM66970	ABm66970 Photorhab
43	71	15.3	511	9	ABM96738	ABm96738 M. xanthu
44	70	15.1	355	8	ADT57590	Adt57590 Plant pol
45	70	15.1	376	8	ADY09636	AdY09636 Plant ful
46	69.5	14.9	1104	7	ADB64352	AdB64352 Human pro
47	68.5	14.7	532	8	ADX73216	Adx73216 Plant ful
48	68.5	14.7	860	8	ADX93806	Adx93806 Plant ful
49	67	14.4	186	7	ADE08482	AdE08482 Novel pro
50	67	14.4	197	7	ABO67819	AbO67819 Protein e
51	67	14.4	265	6	ABU18123	AbU18123 Drosophi
52	66.5	14.3	869	4	ABB60212	Abb60212 Drosophi
53	66	14.2	354	7	ADH54604	Adh54604 Mouse dec
54	66	14.2	446	2	AAAY08889	AAy08889 Tobaccoc
55	66	14.2	722	5	AAAG90502	AAg90502 C glutami
56	65.5	14.1	409	4	ABB54118	Abb54118 Lactococc
57	65.5	14.1	678	5	ABB47819	Abb47819 Listeria
58	65.5	14.1	5024	4	AAAG82935	AAg82935 S. epider
59	65	14.0	222	9	ABM92850	ABm92850 M. xanthu
60	65	14.0	285	3	AAAG28710	AAg28710 Arabidops
61	65	14.0	510	5	ABB90889	Abb90889 Herbicida
62	65	14.0	510	8	ADN74505	Adn74505 Thale cre
63	65	14.0	2188	4	ABB65784	Abb65784 Drosophi
64	64.5	13.9	153	3	AAAG24680	AAg24680 Arabidops
65	64.5	13.9	195	3	AAAG24679	AAg24679 Arabidops
66	64.5	13.9	256	3	AAAG24678	AAg24678 Arabidops
67	64.5	13.9	256	7	ADB31835	AdB31835 Plant (A.
68	64.5	13.9	256	7	ADC46663	AdC46663 Thalecres
69	64.5	13.9	256	7	ADD30524	AdD30524 Plant yie
70	64.5	13.9	256	8	ADI43971	AdI43971 Plant tra
71	64	13.8	396	7	ADB62298	AdB62298 Rat Prote
72	64	13.8	446	2	AAAY08888	AAy08888 Potato Gn
73	64	13.8	508	3	AAAG48146	AAg48146 Arabidops
74	64	13.8	508	5	ABB91938	Abb91938 Herbicida
75	64	13.8	533	3	AAAG48145	AAg48145 Arabidops

ALIGNMENTS

RESULT 1	
ABB78175	ABB78175 standard; protein; 87 AA.
XX	
AC	ABB78175;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	
KW	hydroxyl radical; DNA damage; YggX homologue.
XX	
OS	Unidentified.
XX	
PN	US2002072118-A1.
XX	

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from Salmonella
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 100.0%; Score 465; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARMHCAKLGKEAEGLDPPPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
DB 1 MARMHCAKLGKEAEGLDPPPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
OY 61 RARQYLMKQTEKYPFEGGADQASGYVP 87
DB 61 RARQYLMKQTEKYPFEGGADQASGYVP 87

RESULT 2
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
XX AC ABB78174;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DB Amino acid sequence of a YggX homologue.
XX
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Unidentified.

XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.
XX
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from Salmonella
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 98.7%; Score 459; DB 5; Length 87;
Best Local Similarity 98.9%; Pred. No. 7.6e-50;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MARMHCAKLGKEAEGLDPPPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
DB 1 MARMHCAKLGKEAEGLDPPPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
OY 61 RARQYLMKQTEKYPFEGGADQASGYVP 87
DB 61 RARQYLMKQTEKYPFEGGADQASGYVP 87

RESULT 3
ABB78171
ID ABB78171 standard; protein; 88 AA.
XX
XX AC ABB78171;
XX
XX DT 29-AUG-2003 (revised)
XX DT 05-NOV-2002 (first entry)
XX
XX DE Amino acid sequence of a YggX homologue.

XX
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Neisseria gonorrhoeae.
XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.

XX
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX PI Downs D, Gralnick JA;
XX
XX DR WPI; 2002-589476/63.
XX
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-29
Perfect score: 465
Sequence: 1 MARMHCARKLCKEARGLDLP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: Pirl:*
2: Pirl2:*
3: Pirl3:*
4: Pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	72.9	88	2 H81014	conserved hypothet
2	241	51.8	90	2 C64013	hypothetical prote
3	227	48.8	90	2 H83003	conserved hypothet
4	226	48.6	90	2 C82320	conserved hypothet
5	206	44.3	91	2 AH0879	conserved hypothet
6	206	44.3	91	2 A85954	hypothetical prote
7	206	44.3	91	2 A65082	hypothetical prote
8	206	44.3	91	2 F91108	hypothetical prote
9	199	42.8	90	2 AI0116	conserved hypothet
10	197	42.4	105	2 C82624	conserved hypothet
11	181	38.9	93	2 E84994	hypothetical prote
12	74.5	16.0	203	2 A32009	sporulation repres
13	71	15.3	269	2 A69997	hypothetical prote
14	70	15.1	916	2 S22864	DNA topoisomerase
15	68	14.6	677	2 S33664	flagella-associate
16	67.5	14.5	1215	2 A86595	SWI/SNF family hel
17	67.5	14.5	1215	2 B72029	helicase, Snf2/Rad
18	66	14.2	354	2 A55454	decorin precursor
19	66	14.2	722	2 E86725	conserved hypothet
20	65.5	14.1	192	2 A83798	transcription repr
21	65.5	14.1	678	2 AB1130	penicillin-binding
22	65	14.0	260	2 F87276	hydrolyase, alpha/b
23	65	14.0	443	2 S21909	translational elonga
24	65	14.0	512	2 H86206	hypothetical prote
25	65	14.0	853	2 T08162	amylopullulanase (
26	65	14.0	2186	2 T13169	tiggrin - fruit fl
27	64.5	13.9	256	2 T45817	MADS transcription
28	64	13.8	396	2 T58168	growth factor arg3
29	64	13.8	508	2 T02486	hypothetical prote

30	64	13.8	823	2 A90761	hypothetical prote
31	64	13.8	823	2 B85822	hypothetical prote
32	64	13.8	823	2 F85624	hypothetical prote
33	63.5	13.7	252	2 B82181	oxidoreductase, sh
34	63.5	13.7	271	2 A84643	probable WRKY-type
35	63.5	13.7	1124	2 JX0293	zinc finger protei
36	63.5	13.7	1154	2 A56242	E-box-binding repr
37	63.5	13.7	1509	2 B89985	hypothetical prote
38	63	13.5	164	2 H95176	acetyltransferase,
39	63	13.5	164	2 B98043	conserved hypothet
40	63	13.5	434	2 F75425	tRNA nucleotidyltr
41	63	13.5	610	2 F86453	granule-bound star
42	62.5	13.4	134	2 H82969	hypothetical prote
43	62.5	13.4	236	1 T46967	diheme cytochrome
44	62.5	13.4	258	2 D95910	probable membrane-
45	62.5	13.4	399	2 F83633	hypothetical prote
46	62.5	13.4	488	2 AH2792	L-serine dehydrata
47	62.5	13.4	488	2 G97571	1-serine dehydrata
48	62.5	13.4	712	2 T48961	hypothetical prote
49	62	13.3	242	2 T18588	probable protein p
50	62	13.3	260	2 AH1639	hypothetical prote
51	62	13.3	295	2 AG1291	transcription acti
52	62	13.3	354	2 S29145	decorin precursor
53	62	13.3	413	2 T01043	hypothetical prote
54	62	13.3	489	2 D72762	hypothetical prote
55	62	13.3	611	2 A72393	hypothetical prote
56	61.5	13.2	295	2 T50798	hypothetical prote
57	61.5	13.2	373	2 S47911	PDS1 protein - yea
58	61.5	13.2	726	2 S52141	ATPase - Erwinia a
59	61	13.1	82	2 C71676	hypothetical prote
60	61	13.1	306	2 A97249	Zn-binding lipopro
61	61	13.1	441	2 A41591	endothelin recepto
62	61	13.1	823	2 T02959	kaurene synthase A
63	60.5	13.0	326	2 H82455	ISS transposase VC
64	60.5	13.0	635	2 S75668	DNA primase (EC 2.
65	60.5	13.0	1553	2 S67483	adenosinetriphosph
66	60.5	13.0	1827	1 UDHU	sucrose alpha-gluc
67	60.5	13.0	1867	2 S22775	MOT1 protein - yea
68	60	12.9	136	2 T17621	hypothetical prote
69	60	12.9	138	2 T15806	hypothetical prote
70	60	12.9	260	2 AH1276	hypothetical prote
71	60	12.9	282	2 D97138	DNA replication pr
72	60	12.9	333	1 S39699	monooxygenase homo
73	60	12.9	383	2 T17722	hypothetical prote
74	60	12.9	603	2 T02677	hypothetical prote
75	59.5	12.8	205	2 A30836	chlorophyll a/b-bl

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MCS8
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve,
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A/Experimental source: serogroup B, strain MCS8
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagsels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-29
Perfect score: 465
Sequence: 1 MARMHCAGKLGKAGLDPP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	91	1 FETP_BURMA	Q62iu9 burkholderi
2	465	100.0	91	1 FETP_BURPS	Q63sj4 burkholderi
3	442	95.1	91	2 Q4LS19_9BURK	Q4le19 burkholderi
4	409	88.0	91	1 FETP_RALSO	Q8y010 ralstonia s
5	355	76.3	90	1 FETP_CHRVO	Q7nsr4 chromobacte
6	339	72.9	88	1 FETP_NEIG1	Q5f553 neisseria g
7	339	72.9	88	1 FETP_NEIMA	P67615 neisseria m
8	339	72.9	88	1 FETP_NEIMB	P67616 neisseria m
9	330	71.0	90	1 FETP_NITEU	Q82xf2 nitrosomona
10	300	64.5	90	1 FETP_BORBR	Q7wh06 bordetella
11	300	64.5	90	1 FETP_BORPA	Q7w9q2 bordetella
12	300	64.5	90	1 FETP_BORPE	Q7wvc4 bordetella
13	282	60.6	89	1 FETP_LEGPL	Q5wvc4 legionella
14	278	59.8	89	1 FETP_LEGPA	Q5x3x9 legionella
15	278	59.8	89	1 FETP_LEGPH	Q5zu80 legionella
16	276	59.4	90	1 FETP_METCA	Q60aj7 methylococc
17	263	56.6	90	1 FETP_COXBU	Q83d06 coxiella bu
18	255	54.8	94	1 FETP_HABDU	Q7vkb6 haemophilus
19	243	52.3	90	1 FETP_IDILO	Q5qy58 idiominaria
20	241	51.8	90	1 FETP_HABIN	P44048 haemophilus
21	241	51.8	90	2 Q4OMD9_HAB18	Q4qmd9 haemophilus
22	240	51.6	92	2 Q4NM04_9DELT	Q4nmq4 anaeromycob
23	238	51.2	90	1 FETP_PASMU	Q9c1b9 pasteurella
24	238	51.2	91	1 FETP_XANAC	Q8pjh7 xanthomonas
25	237.5	51.1	90	1 FETP_AC1AD	Q6f1b3 acinetobact
26	237	51.0	90	2 Q4J228_AZOV1	Q4j228 azotobacter
27	236	50.8	92	1 FETP_XANOR	Q5gy22 xanthomonas
28	233	50.1	90	1 FETP_VIBPA	Q87115 vibrio para
29	232	49.9	90	1 FETP_VIBF1	Q5e7c0 vibrio fisc
30	231	49.7	90	1 FETP_VIBVU	Q8dc55 vibrio vuln
31	231	49.7	90	1 FETP_VIBVY	Q7mh14 vibrio vuln

32	230	49.5	90	2 Q6T7F6_PSEFL	Q6t7f6 pseudomonas
33	229	49.2	90	1 FETP_PSEBK	Q88r49 pseudomonas
34	228	49.0	92	1 FETP_XANCP	Q8p829 xanthomonas
35	228	49.0	92	2 Q4UW14_XANCP	Q4uw14 xanthomonas
36	227	48.8	90	1 FETP_PSEAR	Q9hu36 pseudomonas
37	226	48.6	90	1 FETP_VIBCH	Q9kur4 vibrio chol
38	226	48.6	92	1 FETP_MANSN	Q8bxc6 shewanella
39	223	48.0	91	1 FETP_PHOLL	Q65vc7 mannheimia
40	222	47.7	90	1 FETP_PSESM	Q7n711 photorhabdu
41	219	47.1	90	2 Q4KJ12_PSEF5	Q4kjt2 pseudomonas
42	216	46.5	96	2 Q4FVJ7_9GAMM	Q4fvj7 psychrobact
43	212	45.6	90	1 FETP_PHOPR	Q6lmk7 photobacter
44	208	44.7	90	1 FETP_PSESM	Q87uf5 pseudomonas
45	208	44.7	90	2 Q4ZLP3_PSESY	Q4zlp3 pseudomonas
46	207	44.5	90	1 FETP_YERPS	Q66wm3 yersinia ps
47	204	43.9	90	1 FETP_XYLFT	Q87d06 xylella fas
48	203.5	43.8	87	1 FETP_FRATT	Q5nhj8 francisella
49	201	43.2	90	1 FETP_ECOLI	P0a8p3 escherichia
50	201	43.2	90	1 FETP_BRWCT	Q6d8j9 erwinia car
51	201	43.2	90	1 FETP_SALCH	Q57k04 salmonella
52	201	43.2	90	1 FETP_SALPA	Q5pmn1 salmonella
53	201	43.2	90	1 FETP_SALTI	P67618 salmonella
54	201	43.2	90	1 FETP_SALTY	P67617 salmonella
55	201	43.2	90	1 FETP_SHIFL	P0a8p5 shigella fl
56	201	42.8	90	1 FETP_YERPE	Q8zhe7 yersinia pe
57	199	42.4	90	1 FETP_BCOL6	Q8fel9 escherichia
58	197	42.4	90	1 FETP_XYLF1	Q9pc73 xylella fas
59	197	42.4	90	1 FETP_BUCAP	Q8k925 buchnera ap
60	189	40.6	78	1 FETP_BUCAP	Q7vrg9 candidatus
61	183	39.4	79	1 FETP_BUCBP	P57618 buchnera ap
62	181	38.9	77	1 FETP_BUCAI	Q8d3c5 wiggleswort
63	169	36.3	78	1 FETP_BUCBP	Q89a44 buchnera ap
64	150	32.3	87	1 FETP_BUCBP	Q63pv8 burkholderi
65	75.5	16.2	661	2 Q63PV8_BURPS	Q7ng45 gloebacter
66	75	16.1	1222	2 Q7NG45_GLOVI	P11065 bacillus su
67	74.5	16.0	203	1 HPR_BACSU	Q82xa7 nitrosomona
68	74.5	16.0	461	2 Q82XA7_NITEU	Q72je7 thermus the
69	73	15.7	187	2 Q5CR96_CRYPV	Q5cr96 cryptospori
70	72.5	15.6	1328	2 Q5CR96_CRYPV	Q51wz9 anaeromycob
71	72	15.5	917	1 ATG9_MAGGR	Q4ng77 anaeromycob
72	71.5	15.4	192	2 Q4NQ77_9DELT	Q4ng77 anaeromycob
73	71.5	15.4	206	2 Q65LS8_BACLD	Q65l88 bacillus li
74	71.5	15.4	5457	2 Q7N2F7_PHOLL	Q7n2f7 photorhabdu
75	71	15.3	269	2 Q34935_BACSU	Q34935 bacillus su

ALIGNMENTS

RESULT 1
FETP_BURMA
ID FETP_BURMA STANDARD: PRT; 91 AA.
AC Q62IU9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BMA1752;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Nierman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarría S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;


```
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; CP000010; AAU48201.1; -; Genomic_DNA.
DR TIGR; BMA1752; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;

Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
   |||||
DB 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
   |||||
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87

RESULT 2
FETP BURPS
ID _FETP BURPS STANDARD; PRT; 91 AA.
AC O63SJ4;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BPSL2326;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.-M.,
RA Aktine T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagers K.,
RA Keith K.B., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songelvilai S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RA "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
```

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; BX571965; CAH36329.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;

Query Match 100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
   |||||
DB 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
   |||||
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87

RESULT 3
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ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laximer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Laximer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAL0100021; EAM18958.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match 95.1%; Score 442; DB 2; Length 91;
Best Local Similarity 94.3%; Pred. No. 2e-40;
Matches 82; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
   |||||
DB 1 MARMIHCAKLGKEAEGDFFPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
   |||||
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-29

Perfect score: 465
Sequence: 1 MARMHCAGKLGKAEGLDFP.....KQTEKVFEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	245.5	52.8	92	2	US-09-328-352-5456 Sequence 5456, Ap
2	227	48.8	122	2	US-09-252-991A-23355 Sequence 23355, A
3	218	46.9	93	2	US-09-543-681A-5443 Sequence 5443, Ap
4	211	45.4	107	2	US-09-489-039A-11962 Sequence 11962, A
5	181	38.9	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	15.3	511	2	US-09-902-540-15937 Sequence 15937, A
7	69.5	14.9	1104	2	US-10-104-047-2506 Sequence 2506, Ap
8	67.5	14.5	1218	2	US-09-438-185A-837 Sequence 837, App
9	67	14.4	197	2	US-09-489-039A-14336 Sequence 14336, A
10	66	14.2	446	2	US-09-591-466C-4 Sequence 4, Appli
11	65.5	14.1	342	2	US-09-605-703B-1526 Sequence 1526, Ap
12	65.5	14.1	342	2	US-09-605-703B-1528 Sequence 1528, Ap
13	65.5	14.1	5024	2	US-09-710-279-2964 Sequence 2964, Ap
14	65	14.0	222	2	US-09-902-540-12049 Sequence 12049, A
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16	64	13.8	1479	2	US-08-840-062-4 Sequence 4, Appli
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31	62	13.3	503	2	US-09-058-260-10	Sequence 10, Appli
32	62	13.3	503	2	US-09-058-260-12	Sequence 12, Appli
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34	62	13.3	503	2	US-09-058-260-30	Sequence 30, Appli
35	62	13.3	636	2	US-10-138-075-4	Sequence 4, Appli
36	62	13.3	1564	2	US-09-976-594-309	Sequence 309, Appl
37	62	13.3	2012	2	US-09-602-787A-50	Sequence 50, Appl
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43	61	13.1	823	1	US-08-405-254-5	Sequence 5, Appli
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47	60.5	13.0	277	2	US-09-902-540-14772	Sequence 14772, A
48	60.5	13.0	455	2	US-09-270-767-45790	Sequence 45790, A
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51	60.5	13.0	1827	2	US-09-079-723-179	Sequence 179, App
52	60.5	13.0	1867	2	US-09-824-574-5	Sequence 5, Appli
53	60	12.9	292	2	US-09-328-352-5836	Sequence 5836, Ap
54	60	12.9	414	2	US-09-902-540-12109	Sequence 12109, A
55	59.5	12.8	103	2	US-09-081-320-33	Sequence 33, Appli
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59	59.5	12.8	236	2	US-09-270-767-37158	Sequence 37158, A
60	59.5	12.8	236	2	US-09-270-767-52375	Sequence 52375, A
61	59.5	12.8	1017	2	US-09-762-724-12	Sequence 12, Appli
62	59.5	12.8	1023	2	US-09-762-724-14	Sequence 14, Appli
63	59.5	12.8	1792	1	US-08-962-284-4	Sequence 4, Appli
64	59.5	12.8	1838	2	US-09-431-614-8	Sequence 8, Appli
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66	59.5	12.8	1838	2	US-09-412-100-28	Sequence 28, Appli
67	59.5	12.7	510	2	US-09-248-796A-14490	Sequence 14490, A
68	59	12.7	925	2	US-09-902-540-15299	Sequence 15299, A
69	58.5	12.6	259	2	US-09-081-320-11	Sequence 11, Appli
70	58.5	12.6	259	2	US-09-574-141A-11	Sequence 11, Appli
71	58.5	12.6	259	2	US-09-707-780-11	Sequence 11, Appli
72	58.5	12.6	259	2	US-09-568-189A-11	Sequence 11, Appli
73	58.5	12.6	421	2	US-09-710-279-1820	Sequence 1820, Ap
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ALIGNMENTS

RESULT 1
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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RESULT 2
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Best Local Similarity	47.1%;	Pred. No. 9.4e-22;		
Matches 41; Conservative	17;	Mismatches 29;	Indels 0;	Gaps 0;

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RESULT 3
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; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
;
; LENGTH: 93
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; TYPE: PRT
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; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Db      64 DDRKLLIQEMVRFLF-EGDHVIDGYTP 90

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RESULT 4
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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RESULT 5
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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
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US-09-540-236-2859

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Best Local Similarity	39.3%;	Pred. No. 8.3e-16;		
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QY 64 QYLMKQTEKYFFEGADQASGYVP 87
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 Db 84 KYLNEQREKFLDNGDYEKDPAGYKP 107

RESULT 6
US-09-902-540-15937
; Sequence 15937, Application US/09902540

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Title: US-09-955-502A-29

Perfect score: 465

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and is derived by analysis of the total score distribution.

SUMMARIES

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4	339	72.9	88	3	US-09-955-502-27 Sequence 27, Appl
5	339	72.9	88	3	US-09-955-502-28 Sequence 28, Appl
6	310	66.7	87	3	US-09-955-502-31 Sequence 31, Appl
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8	300	64.5	87	3	US-09-955-502-3 Sequence 3, Appl
9	282.5	60.8	86	3	US-09-955-502-4 Sequence 4, Appl
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11	263	56.6	88	3	US-09-955-502-33 Sequence 33, Appl
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14	241	51.8	87	3	US-09-955-502-7 Sequence 7, Appl
15	238	49.2	87	3	US-09-955-502-6 Sequence 6, Appl
16	229	48.8	87	3	US-09-955-502-24 Sequence 24, Appl
17	227	48.6	87	3	US-09-955-502-25 Sequence 25, Appl
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21	206	44.3	88	3	US-09-955-502-15 Sequence 15, Appl
22	206	44.3	91	3	US-09-955-502-11 Sequence 11, Appl
23	206	44.3	91	3	US-09-955-502-12 Sequence 12, Appl
24	206	44.3	91	3	US-09-955-502-13 Sequence 13, Appl
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27	206	44.3	91	3	US-09-955-502-17 Sequence 17, Appl

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38	68.5	14.7	532	4	US-10-425-114-42582	Sequence 42582, A
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40	68.5	14.7	942	4	US-10-425-115-349562	Sequence 349562,
41	67.5	14.5	1027	4	US-10-437-963-156087	Sequence 156087,
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45	67	14.4	439	4	US-10-437-963-166724	Sequence 166724,
46	67	14.4	443	5	US-10-732-923-17533	Sequence 17533, A
47	66.5	14.3	869	6	US-11-097-143-7428	Sequence 7428, Ap
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53	65.5	14.1	409	3	US-09-738-626-4256	Sequence 4256, Ap
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55	65.5	14.1	851	4	US-10-437-963-113913	Sequence 113913,
56	65	14.0	443	5	US-10-732-923-17535	Sequence 17535, A
57	65	14.0	2188	6	US-11-097-143-24144	Sequence 24144, A
58	64.5	13.9	142	4	US-10-437-963-172454	Sequence 172454,
59	64.5	13.9	256	4	US-10-286-264-62	Sequence 62, Appl
60	64.5	13.9	256	4	US-10-295-403-68	Sequence 68, Appl
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63	64.5	13.9	256	5	US-10-732-923-16227	Sequence 16227, A
64	64.5	13.9	256	5	US-10-732-923-16236	Sequence 16236, A
65	64.5	13.9	256	5	US-10-225-066A-556	Sequence 556, App
66	64	13.8	237	4	US-10-425-115-319141	Sequence 319141,
67	64	13.8	446	4	US-10-615-144-2	Sequence 2, Appl
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75	63.5	13.7	271	4	US-10-412-699B-652	Sequence 652, App

ALIGNMENTS

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; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234, 588
; PRIOR FILING DATE: 2000-09-22
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

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SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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5	63.5	13.7	398	6	US-10-793-626-44 Sequence 44, Appl1
6	63.5	13.7	398	6	US-10-793-626-1498 Sequence 1498, Ap
7	59.5	12.8	832	7	US-11-098-686-10182 Sequence 10182, A
8	59.5	12.8	1841	7	US-11-057-058-63 Sequence 63, Appl1
9	58.5	12.6	421	6	US-10-793-626-1820 Sequence 1820, Ap
10	57.5	12.4	447	7	US-11-024-959-286 Sequence 286, App
11	57.5	12.4	787	6	US-10-467-657-2832 Sequence 2832, Ap
12	57	12.3	209	5	US-09-995-493-94 Sequence 94, Appl1
13	56.5	12.2	575	7	US-11-098-686-10635 Sequence 10635, A
14	56.5	12.2	1077	7	US-11-054-281-110 Sequence 110, App
15	56	12.0	381	7	US-11-098-686-11284 Sequence 11284, A
16	56	12.0	867	7	US-11-072-512-3052 Sequence 3052, Ap
17	56	12.0	3803	6	US-10-995-561-773 Sequence 773, App
18	56	12.0	3960	6	US-10-995-561-771 Sequence 771, App
19	56	12.0	5335	6	US-10-995-561-777 Sequence 777, App
20	56	12.0	5405	6	US-10-995-561-774 Sequence 774, App
21	56	12.0	5415	6	US-10-995-561-779 Sequence 779, App
22	56	12.0	5464	6	US-10-995-561-775 Sequence 775, App
23	55.5	11.9	360	7	US-11-019-711-67 Sequence 67, Appl1
24	55.5	11.9	563	7	US-11-072-512-3460 Sequence 3460, Ap
25	55.5	11.9	622	7	US-11-070-080-22 Sequence 22, Appl1

26	54.5	11.7	107	5	US-09-995-493-34	Sequence 34, Appl1
27	54.5	11.7	299	6	US-10-362-772-2	Sequence 2, Appl1
28	54.5	11.7	355	6	US-10-878-556A-10	Sequence 10, Appl1
29	54.5	11.7	505	7	US-11-072-512-3519	Sequence 3519, Ap
30	54.5	11.7	668	7	US-11-111-239-13	Sequence 13, Appl1
31	54.5	11.7	805	7	US-11-108-539-2	Sequence 2, Appl1
32	54.5	11.7	1134	7	US-11-043-889-34	Sequence 34, Appl1
33	54.5	11.7	1187	7	US-11-043-889-46	Sequence 46, Appl1
34	54.5	11.7	1476	6	US-10-647-956A-4	Sequence 4, Appl1
35	54	11.6	437	6	US-10-454-437-84	Sequence 84, Appl1
36	54	11.6	593	7	US-11-194-246-317	Sequence 317, App
37	54	11.6	629	6	US-10-821-234-1528	Sequence 1528, Ap
38	54	11.6	634	7	US-11-072-512-2300	Sequence 2300, Ap
39	54	11.6	8746	7	US-11-098-686-10232	Sequence 10232, A
40	53.5	11.5	389	7	US-11-012-762-72	Sequence 72, Appl1
41	53.5	11.5	757	7	US-11-067-121-16	Sequence 16, Appl1
42	53.5	11.5	757	7	US-11-186-284-41	Sequence 41, Appl1
43	53	11.4	532	6	US-10-063-703-72	Sequence 72, Appl1
44	53	11.4	532	7	US-11-102-240-72	Sequence 72, Appl1
45	53	11.4	620	6	US-10-453-372-1130	Sequence 1130, Ap
46	53	11.4	624	6	US-10-453-372-1126	Sequence 1126, Ap
47	53	11.4	925	6	US-10-453-372-1124	Sequence 1124, Ap
48	53	11.4	931	7	US-11-230-145-2	Sequence 2, Appl1
49	53	11.4	966	6	US-10-877-346-32	Sequence 32, Appl1
50	53	11.4	972	6	US-10-453-372-1128	Sequence 1128, Ap
51	52.5	11.3	160	6	US-10-821-234-1359	Sequence 1359, Ap
52	52.5	11.3	384	7	US-11-219-282-19	Sequence 19, Appl1
53	52.5	11.3	398	7	US-11-012-762-74	Sequence 74, Appl1
54	52.5	11.3	407	6	US-10-995-561-1014	Sequence 1014, Ap
55	52.5	11.3	470	6	US-10-485-517-319	Sequence 319, App
56	52.5	11.3	481	6	US-10-467-657-420	Sequence 420, App
57	52.5	11.3	1261	7	US-11-234-786-538	Sequence 538, App
58	52.5	11.3	1325	6	US-10-329-258-10	Sequence 10, Appl1
59	52.5	11.3	1325	7	US-11-124-367A-410	Sequence 410, App
60	52	11.2	190	6	US-10-467-657-1426	Sequence 1426, Ap
61	52	11.2	241	6	US-10-873-528-116	Sequence 116, App
62	52	11.2	271	7	US-11-098-686-10795	Sequence 10795, A
63	52	11.2	291	6	US-10-883-512-103	Sequence 103, App
64	52	11.2	383	7	US-11-072-512-3579	Sequence 3579, Ap
65	52	11.2	436	7	US-11-072-512-2338	Sequence 2338, Ap
66	52	11.2	457	6	US-10-131-826A-236	Sequence 236, App
67	52	11.2	465	6	US-10-467-657-5040	Sequence 5040, App
68	52	11.2	495	7	US-11-072-512-3469	Sequence 3469, Ap
69	52	11.2	617	6	US-10-982-545-2	Sequence 2, Appl1
70	52	11.2	922	7	US-10-072-512-2694	Sequence 2694, Ap
71	51.5	11.1	117	6	US-10-771-257-60	Sequence 60, Appl1
72	51.5	11.1	117	7	US-11-127-677-58	Sequence 58, Appl1
73	51.5	11.1	662	7	US-11-072-175-184	Sequence 184, App
74	51.5	11.1	893	7	US-11-072-512-3504	Sequence 3504, Ap
75	51.5	11.1	1438	6	US-10-511-559-73	Sequence 73, Appl1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCAXLCKEAREGLDFP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq 21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	87	5	ABB78175 Amino aci
2	459	98.7	87	5	ABB78174 Amino aci
3	339	72.9	88	5	ABB78171 Amino aci
4	339	72.9	88	5	ABB78172 Amino aci
5	339	72.9	88	5	ABB78173 Amino aci
6	339	72.9	88	6	ABP77219 N. gonorr
7	310	66.7	87	5	ABB78176 Amino aci
8	300	64.5	87	5	ABB78148 Amino aci
9	300	64.5	87	5	ABB78147 Amino aci
10	282.5	60.8	86	5	ABB78149 Amino aci
11	278	59.8	89	9	AEB41576 L. pneumo
12	278	59.8	89	9	AEB38294 L. pneumo
13	276	59.4	87	5	ABB78177 Amino aci
14	263	56.6	88	5	ABB78178 Amino aci
15	255	54.8	87	5	ABB78153 Amino aci
16	245.5	52.8	92	6	ADA34169 Acinetoba
17	242	52.0	91	5	ABB78150 Amino aci
18	241	51.8	87	5	ABB78152 Amino aci
19	238	51.2	87	5	ABB78151 Amino aci
20	229	49.2	87	5	ABB78169 Amino aci
21	227	48.8	87	5	ABB78170 Amino aci
22	227	48.8	122	7	ABO74609 Pseudomon
23	226	48.6	88	5	ABB78154 Amino aci
24	226	48.6	90	5	ABB78155 Amino aci

25	218	46.9	93	7	ADP05158	Adf05158 Bacterial
26	211	45.4	107	7	ABO65445	ABO65445 Klebsiell
27	208	44.7	90	5	ABB78168	Abb78168 Amino aci
28	206	44.3	88	5	ABB78160	Abb78160 Amino aci
29	206	44.3	91	5	ABB78161	Abb78161 Amino aci
30	206	44.3	91	5	ABB78158	Abb78158 Amino aci
31	206	44.3	91	5	ABB78159	Abb78159 Amino aci
32	206	44.3	91	5	ABB78162	Abb78162 Amino aci
33	206	44.3	91	5	ABB78157	Abb78157 Amino aci
34	206	44.3	91	5	ABB78156	Abb78156 Amino aci
35	199	42.8	90	5	ABB78165	Abb78165 Amino aci
36	199	42.8	91	5	ABB78163	Abb78163 Amino aci
37	197.5	42.5	78	5	ABB78164	Abb78164 Amino aci
38	189.5	40.8	90	5	ABB78167	Abb78167 Amino aci
39	181	38.9	76	5	ABB78166	Abb78166 Amino aci
40	181	38.9	110	8	ADL05173	Adl05173 M. catar
41	71.5	15.4	206	7	ADS92530	Ads92530 B. lichen
42	71.5	15.4	5458	6	ABM66970	Abm66970 Phototrab
43	71	15.3	511	9	ABM96738	Abm96738 M. xanthu
44	70	15.1	355	8	ADT57590	Adt57590 Plant pol
45	70	15.1	376	8	ADY09636	Ady09636 Plant ful
46	69.5	14.9	1104	7	ADB64352	Adb64352 Human pro
47	68.5	14.7	532	8	ADX73216	Adx73216 Plant ful
48	68.5	14.7	860	8	ADX93806	Adx93806 Plant ful
49	67	14.4	186	7	ADB08482	Adb08482 Novel pro
50	67	14.4	197	7	ABO67819	Aboc67819 Klebsiell
51	67	14.4	265	6	ABU18123	Abu18123 Protein e
52	66.5	14.3	869	4	ABB60212	Abb60212 Drosophil
53	66	14.2	354	7	ADH54604	Adh54604 Mouse dec
54	66	14.2	446	2	AAV08889	Aav08889 Tobacco G
55	66	14.2	722	5	ABB54118	Abb54118 Lactococc
56	65.5	14.1	409	4	AAQ90502	Aaq90502 C glutam
57	65.5	14.1	678	5	ABB47819	Abb47819 Listeria
58	65.5	14.1	5024	4	AAQ82935	Aaq82935 S. epider
59	65	14.0	222	9	ABM92850	Abm92850 M. xanthu
60	65	14.0	285	3	AAQ28710	Aaq28710 Arabidops
61	65	14.0	510	5	ABB90889	Abb90889 Herbicida
62	65	14.0	510	8	ADN74505	Adn74505 Thale cre
63	65	14.0	2188	4	ABB65784	Abb65784 Drosophil
64	64.5	13.9	153	3	AAQ24680	Aaq24680 Arabidops
65	64.5	13.9	195	3	AAQ24679	Aaq24679 Arabidops
66	64.5	13.9	256	3	AAQ24678	Aaq24678 Arabidops
67	64.5	13.9	256	7	ADB31835	Adb31835 Plant (A.
68	64.5	13.9	256	7	ADC46663	Adc46663 Thalecres
69	64.5	13.9	256	7	ADD30524	Add30524 Plant yie
70	64.5	13.9	256	8	ADI43971	Adi43971 Plant tra
71	64	13.8	396	7	ADB62298	Adb62298 Rat Prote
72	64	13.8	446	2	AAV08888	Aav08888 Potato Gn
73	64	13.8	508	3	AAQ48146	Aaq48146 Arabidops
74	64	13.8	508	5	ABB91938	Abb91938 Herbicida
75	64	13.8	533	3	AAQ48145	Aaq48145 Arabidops

ALIGNMENTS

RESULT 1	
ABB78175	standard; protein; 87 AA.
ID	ABB78175
XX	
AC	ABB78175;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM	hydroxyl radical; DNA damage; YggX homologue.
XX	
OS	Unidentified.
XX	
PN	US2002072118-A1.
XX	

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;
SQ
Query Match 100.0%; Score 465; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.3e-50;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARMHCAKLGKEAEGLDFFPPLPGELGKRLYESVSKQAWQDWLKKQQTMLINENRLNMADP 60
DB 1 MARMHCAKLGKEAEGLDFFPPLPGELGKRLYESVSKQAWQDWLKKQQTMLINENRLNMADP 60
QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB
RESULT 2
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
AC ABB78174;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;
SQ
Query Match 98.7%; Score 459; DB 5; Length 87;
Best Local Similarity 98.9%; Pred. No. 7.6e-50;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MARMHCAKLGKEAEGLDFFPPLPGELGKRLYESVSKQAWQDWLKKQQTMLINENRLNMADP 60
DB 1 MARMHCAKLGKEAEGLDFFPPLPGELGKRLYESVSKQAWQDWLKKQQTMLINENRLNMADP 60
QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
DB
RESULT 3
ABB78171
ID ABB78171 standard; protein; 88 AA.
XX
AC ABB78171;
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Neisseria gonorrhoeae.
OS
XX
XX US2002072118-A1.
XX
XX 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
XX
XX Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-30

Perfect score: 465
Sequence: 1 MARMHCALGKRAEGLDFP.....KQTEKYFPGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	72.9	88	2	H81014 conserved hypot
2	241	51.8	90	2	C64013 hypothetical prote
3	227	48.8	90	2	H83003 conserved hypot
4	226	48.6	90	2	C82320 conserved hypot
5	206	44.3	91	2	AH0879 conserved hypot
6	206	44.3	91	2	A85954 hypothetical prote
7	206	44.3	91	2	A65082 hypothetical prote
8	206	44.3	91	2	F91108 hypothetical prote
9	199	42.8	90	2	AI0116 conserved hypot
10	197	42.4	105	2	C82624 conserved hypot
11	181	38.9	93	2	E84994 hypothetical prote
12	74.5	16.0	203	2	A32009 sporulation repres
13	71	15.3	269	2	A69997 hypothetical prote
14	70	15.1	916	2	S22864 DNA topoisomerase
15	68	14.6	677	2	S33664 flagella-associate
16	67.5	14.5	1215	2	A86595 SWI/SNF family hel
17	67.5	14.5	1215	2	B72029 helicase, Snf2/Rad
18	66	14.2	354	2	A55454 decorin precursor
19	66	14.2	722	2	B86725 conserved hypot
20	65.5	14.1	192	2	A83798 transcription repr
21	65.5	14.1	678	2	AB1130 penicillin-binding
22	65	14.0	260	2	F87276 hydrolase, alpha/b
23	65	14.0	443	2	S21909 translation elonga
24	65	14.0	512	2	H86206 hypothetical prote
25	65	14.0	853	2	T08162 amylopolyluanase (
26	65	14.0	2186	2	T13169 tigrin - fruit fl
27	64.5	13.9	256	2	T45817 MDS transcription
28	64	13.8	396	2	I58168 growth factor arg3
29	64	13.8	508	2	T02486 hypothetical prote

30	64	13.8	823	2	A90761 hypothetical prote
31	64	13.8	823	2	B85822 hypothetical prote
32	64	13.8	823	2	F85624 hypothetical prote
33	63.5	13.7	252	2	B82181 oxidoreductase, sh
34	63.5	13.7	271	2	A84643 probable WRKY-type
35	63.5	13.7	1124	2	JX0293 zinc finger protei
36	63.5	13.7	1154	2	A56242 E-box-binding repr
37	63.5	13.7	1509	2	B89985 hypothetical prote
38	63	13.5	164	2	H95176 acetyltransferase,
39	63	13.5	164	2	B98043 conserved hypot
40	63	13.5	434	2	F75425 tRNA nucleotidyltr
41	63	13.5	610	2	F86453 granule-bound star
42	62.5	13.4	134	2	H82969 hypothetical prote
43	62.5	13.4	236	1	T46967 dihem cytochrome
44	62.5	13.4	258	2	D95910 probable membrane-
45	62.5	13.4	399	2	F83633 L-serine dehydrata
46	62.5	13.4	488	2	AH2792 1-serine dehydrata
47	62.5	13.4	488	2	G97571 hypothetical prote
48	62.5	13.4	712	2	T48961 probable protein p
49	62	13.3	242	2	T18588 hypothetical prote
50	62	13.3	260	2	AH1639 transcription acti
51	62	13.3	295	2	AG1291 decarin precursor
52	62	13.3	354	2	S29145 hypothetical prote
53	62	13.3	413	2	T01043 hypothetical prote
54	62	13.3	489	2	D72762 hypothetical prote
55	62	13.3	611	2	A72393 hypothetical prote
56	61.5	13.2	295	2	T50798 pps1 protein - yea
57	61.5	13.2	373	2	S47911 ATPase - Brwinia a
58	61.5	13.2	726	2	S52141 hypothetical prote
59	61	13.1	82	2	C71676 Zn-binding lipopro
60	61	13.1	306	2	A97249 endothelin recepto
61	61	13.1	441	2	A41591 kaurene synthase A
62	61	13.1	823	2	T02959 ISS transposase VC
63	60.5	13.0	326	2	H82455 DNA primase (BC 2.
64	60.5	13.0	635	2	S75668 adenosinetriphosph
65	60.5	13.0	1553	2	S67483 sucrose alpha-gluc
66	60.5	13.0	1827	1	UUHU MORT1 protein - yea
67	60.5	13.0	1867	2	S22775 hypothetical prote
68	60	12.9	136	2	T17621 hypothetical prote
69	60	12.9	138	2	T15806 hypothetical prote
70	60	12.9	260	2	AH1276 DNA replicatio pr
71	60	12.9	282	2	D97138 monooxygenase homo
72	60	12.9	333	1	S39699 hypothetical prote
73	60	12.9	383	2	T17722 hypothetical prote
74	60	12.9	603	2	T02677 chlorophyll a/b-bl
75	59.5	12.8	205	2	A30836

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tetelin, H.; Saunderson, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A/Experimental source: serogroup B, strain MC58
R/Parhill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-30

Perfect score: 465
Sequence: 1 MARMHCALGKARGGLDFP.....KQTEKYFEGGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	91	1	FETP_BURMA
2	465	100.0	91	1	FETP_BURPS
3	442	95.1	91	2	Q4LS19_9BURK
4	409	88.0	91	1	FETP_RALSO
5	355	76.3	90	1	FETP_CHRVO
6	339	72.9	88	1	FETP_NEIGI
7	339	72.9	88	1	FETP_NEIMA
8	339	72.9	88	1	FETP_NEIMB
9	330	71.0	90	1	FETP_NITEU
10	300	64.5	90	1	FETP_BORBR
11	300	64.5	90	1	FETP_BORPA
12	300	64.5	90	1	FETP_BORPE
13	282	60.6	89	1	FETP_LEGPL
14	278	59.8	89	1	FETP_LEGPA
15	278	59.8	89	1	FETP_LEGPH
16	276	59.4	90	1	FETP_METCA
17	263	56.6	90	1	FETP_COXBU
18	255	54.8	94	1	FETP_HAEDU
19	243	52.3	90	1	FETP_IDILO
20	241	51.8	90	1	FETP_HAEIN
21	241	51.8	90	2	Q4QMD9_HAE18
22	240	51.6	92	2	Q4NMQ4_9DELT
23	238	51.2	90	1	FETP_PASMU
24	238	51.2	91	1	FETP_XANAC
25	237.5	51.1	90	1	FETP_XANAD
26	237	51.0	90	2	Q4J228_AZOV1
27	236	50.8	92	1	FETP_XANOR
28	233	50.1	90	1	FETP_VIBPA
29	232	49.9	90	1	FETP_VIBFI
30	231	49.7	90	1	FETP_VIBVU
31	231	49.7	90	1	FETP_VIBVY

ALIGNMENTS

RESULT 1	ALIGNMENTS
FETP_BURMA	Q6T7F6_PSEFL
ID FETP_BURMA	Q88r49_pseudomonas
AC Q62IU9;	Q8p829_xanthomonas
DT 13-SEP-2005 (Rel. 48, Created)	Q4uW14_xanCP
DT 13-SEP-2005 (Rel. 48, Last sequence update)	Q9hu36_pseudomonas
DT 13-SEP-2005 (Rel. 48, Last annotation update)	Q9kur4_vibrio chol
DB Probable Fe(2+) trafficking protein.	Q8ebx6_shewanella
GN Ordered locus names=BMA1752;	Q65vt7_mannheimia
OS Burkholderia mallei (Pseudomonas mallei).	Q7n7i1_photorhabdu
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;	Q4Kjt2_pseudomonas
OC Burkholderiaceae; Burkholderia.	Q4fvj7_psychrobact
OX NCBI_TaxID=13373;	Q61mk7_photobacter
RN [1]	Q87uf5_pseudomonas
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	Q66m3_yersinia ps
RC STRAIN=ATCC 23344;	Q5nhj8_francisella
RX PubMed=15377793; DOI=10.1073/pnas.040306101;	P0a8p4_escherichia
RA Nieman W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,	Q6d8j9_erwinia car
RA Feldblyum T.V., Ulrich R.L., Roming C.M., Brinkac L.M.,	Q5pmm1_salmonella
RA Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,	P67618_salmonella
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,	P67617_salmonella
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,	P0a8ps_shigella fl
RA Sarría S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,	Q8zhe7_yersinia pe
RA Zafar N., Zhou L., Fraser C.M.;	Q8fcl9_escherichia


```
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; CP000010; AAU48201.1; -; Genomic_DNA.
DR TIGR; BMA1752; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9gX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_Y9gX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;

Query Match          100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMHCAGLGEAEGLDFFPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMAPD 60
   |||||
DB 1 MARMHCAGLGEAEGLDFFPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMAPD 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
   |||||
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87

RESULT 2
FETP_BURPS
ID FETP_BURPS STANDARD; PRT; 91 AA.
AC Q63S54;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BPSL2326;
OS Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosslet B., Davis P., Deshazer D.,
RA Feltham T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA Songsiyilai S., Stevens K., Tumapa S., Vesaratchavee M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei."
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9gX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_Y9gX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;

Query Match          100.0%; Score 465; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 6e-43;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMHCAGLGEAEGLDFFPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMAPD 60
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DB 1 MARMHCAGLGEAEGLDFFPLPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMAPD 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
   |||||
DB 61 RARQYLMKQTEKYFFEGADQASGYVP 87

RESULT 3
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ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cecapcia complex.
OX NCBI_TaxID=331272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israeli S., Pitluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAL0100021; EAM18958.1; -; Genomic_DNA.
KW Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match          95.1%; Score 442; DB 2; Length 91;
Best Local Similarity 94.3%; Pred. No. 2e-40;
Matches 82; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

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DB 1 MARMHCAGLGEAEGLDFFPLPGELGKRLYESVSKAWQDWLKKQOTMLINENRLNMAPD 60

QY 61 RARQYLMKQTEKYFFEGADQASGYVP 87
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCAGKLGKAEGLDFP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCFUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	245.5	52.8	92	2	US-09-328-352-5456 Sequence 5456, Ap
2	227	48.8	122	2	US-09-252-991A-23355 Sequence 23355, A
3	218	46.9	93	2	US-09-543-681A-5443 Sequence 5443, Ap
4	211	45.4	107	2	US-09-489-039A-11962 Sequence 11962, A
5	181	38.9	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	15.3	511	2	US-09-902-540-15937 Sequence 15937, A
7	69.5	14.9	1104	2	US-10-104-047-2506 Sequence 2506, Ap
8	67.5	14.5	1218	2	US-09-438-185A-837 Sequence 837, App
9	67	14.4	197	2	US-09-489-039A-14336 Sequence 14336, A
10	66	14.2	446	2	US-09-591-466C-4 Sequence 4, Appli
11	65.5	14.1	342	2	US-09-605-703B-1526 Sequence 1526, Ap
12	65.5	14.1	342	2	US-09-605-703B-1528 Sequence 1528, Ap
13	65.5	14.1	5024	2	US-09-710-279-2964 Sequence 2964, Ap
14	65	14.0	222	2	US-09-902-540-12049 Sequence 12049, A
15	64	13.8	446	2	US-09-591-466C-2 Sequence 2, Appli
16	64	13.8	1479	2	US-08-840-062-4 Sequence 4, Appli
17	63.5	13.7	398	2	US-09-710-279-44 Sequence 44, Appli
18	63.5	13.7	398	2	US-09-710-279-1498 Sequence 1498, Ap
19	63.5	13.7	417	2	US-09-134-001C-3810 Sequence 3810, Ap
20	63.5	13.7	1125	2	US-09-949-016-10194 Sequence 10194, A
21	63.5	13.7	1509	2	US-09-676-519-27 Sequence 27, Appli
22	63.5	13.7	10182	2	US-09-134-001C-3159 Sequence 3159, Ap
23	62.5	13.4	179	2	US-09-252-991A-17099 Sequence 17099, A
24	62.5	13.4	401	2	US-09-252-991A-17272 Sequence 17272, A
25	62	13.3	498	2	US-09-058-260-16 Sequence 16, Appli
26	62	13.3	503	1	US-08-781-802-2 Sequence 2, Appli
27	62	13.3	503	1	US-08-781-802-10 Sequence 10, Appli

28	62	13.3	503	1	US-08-781-802-12	Sequence 12, Appli
29	62	13.3	503	2	US-08-694-078-2	Sequence 2, Appli
30	62	13.3	503	2	US-09-058-260-2	Sequence 2, Appli
31	62	13.3	503	2	US-09-058-260-10	Sequence 10, Appli
32	62	13.3	503	2	US-09-058-260-12	Sequence 12, Appli
33	62	13.3	503	2	US-09-058-260-28	Sequence 28, Appli
34	62	13.3	503	2	US-09-058-260-30	Sequence 30, Appli
35	62	13.3	636	2	US-10-138-075-4	Sequence 4, Appli
36	62	13.3	1564	2	US-09-976-594-309	Sequence 309, App
37	62	13.3	2012	2	US-09-602-787A-50	Sequence 50, Appli
38	61.5	13.2	125	2	US-09-640-211A-762	Sequence 762, App
39	61.5	13.2	555	2	US-09-328-352-5873	Sequence 5873, Ap
40	61.5	13.2	1277	2	US-09-602-787A-54	Sequence 54, Appli
41	61	13.1	163	2	US-09-270-767-33714	Sequence 33714, A
42	61	13.1	823	1	US-08-261-465-1	Sequence 1, Appli
43	61	13.1	823	1	US-08-405-254-5	Sequence 5, Appli
44	60.5	13.0	266	2	US-09-252-991A-21786	Sequence 21786, A
45	60.5	13.0	269	2	US-09-270-767-33833	Sequence 33833, A
46	60.5	13.0	269	2	US-09-270-767-49050	Sequence 49050, A
47	60.5	13.0	277	2	US-09-902-540-14772	Sequence 14772, A
48	60.5	13.0	455	2	US-09-270-767-45790	Sequence 45790, A
49	60.5	13.0	1003	2	US-09-949-016-10627	Sequence 10627, A
50	60.5	13.0	1827	2	US-09-443-780C-14	Sequence 14, Appli
51	60.5	13.0	1827	2	US-09-079-723-179	Sequence 179, App
52	60.5	13.0	1867	2	US-09-824-574-5	Sequence 5, Appli
53	60	12.9	292	2	US-09-328-352-5836	Sequence 5836, Ap
54	60	12.9	414	2	US-09-902-540-12109	Sequence 12109, A
55	59.5	12.8	103	2	US-09-081-320-33	Sequence 33, Appli
56	59.5	12.8	103	2	US-09-574-141A-33	Sequence 33, Appli
57	59.5	12.8	103	2	US-09-707-780-33	Sequence 33, Appli
58	59.5	12.8	103	2	US-09-568-189A-33	Sequence 33, Appli
59	59.5	12.8	236	2	US-09-270-767-37158	Sequence 37158, A
60	59.5	12.8	236	2	US-09-762-724-12	Sequence 12, Appli
61	59.5	12.8	1017	2	US-09-962-284-4	Sequence 4, Appli
62	59.5	12.8	1023	2	US-08-962-284-2	Sequence 2, Appli
63	59.5	12.8	1792	2	US-09-431-614-8	Sequence 8, Appli
64	59.5	12.8	1838	2	US-09-596-784-2	Sequence 2, Appli
65	59.5	12.8	1838	2	US-09-412-100-28	Sequence 28, Appli
66	59.5	12.8	1838	2	US-09-248-796A-14490	Sequence 14490, A
67	59	12.7	510	2	US-09-902-540-15299	Sequence 15299, A
68	59	12.7	925	2	US-09-081-320-11	Sequence 11, Appli
69	58.5	12.6	259	2	US-09-574-141A-11	Sequence 11, Appli
70	58.5	12.6	259	2	US-09-707-780-11	Sequence 11, Appli
71	58.5	12.6	259	2	US-09-568-189A-11	Sequence 11, Appli
72	58.5	12.6	421	2	US-09-710-279-1820	Sequence 1820, Ap
73	58.5	12.6	427	2	US-09-134-001C-5141	Sequence 5141, Ap
74	58.5	12.6				
75	58.5	12.6				

ALIGNMENTS

RESULT 1
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456
Query Match 52.8%; Score 245.5; DB 2; Length 92;
Best Local Similarity 51.1%; Pred. No. 2.5e-24;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCAGKIGKAEGLDFP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*

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5:	/cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6:	/cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	100.0	87	3	US-09-955-502-29 Sequence 29, Appl
2	465	100.0	87	3	US-09-955-502-30 Sequence 30, Appl
3	339	72.9	88	3	US-09-955-502-26 Sequence 26, Appl
4	339	72.9	88	3	US-09-955-502-27 Sequence 27, Appl
5	339	72.9	88	3	US-09-955-502-28 Sequence 28, Appl
6	310	66.7	87	3	US-09-955-502-31 Sequence 31, Appl
7	300	64.5	87	3	US-09-955-502-2
8	300	64.5	87	3	US-09-955-502-3
9	282.5	60.8	86	3	US-09-955-502-4
10	276	59.4	87	3	US-09-955-502-32
11	263	56.6	88	3	US-09-955-502-33
12	255	54.8	87	3	US-09-955-502-8
13	242	52.0	91	3	US-09-955-502-5
14	241	51.8	87	3	US-09-955-502-7
15	238	51.2	87	3	US-09-955-502-6
16	229	49.2	87	3	US-09-955-502-24
17	227	48.8	87	3	US-09-955-502-25
18	226	48.6	88	3	US-09-955-502-9
19	226	48.6	90	3	US-09-955-502-10
20	208	44.7	90	3	US-09-955-502-23
21	206	44.3	88	3	US-09-955-502-15
22	206	44.3	91	3	US-09-955-502-11
23	206	44.3	91	3	US-09-955-502-12
24	206	44.3	91	3	US-09-955-502-13
25	206	44.3	91	3	US-09-955-502-14
26	206	44.3	91	3	US-09-955-502-16
27	206	44.3	91	3	US-09-955-502-17

28	199	42.8	90	3	US-09-955-502-20	Sequence 20, Appl
29	199	42.8	91	3	US-09-955-502-18	Sequence 18, Appl
30	197.5	42.5	78	3	US-09-955-502-19	Sequence 19, Appl
31	197	42.4	89	3	US-09-955-502-22	Sequence 22, Appl
32	181	38.9	76	3	US-09-955-502-21	Sequence 21, Appl
33	71.5	15.4	206	5	US-10-510-812-76	Sequence 76, Appl
34	70	15.1	355	5	US-10-739-930-7667	Sequence 7667, Ap
35	70	15.1	376	4	US-10-425-114-65451	Sequence 65451, A
36	69.5	14.9	1104	4	US-10-104-047-2506	Sequence 2506, Ap
37	69	14.8	313	4	US-10-437-963-173240	Sequence 173240,
38	68.5	14.7	532	4	US-10-425-114-42582	Sequence 42582, A
39	68.5	14.7	860	4	US-10-425-114-56470	Sequence 56470, A
40	67.5	14.5	942	4	US-10-425-115-349562	Sequence 349562,
41	67.5	14.5	1027	4	US-10-437-963-156087	Sequence 156087,
42	67.5	14.5	1215	5	US-10-732-923-8185	Sequence 8185, Ap
43	67.5	14.5	1215	5	US-10-732-923-8195	Sequence 8195, Ap
44	67	14.4	265	4	US-10-282-122A-46047	Sequence 46047, A
45	67	14.4	439	4	US-10-437-963-166724	Sequence 166724,
46	67	14.4	443	5	US-10-732-923-17533	Sequence 17533, A
47	66.5	14.3	869	6	US-11-097-143-7428	Sequence 7428, Ap
48	66	14.2	354	4	US-10-319-130-20	Sequence 20, Appl
49	66	14.2	362	4	US-10-424-599-248696	Sequence 248696,
50	66	14.2	374	5	US-10-732-923-17415	Sequence 17415, A
51	66	14.2	446	4	US-10-615-144-4	Sequence 4, Appli
52	66	14.2	526	4	US-10-437-963-156176	Sequence 156176,
53	65.5	14.1	409	3	US-09-738-626-4256	Sequence 4256, Ap
54	65.5	14.1	546	5	US-10-732-923-10268	Sequence 10268, A
55	65.5	14.1	851	4	US-10-437-963-113913	Sequence 113913,
56	65	14.0	443	5	US-10-732-923-17535	Sequence 17535, A
57	65	14.0	2188	6	US-11-097-143-24144	Sequence 24144, A
58	64.5	13.9	142	4	US-10-437-963-172454	Sequence 172454,
59	64.5	13.9	256	4	US-10-286-264-62	Sequence 62, Appl
60	64.5	13.9	256	4	US-10-225-066A-556	Sequence 556, App
61	64.5	13.9	256	4	US-10-374-780A-2434	Sequence 2434, Ap
62	64.5	13.9	256	5	US-10-732-923-16227	Sequence 16227, A
63	64.5	13.9	256	5	US-10-732-923-16236	Sequence 16236, A
64	64.5	13.9	256	5	US-10-225-066A-556	Sequence 556, App
65	64.5	13.9	256	5	US-10-425-115-319141	Sequence 319141,
66	64	13.8	237	4	US-10-615-144-2	Sequence 2, Appli
67	64	13.8	446	4	US-10-424-599-164730	Sequence 164730,
68	64	13.8	485	4	US-10-437-963-173228	Sequence 173228,
69	64	13.8	1011	4	US-10-732-923-7779	Sequence 7779, Ap
70	63.5	13.7	205	5	US-10-282-122A-77306	Sequence 77306, A
71	63.5	13.7	252	4	US-10-295-403-88	Sequence 88, Appl
72	63.5	13.7	271	4	US-10-225-066A-942	Sequence 942, App
73	63.5	13.7	271	4	US-10-374-780A-2068	Sequence 2068, Ap
74	63.5	13.7	271	4	US-10-412-699B-652	Sequence 652, App
75	63.5	13.7	271	4		

ALIGNMENTS

RESULT 1
US-09-955-502-29
; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-30
Perfect score: 465
Sequence: 1 MARMHCAGLGRKAEGLDFP.....KQTEKYFFGEGADQASGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*

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2:	/cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
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4:	/cgn2_6/ptodata/2/pubpaa/PCr_NEW_PUB.pep:*
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7:	/cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8:	/cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	339	72.9	88	6	US-10-467-657-968 Sequence 968, App
2	69.5	14.9	1104	7	US-11-072-512-2506 Sequence 2506, App
3	67	14.4	446	7	US-11-119-351-8 Sequence 8, Appl1
4	65.5	14.1	5024	6	US-10-793-626-2964 Sequence 2964, Ap
5	63.5	13.7	398	6	US-10-793-626-44 Sequence 44, Appl1
6	63.5	13.7	398	6	US-10-793-626-1498 Sequence 1498, Ap
7	59.5	12.8	832	7	US-11-098-686-10182 Sequence 10182, A
8	59.5	12.8	1841	7	US-11-057-058-63 Sequence 63, Appl1
9	58.5	12.6	421	6	US-10-793-626-1820 Sequence 1820, Ap
10	57.5	12.4	447	7	US-11-024-959-286 Sequence 286, App
11	57.5	12.4	787	6	US-10-467-657-2832 Sequence 2832, Ap
12	57	12.3	209	5	US-09-995-493-94 Sequence 94, Appl1
13	56.5	12.2	575	7	US-11-098-686-10635 Sequence 10635, A
14	56.5	12.2	1077	7	US-11-054-281-110 Sequence 110, App
15	56	12.0	381	7	US-11-098-686-11284 Sequence 11284, A
16	56	12.0	867	7	US-11-072-512-3052 Sequence 3052, Ap
17	56	12.0	3803	6	US-10-995-561-773 Sequence 773, App
18	56	12.0	3960	6	US-10-995-561-771 Sequence 771, App
19	56	12.0	5335	6	US-10-995-561-777 Sequence 777, App
20	56	12.0	5406	6	US-10-995-561-774 Sequence 774, App
21	56	12.0	5415	6	US-10-995-561-779 Sequence 779, App
22	56	12.0	5464	6	US-10-995-561-775 Sequence 775, App
23	55.5	11.9	360	7	US-11-019-711-67 Sequence 67, Appl1
24	55.5	11.9	563	7	US-11-072-512-3460 Sequence 3460, Ap
25	55.5	11.9	622	7	US-11-070-080-22 Sequence 22, Appl1

26	54.5	11.7	107	5	US-09-995-493-34	Sequence 34, Appl
27	54.5	11.7	299	6	US-10-362-772-2	Sequence 2, Appli
28	54.5	11.7	355	6	US-10-878-556A-10	Sequence 10, Appl
29	54.5	11.7	505	7	US-11-072-512-3519	Sequence 3519, Ap
30	54.5	11.7	668	7	US-11-111-239-13	Sequence 13, Appl
31	54.5	11.7	805	7	US-11-108-539-2	Sequence 2, Appli
32	54.5	11.7	1134	7	US-11-043-889-34	Sequence 34, Appl
33	54.5	11.7	1187	7	US-11-043-889-46	Sequence 46, Appl
34	54.5	11.7	1476	6	US-10-647-956A-4	Sequence 4, Appli
35	54	11.6	437	6	US-10-454-437-84	Sequence 84, Appl
36	54	11.6	593	7	US-11-194-246-317	Sequence 317, App
37	54	11.6	629	6	US-10-821-234-1528	Sequence 1528, Ap
38	54	11.6	634	7	US-11-072-512-2300	Sequence 2300, Ap
39	54	11.6	8746	7	US-11-098-686-10232	Sequence 10232, A
40	53.5	11.5	389	7	US-11-012-762-72	Sequence 72, Appl
41	53.5	11.5	757	7	US-11-067-121-16	Sequence 16, Appl
42	53.5	11.5	757	7	US-11-186-284-41	Sequence 41, Appl
43	53.5	11.5	532	6	US-10-063-703-72	Sequence 72, Appl
44	53	11.4	532	7	US-11-102-240-72	Sequence 72, Appl
45	53	11.4	620	6	US-10-453-372-1130	Sequence 1130, Ap
46	53	11.4	624	6	US-10-453-372-1126	Sequence 1126, Ap
47	53	11.4	925	6	US-10-453-372-1124	Sequence 1124, Ap
48	53	11.4	931	7	US-11-230-145-2	Sequence 2, Appli
49	53	11.4	966	6	US-10-877-346-32	Sequence 32, Appl
50	53	11.4	972	6	US-10-453-372-1128	Sequence 1128, Ap
51	52.5	11.3	160	6	US-10-821-234-1359	Sequence 1359, Ap
52	52.5	11.3	384	7	US-11-219-282-19	Sequence 19, Appl
53	52.5	11.3	398	7	US-11-012-762-74	Sequence 74, Appl
54	52.5	11.3	407	6	US-10-995-561-1014	Sequence 1014, Ap
55	52.5	11.3	470	6	US-10-467-657-420	Sequence 420, App
56	52.5	11.3	481	6	US-11-234-786-538	Sequence 538, App
57	52.5	11.3	1261	7	US-10-329-258-10	Sequence 10, Appl
58	52.5	11.3	1325	6	US-11-124-367A-410	Sequence 410, App
59	52.5	11.3	1325	7	US-10-467-657-1426	Sequence 1426, Ap
60	52	11.2	190	6	US-10-873-528-116	Sequence 116, App
61	52	11.2	241	7	US-11-098-686-10795	Sequence 10795, A
62	52	11.2	271	7	US-10-883-512-103	Sequence 103, App
63	52	11.2	291	6	US-11-072-512-3579	Sequence 3579, Ap
64	52	11.2	383	7	US-11-072-512-2338	Sequence 2338, App
65	52	11.2	436	7	US-10-131-826A-236	Sequence 5040, Ap
66	52	11.2	457	6	US-10-467-657-5040	Sequence 3469, Ap
67	52	11.2	465	6	US-11-072-512-3469	Sequence 2, Appl1
68	52	11.2	495	7	US-10-982-545-2	Sequence 2694, Ap
69	52	11.2	617	6	US-11-072-512-2694	Sequence 60, Appl
70	52	11.2	922	7	US-11-127-677-58	Sequence 58, Appl
71	51.5	11.1	117	6	US-11-072-512-184	Sequence 184, App
72	51.5	11.1	117	7	US-11-072-512-3504	Sequence 3504, Ap
73	51.5	11.1	662	7	US-11-072-512-3504	Sequence 73, Appl
74	51.5	11.1	893	7	US-10-511-559-73	
75	51.5	11.1	1438	6	US-10-511-559-73	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin9, version 1.04

; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 72.9%; Score 339; DB 6; Length 88;
Best Local Similarity 67.8%; Pred. No. 4.5e-33;
Matches 59; Conservative 14; Mismatches 14; Indels 0; Gaps 0;

QY 1 MARMHCAGKLGKAEAGLDPPPLPGLGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADP 60
Db 1 MARMVFCVKLNKEAGMKFPPLPNELGKRLIFENVSGEAWAATRHQOTMLINENRLSLADP 60

QY 61 RARQYLMKQTEKYFFGEGADQASGYVP 87
Db 61 RAREYLAQQMEQYFFGDDGADAVQGYVP 87

RESULT 2

US-11-072-512-2506
; Sequence 2506, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:

; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHICO
; APPLICANT: YOSHIKAWA, TSUTOMU
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2506
; LENGTH: 1104
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2506

Query Match 14.9%; Score 69.5; DB 7; Length 1104;
Best Local Similarity 26.1%; Pred. No. 3.9;
Matches 23; Conservative 12; Mismatches 36; Indels 17; Gaps 4;

QY 13 EAAGL---DFPP---LPGELGKRLYESVSKQAWQDWLKKQOTMLINENRLNMADPRARQY 65
Db 52 DCEGVPEDDLPTDQTVLPERSSER--EGNAKSCWKDIDKDECESDAENEQNHDPNVEZF 109

QY 66 LMKQTEKYFFGE-----GADQASGY 85
Db 110 LQQQDTAVIFPEAPEBDDQGTPEASGH 137

RESULT 3

US-11-119-351-8

; Sequence 8, Application US/11119351
; Publication No. US20060010519A1
; GENERAL INFORMATION:
; APPLICANT: Kadowaki, Koichi
; APPLICANT: Takahashi, Sakiko
; APPLICANT: Kawamukai, Makoto
; APPLICANT: Shimada, Hiroaki
; TITLE OF INVENTION: Method for Producing Ubiquitinone-10 in Plant
; FILE REFERENCE: 59150-8034
; CURRENT APPLICATION NUMBER: US/11/119,351
; CURRENT FILING DATE: 2005-04-29
; PRIOR APPLICATION NUMBER: JP 2004-136906
; PRIOR FILING DATE: 2004-04-30
; PRIOR APPLICATION NUMBER: JP 2005-000984
; PRIOR FILING DATE: 2005-01-05
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Nicotiana tabacum
US-11-119-351-8

Query Match 14.4%; Score 67; DB 7; Length 446;
Best Local Similarity 31.2%; Pred. No. 2.6;
Matches 20; Conservative 8; Mismatches 20; Indels 16; Gaps 4;

QY 19 FPPLPGLGKRLYESVS---KQAWQDWLKKQOTMLINENRLNMADPRARQYLMKQT-EKY 73
Db 264 FPLGWMLSKSTWDELSPKWPKAYWDDWL-----LKENH-----RGRQFIRPEVCRSY 312

QY 74 FPGE 77
Db 313 NFGE 316

RESULT 4

US-10-793-626-2964
; Sequence 2964, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:

; APPLICANT: KIMBERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2964
; LENGTH: 5024
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
; NAME/KEY: MOD RES
; LOCATION: (5024)
; OTHER INFORMATION: variable amino acid
US-10-793-626-2964

Query Match 14.1%; Score 65.5; DB 6; Length 5024;
Best Local Similarity 41.5%; Pred. No. 71;
Matches 17; Conservative 7; Mismatches 16; Indels 1; Gaps 1;

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Db 3822 QNEAKQALQQLNAETSLNGFERLNHARPRALLEYI-KSLBK 3861

RESULT 5

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-31

Perfect score: 471

Sequence: 1 MSRMVQCVKLGHBAGLDRP.....KQMEAYFFGDGAQSPGQYVP 87

Scoring table: BLOSUM62

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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5: geneseqp2002s:*
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7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	471	100.0	87	5	ABB78176	Abb78176 Amino aci
2	310	65.8	87	5	ABB78175	Abb78175 Amino aci
3	304	64.5	87	5	ABB78174	Abb78174 Amino aci
4	294	62.4	88	5	ABB78171	Abb78171 Amino aci
5	294	62.4	88	5	ABB78172	Abb78172 Amino aci
6	294	62.4	88	5	ABB78173	Abb78173 Amino aci
7	294	62.4	88	6	ABP77219	Abp77219 N. gonorr
8	291	61.8	87	5	ABB78177	Abb78177 Amino aci
9	286	60.7	88	5	ABB78178	Abb78178 Amino aci
10	286	60.7	89	9	AEb41576	Aeb41576 L. pneumo
11	286	60.7	95	9	AEb38294	Aeb38294 L. pneumo
12	275	58.4	87	5	ABB78148	Abb78148 Amino aci
13	275	58.4	87	5	ABB78147	Abb78147 Amino aci
14	257.5	54.7	86	5	ABB78149	Abb78149 Amino aci
15	242	51.4	87	5	ABB78170	Abb78170 Amino aci
16	242	51.4	122	7	ABO74609	AbO74609 Pseudomon
17	237	50.3	87	5	ABB78169	Abb78169 Amino aci
18	225.5	47.9	92	6	ADA34169	Ada34169 Acinetoba
19	219	46.5	90	5	ABB78168	Abb78168 Amino aci
20	213	45.2	88	5	ABB78154	Abb78154 Amino aci
21	211	44.8	87	5	ABB78153	Abb78153 Amino aci
22	208.5	44.3	90	5	ABB78167	Abb78167 Amino aci
23	208	44.2	91	5	ABB78150	Abb78150 Amino aci
24	208	44.2	93	7	ADF05158	Adf05158 Bacterial

25	208	44.2	107	7	ABO65445	AbO65445 Klebsiell
26	204	43.3	90	5	ABB78155	Abb78155 Amino aci
27	202	42.9	87	5	ABB78152	Abb78152 Amino aci
28	200	42.5	87	5	ABB78151	Abb78151 Amino aci
29	200	42.5	91	5	ABB78158	Abb78158 Amino aci
30	200	42.5	91	5	ABB78157	Abb78157 Amino aci
31	200	42.5	91	5	ABB78156	Abb78156 Amino aci
32	197	41.8	88	5	ABB78160	Abb78160 Amino aci
33	197	41.8	91	5	ABB78161	Abb78161 Amino aci
34	197	41.8	91	5	ABB78159	Abb78159 Amino aci
35	197	41.8	91	5	ABB78162	Abb78162 Amino aci
36	196	41.6	78	5	ABB78164	Abb78164 Amino aci
37	190	40.3	91	5	ABB78163	Abb78163 Amino aci
38	186	39.5	90	5	ABB78165	Abb78165 Amino aci
39	177	37.6	110	8	ADL05173	Adl05173 M. catarr
40	166	35.2	76	5	ABB78166	Abb78166 Amino aci
41	72.5	15.4	2285	4	ABB63057	Abb63057 Drosophi1
42	71.5	15.2	387	7	ABO82328	AbO82328 Pseudomon
43	71	15.1	523	4	AAU35394	Aau35394 Haemophil
44	71	15.1	523	6	ABU30183	Abu30183 Protein e
45	71	15.1	568	8	ADN22552	Adn22552 Bacterial
46	69	14.6	1263	2	AAW22052	Aaw22052 DNA polym
47	69	14.6	1263	2	AAW97098	Aaw97098 Pfu DNA p
48	69	14.6	1263	3	AAy51659	Aay51659 Pyrococcu
49	69	14.6	1263	3	AAy52030	Aay52030 P. furios
50	68.5	14.5	249	8	ADS28293	Ads28293 Bacterial
51	68	14.4	536	6	ABU40906	Abu40906 Protein e
52	68	14.4	569	7	ADF06692	Adf06692 Bacterial
53	67	14.2	188	9	AEA50037	Aea50037 Rice glob
54	67	14.2	319	6	ADA56784	Ada56784 Human sec
55	67	14.2	319	6	ADA40633	Ada40633 Human sec
56	67	14.2	319	6	ABR47664	AbR47664 Human sec
57	67	14.2	319	6	ABR00028	AbR00028 Human gen
58	67	14.2	319	7	ADB91477	AdB91477 Human sec
59	67	14.2	319	7	ADC74042	Adc74042 Human sec
60	67	14.2	320	2	AAy30730	Aay30730 Amino aci
61	67	14.2	561	6	ADA54803	Ada54803 Human pro
62	67	14.2	907	5	ABG91058	Abg91058 Neisseria
63	67	14.2	915	2	AAy51770	Aay51770 N. gonorr
64	67	14.2	915	2	AAy07476	Aay07476 N. gonorr
65	67	14.2	915	2	AAy80374	Aay80374 N. gonorr
66	67	14.2	915	5	AAE20190	Aae20190 Neisseria
67	67	14.2	950	4	AAU35678	Aau35678 Haemophil
68	67	14.2	950	6	ABU30652	Abu30652 Protein e
69	67	14.2	1798	8	ADN46771	Adn46771 Thermococ
70	66.5	14.1	204	9	AEA50033	Aea50033 Rice glo
71	66.5	14.1	972	4	ABB70158	Abb70158 Drosophi1
72	66	14.0	387	7	ADF58994	Adf58994 Human pol
73	65.5	13.9	186	7	ADC07962	Adc07962 Rice prot
74	65.5	13.9	186	7	ADC07948	Adc07948 Rice prot
75	65.5	13.9	198	4	ABG23100	Abg23100 Novel hum

ALIGNMENTS

RESULT 1
ABB78176
ID ABB78176 standard; protein; 87 AA.
XX ABB78176;
AC
XX
DT 29-AUG-2003 (revised)
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Acidithiobacillus ferrooxidans.
XX
PN US2002072118-A1.

XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A, 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 471; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-51;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHAEGLDRPPYPGALGARIYQEVSKAOWGLKHQTMLINERYLSPIDP 60
Db 1 MSRMVQCVKLGHAEGLDRPPYPGALGARIYQEVSKAOWGLKHQTMLINERYLSPIDP 60

QY 61 KSRTFLEKQMEAYFFGDAQSPGYP 87
Db 61 KSRTFLEKQMEAYFFGDAQSPGYP 87

RESULT 2
ABB78175
ID ABB78175 standard; protein; 87 AA.
XX
AC ABB78175;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX

PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A, 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 65.8%; Score 310; DB 5; Length 87;
Best Local Similarity 64.4%; Pred. No. 4.4e-31;
Matches 56; Conservative 10; Mismatches 21; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHAEGLDRPPYPGALGARIYQEVSKAOWGLKHQTMLINERYLSPIDP 60
Db 1 MARMIHCVKLGKEAEGLDPPPLPGELGRLYESVSKOAWQDWLKHQTMLINENRLMADP 60

QY 61 KSRTFLEKQMEAYFFGDAQSPGYP 87
Db 61 RARQYLMKQTEKYFFGEGADQASGYVP 87

RESULT 3
ABB78174
ID ABB78174 standard; protein; 87 AA.
XX
AC ABB78174;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A, 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-31
Perfect score: 471
Sequence: 1 MSRMVQCVKLGHAEGGLDRP.....KQMEAYFFGDGAQSPGTYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	294	62.4	88	2	H81014	conserved hypothet
2	242	51.4	90	2	H83003	conserved hypothet
3	215	45.6	105	2	C82624	conserved hypothet
4	204	43.3	90	2	C82320	conserved hypothet
5	202	42.9	90	2	C64013	hypothetical prote
6	200	42.5	91	2	A85954	hypothetical prote
7	200	42.5	91	2	A65082	hypothetical prote
8	200	42.5	91	2	F91108	hypothetical prote
9	197	41.8	91	2	AH0879	conserved hypothet
10	186	39.5	90	2	AI0116	conserved hypothet
11	166	35.2	93	2	B84994	hypothetical prote
12	71.5	15.2	383	2	F83321	hypothetical prote
13	71	15.1	523	1	I64055	GMP synthase (glut
14	71	15.1	568	2	T25162	Fritzried-1 protein
15	70	14.9	1197	2	I39613	pyruvate (flavodox
16	70	14.9	1199	2	AD2156	pyruvate-flavodoxi
17	69.5	14.8	501	2	T35009	probable phospholi
18	69	14.6	1263	2	T43934	DNA-directed DNA p
19	68.5	14.5	249	2	A83963	hypothetical prote
20	67.5	14.3	564	2	T49322	related to RNA-bin
21	67	14.2	915	2	A43335	transferrin-bindin
22	67	14.2	950	2	B64135	oxoglutarate dehyd
23	66	14.0	604	2	S36493	E1 protein - human
24	65.5	13.9	186	1	WMR219	19K globulin precu
25	65.5	13.9	186	2	JC4784	alpha-globulin pre
26	65.5	13.9	368	2	T31103	probable GMP synth
27	65	13.8	159	2	AD0348	probable membrane
28	65	13.8	1434	2	G71232	hypothetical prote
29	64.5	13.7	914	2	T17233	hypothetical prote

30	64.5	13.7	4273	2	C69679	polyketide synthas
31	64	13.6	205	2	AD0788	heme exporter prot
32	64	13.6	205	2	AC0960	heme exporter prot
33	64	13.6	306	2	A97249	Zn-binding lipopro
34	64	13.6	364	2	C48376	orf2 5' to phbC -
35	64	13.6	598	2	A75531	hypothetical prote
36	63.5	13.5	376	2	C82310	sulfate ABC transp
37	63.5	13.5	609	2	S36481	E1 protein - human
38	63.5	13.5	1199	2	S77082	pyruvate (flavodox
39	63.5	13.5	1243	2	JC5615	membrane-associate
40	63	13.4	265	2	T46733	citr protein limpo
41	63	13.4	443	2	T48593	hypothetical prote
42	63	13.4	468	2	F87359	leucine aminopepti
43	63	13.4	705	2	S18733	glutenin high mole
44	63	13.4	1455	2	B75199	DNA-directed DNA p
45	62.5	13.3	243	2	J01427	hypothetical 27K p
46	62.5	13.3	289	2	T46370	hypothetical prote
47	62.5	13.3	393	2	T49257	protein kinase-lik
48	62.5	13.3	475	2	S54993	reverse transcript
49	62.5	13.3	475	2	S54994	reverse transcript
50	62.5	13.3	510	2	A96735	hypothetical prote
51	62.5	13.3	513	2	AE1921	hypothetical prote
52	62.5	13.3	605	2	S36469	E1 protein - human
53	62	13.2	316	2	C91272	hypothetical prote
54	62	13.2	316	2	C86113	hypothetical prote
55	62	13.2	503	2	AF2029	hypothetical prote
56	62	13.2	512	1	F0MVG5	gag polyprotein -
57	62	13.2	520	1	F0LJGL	gag polyprotein -
58	62	13.2	662	2	T41215	probable acetate-C
59	61	13.0	254	2	T15187	hypothetical prote
60	61	13.0	316	2	B37318	delta(2)-isopenten
61	61	13.0	430	2	B96031	hypothetical prote
62	61	13.0	450	2	S73419	signal recognition
63	61	13.0	457	1	JC4993	biphenyl dioxygena
64	61	13.0	525	1	SYECGU	GMP synthase (glut
65	61	13.0	525	2	F85894	GMP synthetase (gl
66	61	13.0	525	2	AD0820	GMP synthase (glut
67	61	13.0	525	2	A91050	GMP synthetase [im
68	61	13.0	535	2	AF0103	probable sulfatase
69	61	13.0	915	2	F81196	transferrin-bindin
70	60.5	12.8	359	2	T26813	hypothetical prote
71	60.5	12.8	475	2	S54996	reverse transcript
72	60.5	12.8	475	2	S54998	reverse transcript
73	60	12.7	342	2	T19021	probable inositol
74	60	12.7	352	2	D69410	cell division cont
75	60	12.7	375	2	T39364	probable galactosy

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MCS8
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; P81958
R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MCS8
A/Reference number: AB1000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4B7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:
A/Experimental source: serogroup B, strain MCS8
R/Parikh, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502a-31

Perfect score: 471
Sequence: 1 MSRMVQCVKLGHEAGLDRP.....KQMEAYFFGDGAQSPGTYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	331	70.3	91	2 Q4LS19_9BURK	Q4LS19 burkholderi
2	319	67.7	90	1 FETP_CHRVO	Q7MR4 chromobacte
3	313	66.5	90	1 FETP_NITRU	Q82XF2 nitrosomona
4	310	65.8	91	1 FETP_BURMA	Q621U9 burkholderi
5	310	65.8	91	1 FETP_BURPS	Q63SJ4 burkholderi
6	309	65.6	91	1 FETP_RALSO	Q8Y010 ralstonia s
7	294	62.4	88	1 FETP_NEIGI	Q5F553 neisseria g
8	294	62.4	88	1 FETP_NEIMA	P67615 neisseria m
9	294	62.4	88	1 FETP_NEIMB	P67616 neisseria m
10	291	61.8	90	1 FETP_METCA	Q608J7 methylococc
11	286	60.7	89	1 FETP_LEGPA	Q5X3X9 legionella
12	286	60.7	89	1 FETP_LEGPH	Q5ZU80 legionella
13	286	60.7	90	1 FETP_COXBU	Q83D06 coxiella bu
14	284	60.3	89	1 FETP_LEGPL	Q5WVC4 legionella
15	275	58.4	90	1 FETP_BORBR	Q7WU06 bordetella
16	275	58.4	90	1 FETP_BORPA	Q7W9Q2 bordetella
17	275	58.4	90	1 FETP_BORPE	Q7WVC4 bordetella
18	261	55.4	91	1 FETP_XANAC	Q8PJH7 xanthomonas
19	255	54.1	92	1 FETP_XANOR	Q5GY22 xanthomonas
20	252	53.5	92	1 FETP_XANCP	Q8B829 xanthomonas
21	252	53.5	92	1 FETP_XANCP	Q4UW14 xanthomonas
22	249	52.9	92	2 Q4NM04_9DELT	Q4NW44 anaeromyxob
23	242	51.4	90	1 FETP_PSEAB	Q9HU36 pseudomonas
24	238	50.5	90	1 FETP_IDILO	Q5GY58 idiomarina
25	237	50.3	90	1 FETP_PSEBP	Q8B149 pseudomonas
26	231	49.0	90	2 Q4J228_AZOV1	Q4J228 azotobacter
27	229	48.6	90	2 Q6T7F6_PSEFL	Q6T7F6 pseudomonas
28	224.5	47.7	90	1 FETP_AC1AD	Q6F1B3 acinetobact
29	222	47.1	90	1 FETP_XYLFT	Q87D06 xyloella fas
30	222	47.1	90	2 Q4KJ12_PSEFS	Q4KJ12 pseudomonas
31	220	46.7	90	1 FETP_VIBF1	Q5E710 vibrio flusc

32	219	46.5	90	1 FETP_PSESM	Q87UF5 pseudomonas
33	219	46.5	90	2 Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
34	218	46.3	90	1 FETP_PHOLL	Q7N711 photorhabdu
35	215	45.6	90	1 FETP_XYLFA	Q9PC73 xyloella fas
36	213	45.2	92	1 FETP_SHEON	Q8BX6 shewanella
37	211	44.8	90	1 FETP_VIBVU	Q8DC5 vibrio vuln
38	211	44.8	90	1 FETP_VIBVU	Q7MB14 vibrio vuln
39	211	44.8	94	1 FETP_HAEDU	Q7VKB6 haemophilus
40	208	44.2	90	1 FETP_VIBPA	Q87115 vibrio para
41	204	43.3	90	1 FETP_VIBCH	Q9KUR4 vibrio chol
42	203	43.1	87	1 FETP_FRATT	Q5NHJ8 francisella
43	202	42.9	90	1 FETP_HAEIN	P44048 haemophilus
44	202	42.9	90	2 Q4QMD9_HAEI8	Q4QMD9 haemophilus
45	200	42.5	90	1 FETP_PASMU	Q9CLB9 pasteurella
46	200	42.5	91	1 FETP_MANSN	Q65VC7 mannheimia
47	197	41.8	90	1 FETP_ERWCT	Q6D8J9 erwina car
48	195	41.4	90	1 FETP_ECOS7	Q6D8J9 erwina car
49	195	41.4	90	1 FETP_ECOLI	Q6D8J9 erwina car
50	195	41.4	90	1 FETP_SHIFL	P0A8P4 escherichia
51	194	41.2	90	1 FETP_YERPS	P0A8P5 shigella fl
52	192	40.8	90	1 FETP_PHOPR	Q66CM3 yersinia ps
53	192	40.8	90	1 FETP_SALCH	Q61MK7 photobacter
54	192	40.8	90	1 FETP_SALPA	Q57K04 salmonella
55	192	40.8	90	1 FETP_SALTI	Q5PMU1 salmonella
56	192	40.8	90	1 FETP_SALTY	P67617 salmonella
57	191	40.6	90	1 FETP_ECOL6	Q8FE19 escherichia
58	186	39.5	90	1 FETP_YERPE	Q8ZHE7 yersinia pe
59	179	38.0	78	1 FETP_BUCAP	Q8K925 buchnera ap
60	172	36.5	78	1 FETP_WIGBR	Q8D3C5 wigleswort
61	172	36.5	79	1 FETP_CANBP	Q4FVJ7 psychrobact
62	167	35.5	96	2 Q4FVJ7_9GAMM	P57618 buchnera ap
63	166	35.2	77	1 FETP_BUCAI	Q89A44 buchnera ap
64	142	30.1	87	1 FETP_BUCBP	Q7S1F4 alcaligenes
65	78.5	16.7	825	1 AOXB_ALCPA	Q6WB60 alcaligenes
66	78.5	16.7	826	2 Q6WB60_ALCPA	Q6WB60 alcaligenes
67	72.5	15.4	484	2 Q6MQ14_BDEBA	Q6MG14 bdellovibri
68	72.5	15.4	2308	2 Q9VP17_DROME	Q9VP17 drosophila
69	72	15.3	514	2 Q8VNU2_DESDE	Q8VNU2 desulfovibr
70	71.5	15.2	359	2 Q4N608_THERPA	Q4N608 theileria p
71	71.5	15.2	383	2 Q910P0_PSEAE	Q910P0 pseudomonas
72	71.5	15.2	1200	2 Q4NU62_9DELT	Q4NU62 anaeromyxob
73	71.5	15.2	1322	2 Q75HA9_ORYSA	Q75HA9 oryza sativ
74	71	15.1	523	1 GUAA_HAEIN	P44335 haemophilus
75	71	15.1	523	2 Q4QNW4_HAEI8	Q4QNW4 haemophilus

ALIGNMENTS

RESULT 1
Q4LS19_9BURK
ID Q4LS19_9BURK PRELIMINARY; PRT; 91 AA.
AC Q4LS19;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=Bcen2424DRAFT_3773;
OS Burkholderia cenocepacia HI2424.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; Burkholderia cenocepacia complex.
OX NCBI_TaxID=3311272;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Detter C., Glavina T.,
RT Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Burkholderia cenocepacia
HI2424.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.


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RC STRAIN=HI2424;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Burkholderia cenocepacia
RT HI2424."
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAHL01000021; EAM18958.1; -; Genomic_DNA.
KM Hypothetical protein.
SQ SEQUENCE 91 AA; 10327 MW; 0A540A880A76E284 CRC64;

Query Match
Best Local Similarity 70.3%; Score 331; DB 2; Length 91;
Matches 61; Conservative 7; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHEAEGLDPRPPYPGALGARIYQEVSKAWQGWLKHQTMLINEYRLSPIDP 60
Db 1 MARMIOCAKLGKEAEGLDPPPLPGELGKRIYESVSKAWQGWLKKQTMLINEYRLNLMADP 60

QY 61 KSRTFLEKOMEAYFFGDGAQSPGYVP 87
Db 61 RARQYLMKQTEKYPFGDGADQASGYVP 87

RESULT 2
FETP_CHRVO STANDARD; PRT; 90 AA.
AC 07NSR4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=CV3356;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxId=536;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.U., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogio M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brochi M., Buritly H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcão C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.A., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangelro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Lecl L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA dl Mauro S.M.Z., de Medeiros S.R.B., Meisner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Patxao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.B., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Senanez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassef R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB016922; AAQ61020.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10095 MW; 60492ED67A9ABE78 CRC64;

Query Match
Best Local Similarity 67.7%; Score 319; DB 1; Length 90;
Matches 57; Conservative 11; Mismatches 19; Indels 0; Gaps 0;

QY 1 MSRMVQCVKLGHEAEGLDPRPPYPGALGARIYQEVSKAWQGWLKHQTMLINEYRLSPIDP 60
Db 1 MSRTVNCIKLGREAEGLDPPPLPGELGKRIYESVSKAWQGWLYQTMLINENRLSLADA 60

QY 61 KSRTFLEKOMEAYFFGDGAQSPGYVP 87
Db 61 RARQYLASQLDAYFFGQADAPAGYTP 87

RESULT 3
FETP_NITEU STANDARD; PRT; 90 AA.
AC Q82XF2;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=NE0322;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxId=915;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 19718 / IFO 14298;
RX MEDLINE=22586410; PubMed=12700255;
RA DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX321857; CAD84233.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	225.5	47.9	92	2	US-09-328-352-5456
3	208	44.2	93	2	US-09-543-681A-5443
4	208	44.2	107	2	US-09-489-039A-11962
5	177	37.6	110	2	US-09-540-236-2859
6	71.5	15.2	387	2	US-09-252-991A-31074
7	69	14.6	1263	2	US-09-446-504-6
8	69	14.6	1263	2	US-09-712-266-6
9	69	14.6	1263	2	US-09-091-889A-4
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12	67	14.2	353	2	US-09-716-129-169
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14	67	14.2	915	1	US-08-363-124A-2
15	67	14.2	915	1	US-08-478-435-96
16	67	14.2	915	1	US-08-337-483-96
17	67	14.2	915	1	US-08-478-373-96
18	67	14.2	915	2	US-08-474-671-96
19	67	14.2	915	2	US-08-483-577A-96
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24	67	14.2	915	2	US-08-778-570B-24
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27	64.5	13.7	225	2	US-10-104-047-3107

28	64.5	13.7	502	2	US-09-904-615-69	Sequence 69, Appl
29	64.5	13.7	502	2	US-10-054-988-69	Sequence 69, Appl
30	64	13.6	125	2	US-09-640-211A-762	Sequence 762, App
31	64	13.6	313	2	US-09-513-151A-68	Sequence 68, Appl
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33	63	13.4	162	2	US-09-248-796A-21408	Sequence 21408, A
34	63	13.4	452	2	US-09-284-768A-22	Sequence 22, Appl
35	63	13.4	608	2	US-09-284-768A-4	Sequence 4, Appli
36	63	13.4	657	2	US-09-284-768A-7	Sequence 7, Appli
37	62.5	13.3	225	2	US-09-107-532A-5865	Sequence 5865, Ap
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43	61	13.0	582	2	US-09-902-540-11161	Sequence 11161, A
44	60.5	12.8	425	2	US-09-252-991A-32805	Sequence 32805, A
45	60.5	12.8	1244	2	US-09-938-291A-5	Sequence 5, Appli
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62	58	12.3	145	2	US-09-902-540-13774	Sequence 2, Appli
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64	58	12.3	506	2	US-09-362-633-2	Sequence 2, Appli
65	58	12.3	506	2	US-09-877-476-2	Sequence 2, Appli
66	58	12.3	506	2	US-09-877-476-24	Sequence 24, Appl
67	58	12.3	506	2	US-09-877-476-26	Sequence 30, Appl
68	58	12.3	506	2	US-09-877-476-30	Sequence 36, Appl
69	58	12.3	506	2	US-09-877-476-36	Sequence 38, Appl
70	58	12.3	506	2	US-09-877-476-38	Sequence 40, Appl
71	58	12.3	506	2	US-09-877-476-40	Sequence 2, Appli
72	58	12.3	1302	1	US-08-232-537-2	Sequence 21060, A
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ALIGNMENTS

RESULT 1
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502a-31

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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	310	65.8	87	3	US-09-955-502-29 Sequence 30, Appl
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4	294	62.4	88	3	US-09-955-502-26 Sequence 27, Appl
5	294	62.4	88	3	US-09-955-502-27 Sequence 28, Appl
6	294	62.4	88	3	US-09-955-502-28 Sequence 32, Appl
7	291	61.8	87	3	US-09-955-502-32 Sequence 33, Appl
8	286	60.7	88	3	US-09-955-502-33 Sequence 3, Appl
9	275	58.4	87	3	US-09-955-502-2 Sequence 3, Appl
10	275	58.4	87	3	US-09-955-502-3 Sequence 4, Appl
11	257.5	54.7	86	3	US-09-955-502-4 Sequence 25, Appl
12	242	51.4	87	3	US-09-955-502-25 Sequence 24, Appl
13	237	50.3	87	3	US-09-955-502-24 Sequence 23, Appl
14	219	46.5	90	3	US-09-955-502-23 Sequence 22, Appl
15	215	45.6	89	3	US-09-955-502-22 Sequence 9, Appl
16	213	45.2	88	3	US-09-955-502-9 Sequence 8, Appl
17	211	44.8	87	3	US-09-955-502-8 Sequence 5, Appl
18	208	44.2	91	3	US-09-955-502-5 Sequence 10, Appl
19	204	43.3	90	3	US-09-955-502-10 Sequence 6, Appl
20	202	42.9	87	3	US-09-955-502-7 Sequence 11, Appl
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22	200	42.5	91	3	US-09-955-502-11 Sequence 13, Appl
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24	200	42.5	91	3	US-09-955-502-13 Sequence 15, Appl
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27	197	41.8	91	3	US-09-955-502-16 Sequence 16, Appl

28	197	41.8	91	3	US-09-955-502-17	Sequence 17, Appl
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44	67	14.2	319	5	US-10-472-533-317	Sequence 317, App
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47	67	14.2	907	4	US-10-467-534-82	Sequence 82, Appl
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55	66.5	14.1	972	6	US-11-097-143-37266	Sequence 37266, A
56	66.5	14.1	1125	4	US-10-437-963-129383	Sequence 129383,
57	66.5	14.1	1278	4	US-10-437-963-181016	Sequence 181016,
58	66.5	14.1	1389	4	US-10-437-963-129393	Sequence 129393,
59	65.5	13.9	186	5	US-10-481-032A-214	Sequence 214, App
60	65.5	13.9	186	5	US-10-481-032A-228	Sequence 228, App
61	65.5	13.9	198	5	US-10-450-763-53459	Sequence 53459, A
62	65.5	13.9	523	4	US-10-282-122A-66959	Sequence 66959, A
63	65.5	13.9	870	4	US-10-437-963-154457	Sequence 154457,
64	65.5	13.9	1479	4	US-10-437-963-181030	Sequence 181030,
65	65	13.8	683	4	US-10-156-761-9254	Sequence 9254, Ap
66	64.5	13.7	221	4	US-10-424-599-148972	Sequence 148972,
67	64.5	13.7	225	4	US-10-104-047-3107	Sequence 3107, Ap
68	64.5	13.7	289	4	US-10-767-701-42005	Sequence 42005, A
69	64.5	13.7	328	3	US-09-867-550-1052	Sequence 1052, Ap
70	64.5	13.7	501	4	US-10-181-108-14	Sequence 14, Appl
71	64.5	13.7	501	6	US-11-079-743-14	Sequence 14, Appl
72	64.5	13.7	502	3	US-09-739-254-69	Sequence 69, Appl
73	64.5	13.7	502	3	US-09-904-615-69	Sequence 69, Appl
74	64.5	13.7	502	4	US-10-054-988-69	Sequence 69, Appl
75	64.5	13.7	575	4	US-10-425-115-234031	Sequence 234031,

ALIGNMENTS

RESULT 1
US-09-955-502-31
; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnicks, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiobacillus ferrooxidans

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-31

Perfect score: 471

Sequence: 1 MSRMVQCVRKLGHEAGIDRP.....KOMEAFFGDAQSPGYPV 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Published Applications AA New:*

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- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	294	62.4	88	6	US-10-467-657-968 Sequence 968, App
2	67	14.2	907	7	US-11-103-957-82 Sequence 82, Appl
3	65	13.8	912	6	US-10-467-657-7142 Sequence 7142, Ap
4	64.5	13.7	225	7	US-11-072-512-3107 Sequence 3107, Ap
5	64	13.6	313	7	US-11-237-600-68 Sequence 68, Appl
6	62	13.2	316	7	US-11-156-084-193 Sequence 193, App
7	62	13.2	316	7	US-11-156-084-287 Sequence 287, App
8	62	13.2	1047	7	US-11-072-512-2408 Sequence 2408, Ap
9	61	13.0	216	7	US-11-156-084-244 Sequence 244, App
10	61	13.0	216	7	US-11-156-084-322 Sequence 322, App
11	61	13.0	316	7	US-11-156-084-210 Sequence 210, App
12	61	13.0	316	7	US-11-156-084-280 Sequence 280, App
13	60.5	12.8	1244	6	US-10-531-036-36 Sequence 36, Appl
14	60	12.7	521	6	US-10-467-657-1344 Sequence 1344, Ap
15	59	12.5	306	7	US-11-052-554A-222 Sequence 222, App
16	59	12.5	645	6	US-10-510-386-32 Sequence 32, Appl
17	58.5	12.4	347	7	US-11-186-284-226 Sequence 226, App
18	58.5	12.4	444	7	US-11-072-512-2690 Sequence 2690, Ap
19	58.5	12.4	509	6	US-10-131-826A-108 Sequence 108, App
20	58.5	12.4	553	7	US-11-205-109-25 Sequence 25, Appl
21	58	12.3	506	7	US-11-010-239-38 Sequence 38, Appl
22	57	12.1	304	7	US-11-156-084-291 Sequence 291, App
23	57	12.1	315	7	US-11-156-084-313 Sequence 313, App
24	57	12.1	315	7	US-11-156-084-353 Sequence 353, App
25	57	12.1	336	7	US-11-165-226-125 Sequence 125, App

26	56.5	12.0	1981	6	US-10-374-954-23	Sequence 23, Appl
27	56.5	12.0	1998	6	US-10-374-954-21	Sequence 21, Appl
28	56.5	12.0	2009	6	US-10-374-954-2	Sequence 2, Appl1
29	56	11.9	313	7	US-11-156-084-208	Sequence 208, App
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31	55.5	11.8	295	7	US-11-072-512-3285	Sequence 3285, Ap
32	55	11.7	470	6	US-10-979-821-14	Sequence 14, Appl
33	55	11.7	470	7	US-11-114-922-14	Sequence 14, Appl
34	54.5	11.6	237	6	US-10-467-657-570	Sequence 570, App
35	54.5	11.6	328	6	US-10-848-375-1	Sequence 1, Appl1
36	54.5	11.6	352	7	US-11-018-868-13	Sequence 13, Appl
37	54.5	11.6	697	7	US-11-103-957-39	Sequence 39, Appl
38	54	11.5	316	7	US-11-156-084-213	Sequence 213, App
39	54	11.5	316	7	US-11-156-084-214	Sequence 214, App
40	54	11.5	316	7	US-11-156-084-303	Sequence 303, App
41	54	11.5	348	7	US-11-156-084-267	Sequence 267, App
42	54	11.5	462	7	US-11-055-822-956	Sequence 956, App
43	54	11.5	523	7	US-11-055-822-954	Sequence 954, App
44	53.5	11.4	205	7	US-11-072-512-3387	Sequence 3387, Ap
45	53.5	11.4	290	6	US-10-131-826A-222	Sequence 222, App
46	53.5	11.4	559	6	US-10-873-528-158	Sequence 158, App
47	53.5	11.4	2871	7	US-11-124-367A-264	Sequence 264, App
48	53	11.3	589	7	US-11-072-512-2914	Sequence 2914, Ap
49	52.5	11.1	222	7	US-11-156-084-121	Sequence 121, App
50	52.5	11.1	296	6	US-10-467-657-7994	Sequence 7994, Ap
51	52.5	11.1	352	6	US-10-981-873-29	Sequence 29, Appl
52	52.5	11.1	352	6	US-10-981-873-28	Sequence 28, Appl
53	52.5	11.1	380	6	US-10-525-674-28	Sequence 28, Appl
54	52.5	11.1	393	7	US-11-111-239-11	Sequence 11, Appl
55	52.5	11.1	520	6	US-10-131-826A-144	Sequence 144, App
56	52.5	11.1	726	7	US-11-052-554A-127	Sequence 127, App
57	52.5	11.1	1242	7	US-11-124-367A-338	Sequence 338, App
58	52.5	11.1	1242	7	US-11-124-367A-339	Sequence 339, App
59	52.5	11.1	1717	7	US-11-182-016-20	Sequence 20, Appl
60	52	11.0	296	7	US-11-072-512-2977	Sequence 2977, Ap
61	52	11.0	310	7	US-11-156-084-301	Sequence 301, App
62	52	11.0	380	6	US-10-517-939-140	Sequence 140, App
63	52	11.0	881	7	US-11-077-550-124	Sequence 124, App
64	52	11.0	902	7	US-11-077-550-132	Sequence 132, App
65	52	11.0	912	7	US-11-077-550-116	Sequence 116, App
66	52	11.0	914	7	US-11-077-550-120	Sequence 120, App
67	52	11.0	944	7	US-11-077-550-122	Sequence 122, App
68	52	11.0	950	7	US-11-077-550-118	Sequence 118, App
69	52	11.0	1187	7	US-11-098-686-10523	Sequence 10523, A
70	52	11.0	1254	6	US-10-528-031-47	Sequence 47, Appl
71	52	11.0	1467	6	US-10-507-956-1	Sequence 1, Appl1
72	52	11.0	3353	7	US-11-037-243-64	Sequence 64, Appl
73	51.5	10.9	264	7	US-11-214-199-46	Sequence 46, Appl
74	51.5	10.9	345	6	US-10-467-657-252	Sequence 252, App
75	51.5	10.9	345	6	US-10-467-657-3086	Sequence 3086, Ap

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWln9, version 1.04

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 70.7181 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-32
Perfect score: 466
Sequence: 1 MARRICAKLGIEADGIDAP.....QERREKFLFGGTSTPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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7: geneseqp2003bs:*
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9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	268	57.5	88	5	ABB781178
6	260	55.8	87	5	ABB781148
7	260	55.8	87	5	ABB781147
8	250	53.6	89	9	AEBA1576
9	250	53.6	95	9	AEBA38294
10	243	52.1	88	5	ABB781171
11	243	52.1	88	5	ABB781172
12	243	52.1	88	5	ABB781173
13	243	52.1	88	6	ABP77219
14	242.5	52.0	86	5	ABB781149
15	239	51.3	87	5	ABB781169
16	235.5	50.5	92	6	ADA34169
17	235	50.4	87	5	ABB781170
18	235	50.4	122	7	ABO74609
19	226	48.5	90	5	ABB781168
20	224	48.1	87	5	ABB781152
21	223	47.9	91	5	ABB781150
22	219	47.0	87	5	ABB781151
23	215	46.1	88	5	ABB781154
24	215	46.1	90	5	ABB781155

25	214	45.9	93	7	ADF05158	Adf05158 Bacterial
26	205	44.0	87	5	ABB78153	Abb78153 Amino aci
27	201	43.1	107	7	ABO65445	AbO65445 Klebsiell
28	200	42.9	91	5	ABB78158	Abb78158 Amino aci
29	200	42.9	91	5	ABB78157	Abb78157 Amino aci
30	200	42.9	91	5	ABB78156	Abb78156 Amino aci
31	195	41.8	88	5	ABB78160	Abb78160 Amino aci
32	195	41.8	91	5	ABB78161	Abb78161 Amino aci
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34	195	41.8	91	5	ABB78162	Abb78162 Amino aci
35	193	41.4	110	8	ADL05173	Adl05173 M. catarr
36	191.5	40.6	90	5	ABB78167	Abb78167 Amino aci
37	189	40.6	78	5	ABB78164	Abb78164 Amino aci
38	188	40.3	91	5	ABB78163	Abb78163 Amino aci
39	186	39.9	90	5	ABB78165	Abb78165 Amino aci
40	154	33.0	76	5	ABB78166	Abb78166 Amino aci
41	74	15.9	603	8	ADX91918	Adx91918 Plant ful
42	73.5	15.9	364	3	AAg39023	Aag39023 Arabidops
43	73.5	15.8	388	3	AAg39022	Aag39022 Arabidops
44	73.5	15.8	436	3	AAg39021	Aag39021 Arabidops
45	73.5	15.8	474	7	ABO75727	ABO75727 Pseudomon
46	73	15.7	582	9	ABM91962	Abm91962 M. xanthu
47	71.5	15.3	268	8	ADX95150	Adx95150 Plant ful
48	71.5	15.3	683	8	ADX96168	Adx96168 Plant ful
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50	71	15.2	291	4	AAAB85750	Aaam85750 Human imm
51	71	15.2	329	3	AAAB43482	Aaab43482 Human can
52	71	15.2	427	3	AAAB43107	Aaab43107 Human ORF
53	71	15.2	566	5	ABB97401	Abb97401 Novel hum
54	71	15.2	591	8	ABM82407	Abm82407 Tumour-as
55	71	15.2	615	7	ADJ71113	Adj71113 Human hea
56	70.5	15.1	491	3	AAAB08899	Aab08899 Human sec
57	70.5	15.1	534	5	AAAG68347	Aag68347 Human zin
58	70.5	15.1	840	8	ADM87322	Adm87322 Human pro
59	70	15.0	485	3	AAAG46903	Aag46903 Arabidops
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61	69.5	14.9	438	6	ADG78792	Adg78792 Human sec
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63	69.5	14.9	507	6	ABU41973	Abu41973 Protein e
64	69.5	14.9	564	8	ADM87771	Adm87771 Human EST
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66	69.5	14.9	295	8	AD124548	Adi24548 Human mod
67	68.5	14.7	393	8	ADI67182	Adi67182 Lactobaci
68	68.5	14.7	507	6	ABU40210	Abu40210 Protein e
69	68.5	14.7	646	8	ADT60267	Adt60267 Plant pol
70	68.5	14.7	704	9	ADZ14794	Adz14794 Human tum
71	68.5	14.7	76	9	AEA27813	Aea27813 Rat ortho
72	68	14.6	405	7	ADE71290	Ade71290 Novel hum
73	68	14.6	287	4	AAAB46739	Aab46739 C. tracho
74	67.5	14.5	436	9	ADW17810	Adw17810 Pinus rad
75	67.5	14.5				

ALIGNMENTS

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ID ABB78177 standard; protein; 87 AA.
XX ABB78177;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Methylococcus capsulatus.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PA
XX
PI Downs D, Gralnick JA;
PI
XX
DR WPI; 2002-589476/63.
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
PT
XX
PS Example; Fig 1A; 16bp; English.
PS
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

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Query Match          100.0%; Score 466; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.6e-48;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MARRIICAKLGIEADGLDAPPFGPGQGRIFEHVSKEAWQDWLKLQTMLINEHRLTPFEA 60
        |||
DB      1 MARRIICAKLGIEADGLDAPPFGPGQGRIFEHVSKEAWQDWLKLQTMLINEHRLTPFEA 60

OY      61 SARKELEQEREKFLFGGTTSTPGGYVP 87
        |||
DB      61 SARKELEQEREKFLFGGTTSTPGGYVP 87

RESULT 2
ABB78176
ID      ABB78176 standard; protein; 87 AA.
XX
AC      ABB78176;
XX
DT      29-AUG-2003 (revised)
DT      05-NOV-2002 (first entry)
XX
DE      Amino acid sequence of a YggX homologue.
XX
KW      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW      hydroxyl radical; DNA damage; YggX homologue.
XX
OS      Acidithiobacillus ferrooxidans.
XX
US      US2002072118-A1.
XX
PD      13-JUN-2002.
XX
PF      18-SEP-2001; 2001US-00955502.
XX
PR      22-SEP-2000; 2000US-0234588P.
XX
PA      (DOWN/) DOWNS D.
PA      (GRAL/) GRALNICK J A.
XX
PI      Downs D, Gralnicks JA;

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XX WP1; 2002-589476/63.
XX
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
XX
SQ Sequence 87 AA;

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					0; <td>Gaps</td>	Gaps
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Dd	1 MSRMVQCVKLGHEAEGLDRPPYPGALGARITYQEVSKEAWQWLKHQTMLINEYRSLPIDP					60
QY	61 SAKFLEOEREKFLPGGSTSTPOGYVP					87
Dd	61 KSRTPLEKOMEAFFGDGAQSPEGYVP					87

RESULT 3
ABB78175
ID ABB78175 standard; protein; 87 AA.
XX
AC ABB78175;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium; hydroxyl radical; DNA damage; yggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D. PA (GRAL/) GRALNICK J A.
XX
P1 Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant cell, comprises engineering the cell to produce more YggX protein, a protein identified from Salmonella enterica Serovar Typhimurium.
PT
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.41601 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-32

Perfect score: 466
Sequence: 1 MARRICAKLGIEADGLDAP.....QEREKFLFGGTSTPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	52.1	88	2	H81014 conserved hypothet
2	235	50.4	90	2	H83003 conserved hypothet
3	224	48.1	90	2	C64013 hypothetical prote
4	215	46.1	90	2	C82320 conserved hypothet
5	201	43.1	105	2	C82624 conserved hypothet
6	200	42.9	91	2	A85954 hypothetical prote
7	200	42.9	91	2	A65082 hypothetical prote
8	200	42.9	91	2	F91108 hypothetical prote
9	195	41.8	91	2	AH0879 conserved hypothet
10	186	39.9	90	2	AI0116 conserved hypothet
11	154	33.0	93	2	B84994 hypothetical prote
12	73.5	15.8	507	2	A83105 conserved fumarse
13	72.5	15.6	313	2	D69756 conserved hypothet
14	71	15.2	427	2	T46265 hypothetical prote
15	70	15.0	499	2	T04433 hypothetical prote
16	70	15.0	499	2	A85216 hypothetical prote
17	68.5	14.7	520	2	B96517 hypothetical prote
18	68	14.6	374	2	B86198 hypothetical prote
19	67.5	14.5	261	2	TI3932 gag protein - fru
20	67.5	14.5	472	2	H81665 replicative DNA he
21	67.5	14.5	472	2	G71503 probable replicati
22	67	14.4	353	1	FOMVGR gag polypote
23	67	14.4	512	2	C96517 hypothetical prote
24	66	14.2	611	2	C84863 hypothetical prote
25	66	14.2	639	2	G86455 hypothetical prote
26	65	13.9	165	1	XUBSM1 methylated-DNA-lpr
27	65	13.9	591	1	FOMVMM gag polypote
28	65	13.9	603	2	F86442 unknown prote
29	65	13.9	802	2	G89893 p1A, primosomal p

30	65	13.9	994	2	B82843 valyl-tRNA synthet
31	65	13.9	1324	2	T00386 hypothetical prote
32	64.5	13.8	1475	2	S42718 nuclear pore compl
33	64	13.7	424	2	H84295 glycine hydroxymet
34	64	13.7	732	2	S23001 tral protein - Esc
35	64	13.7	3187	2	JC5837 364K Golgi complex
36	63.5	13.6	302	2	B96520 hypothetical prote
37	63.5	13.6	439	1	QXFF71 hypothetical prote
38	63.5	13.6	2201	2	AH0095 probable sideropho
39	63	13.5	198	2	AF0968 hypothetical prote
40	63	13.5	387	2	T25452 hypothetical prote
41	63	13.5	398	2	S34638 gag protein - fru
42	63	13.5	633	2	T04179 hypothetical prote
43	62.5	13.4	158	2	AD2410 hypothetical prote
44	62.5	13.4	283	2	F82779 site-specific DNA-
45	62.5	13.4	482	2	AI2259 site-specific DNA-
46	62.5	13.4	482	2	S72471 potassium efflux s
47	62.5	13.4	970	2	AI3605 hypothetical prote
48	62	13.3	168	2	AD2450 phosphoribosylamin
49	62	13.3	306	1	JQ1395 L-serine dehydrata
50	62	13.3	488	2	AH2792 heat shock protein
51	62	13.3	488	2	G97571 DNA primase [impor
52	62	13.3	537	2	T04745 DNA primase (AF299
53	62	13.3	619	2	C83168 actin binding prot
54	62	13.3	661	2	AG2842 probable ATP /GTP
55	62	13.3	661	2	H97619 hypothetical prote
56	62	13.3	2033	2	T30849 homoserine O-acety
57	61.5	13.2	609	2	B81385 GMP synthase (glut
58	61	13.1	371	2	F90581 conserved hypothet
59	61	13.1	401	2	G84392 hypothetical prote
60	61	13.1	523	1	I64055 internalin homolog
61	61	13.1	686	2	T25743 probable GMP synth
62	61	13.1	956	2	H81654 oligoendopeptidase
63	60.5	13.0	236	2	AH1936 NADPH-ferrihemopro
64	60.5	13.0	300	2	AB1380 6-phosphofructokin
65	60.5	13.0	368	2	T31103 WD-repeat protein
66	60.5	13.0	601	1	A55485 probable amino aci
67	60.5	13.0	601	2	G86840 translation elonga
68	60.5	13.0	692	2	S37159 probable membrane
69	60.5	13.0	780	1	KIRBF conjugal transfer
70	60.5	13.0	1551	2	AB2410 conserved hypothet
71	60	12.9	333	2	D95968
72	60	12.9	447	2	S39505
73	60	12.9	602	2	S58336
74	60	12.9	815	2	G82861
75	59.5	12.8	185	1	B69374

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein MMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathavan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI000000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN:.
A/Experimental source: serogroup B, strain MC58
R/Parthill, J.; Achman, M.; James, R.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

[illegible]

```

A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:LA2023; NID:g15;
C/Superfamily: fe(II) trafficking protein YggX

Query Match      48.1%; Score 224; DB 2; Length 90;
Best Local Similarity 51.7%; Pred. No. 3.9e-18;
Matches 45; Conservative 11; Mismatches 31; Indels 0; Gaps 0;

OY      1 MARRICAKLGIEADGLDADPPFPPOGORIFEHVSKEAWQDWLKLQTMLINEHRLTPFEA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MARTVFCBYLKKKEAGLDLQLYPGLGKRIFDSVSKQAWGEWIKKQTMVNEKLLNMDNA 60

OY      61 SARKFLEQEREKFLFGGCTSTPGYVP 87
      ||||| ||| |||:|:|
Db      61 EHRKLLQEMVNFLEFGKDVHIEGYTP 87

RESULT 4
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Babs, S.; Qin, H.; Dragol, I.; Sellers, P
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein YggX

Query Match      46.1%; Score 215; DB 2; Length 90;
Best Local Similarity 49.4%; Pred. No. 4.1e-17;
Matches 43; Conservative 10; Mismatches 34; Indels 0; Gaps 0;

OY      1 MARRICAKLGIEADGLDADPPFPPOGORIFEHVSKEAWQDWLKLQTMLINEHRLTPFEA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MARTVFCBYLKKKEAGLDLQLYPGLGKRIFDSVSKQAWGEWIKKQTMVNEKLLNMDP 60

OY      61 SARKFLEQEREKFLFGGCTSTPGYVP 87
      ||||| ||| |||:|:|
Db      61 EHRKLLQEMVNFLEFGKDVHIEGYTP 87

RESULT 5
C82624
conserved hypothetical protein XFI908 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82624
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-105 <SIM>
A/Cross-references: UNIPARC:UPI00000C288F; GB:AB004010; GB:AE003849; NID:g9106992; PIDN:
A/Experimental source: strain 9a5c

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.2638 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-32
Perfect score: 466
Sequence: 1 MARRICAKLGIEADGLDAP.....QEREKFLGGGTSTPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	90	1	FETP_METCA
2	276	59.2	91	1	FETP_BURMA
3	276	59.2	91	1	FETP_BURPS
4	275	59.0	91	2	Q4LSI9_9BURK
5	268	57.5	90	1	FETP_COXBU
6	261	56.0	90	1	FETP_CHRVO
7	261	56.0	90	1	FETP_NITRU
8	260	55.8	90	1	FETP_BORBR
9	260	55.8	90	1	FETP_BORPA
10	260	55.8	90	1	FETP_BORPE
11	250	53.6	89	1	FETP_LEGPA
12	250	53.6	89	1	FETP_LEGPH
13	250	53.6	89	1	FETP_LEGPL
14	248	53.2	91	1	FETP_RALSO
15	243	52.1	88	1	FETP_NEIGI
16	243	52.1	88	1	FETP_NEIMA
17	243	52.1	88	1	FETP_NEIMB
18	239	51.3	90	1	FETP_PSEPK
19	235	50.4	90	1	FETP_PSEAB
20	232	49.8	92	1	FETP_XANOR
21	230	49.4	90	2	Q4J2Z8_AZOV1
22	229.5	49.2	90	1	FETP_ACIAD
23	227	48.7	91	1	FETP_XANAC
24	226	48.5	90	1	FETP_PSESM
25	226	48.5	90	2	Q4ZLF3_PSESY
26	226	48.5	90	2	Q4KJT2_PSEFS
27	224	48.1	90	1	FETP_HAEIN
28	224	48.1	90	2	Q4QMD9_HAEI8
29	222	47.6	90	2	Q6T7F6_PSEFL
30	221	47.4	92	1	FETP_XANCP
31	221	47.4	92	2	Q4UW14_XANCP

32	219	47.0	90	1	FETP_PASMU	Q9C1B9 pasteurella
33	219	47.0	91	1	FETP_MANSM	Q65V77 manheimia
34	218	46.8	90	1	FETP_IDILO	Q5QY58 idiomarina
35	218	46.8	90	1	FETP_VIBF1	Q5E7C0 vibrio fisc
36	216	46.4	90	1	FETP_VIBVU	Q8DCC5 vibrio fisc
37	216	46.4	90	1	FETP_VIBVY	Q7MB14 vibrio vuln
38	215	46.1	90	1	FETP_VIBCH	Q9KUR4 vibrio chol
39	215	46.1	92	1	FETP_SHEON	Q8EBX6 shewanella
40	214	45.9	90	1	FETP_PHOHL	Q7N711 photorhabdu
41	207	44.4	90	1	FETP_PHOPR	Q61MK7 photobacter
42	207	44.4	90	1	FETP_VIBPA	Q87115 vibrio para
43	205	44.0	94	1	FETP_HABDU	Q7VKB6 haemophilus
44	204	43.8	90	1	FETP_XYLFT	Q87D06 xylella fas
45	201	43.1	90	1	FETP_XYLPFA	Q9PC73 xylella fas
46	199	42.7	90	1	FETP_ERWCT	Q6D8J9 erwina car
47	198	42.5	92	2	Q4NMQ4_9DELT	Q4NWQ4 anaeromyxob
48	195	41.8	90	1	FETP_ECO57	Q4ABP4 escherichia
49	195	41.8	90	1	FETP_ECOLI	Q0A8P3 escherichia
50	195	41.8	90	1	FETP_SHIFL	Q0A8P5 shigella fl
51	194	41.6	90	1	FETP_YERPS	Q66FM3 yersinia ps
52	191	41.0	90	1	FETP_ECOL6	Q8FE19 escherichia
53	190	40.8	90	1	FETP_SALCH	Q57K04 salmonella
54	190	40.8	90	1	FETP_SALPA	Q5PMN1 salmonella
55	190	40.8	90	1	FETP_SALTI	Q67618 salmonella
56	190	40.8	90	1	FETP_SALTY	Q67617 salmonella
57	186	39.9	90	1	FETP_YERPE	Q8ZHE7 yersinia pe
58	183	39.3	87	1	FETP_FRATT	Q5NHJ8 francisella
59	183	39.3	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
60	165	35.4	78	1	FETP_BUCAP	Q8K925 buchnera ap
61	154	33.0	77	1	FETP_BUCAI	Q57618 buchnera ap
62	154	33.0	79	1	FETP_CANBF	Q7VRG9 candidatus
63	152	32.6	78	1	FETP_WICGBR	Q8D3C5 wiglesworth
64	130	27.9	87	1	FETP_BUCBP	Q89A44 buchnera ap
65	77	16.5	443	2	Q4URX4_XANCP	Q4URX4 xanthomonas
66	77	16.5	443	2	Q8PBW5_XANCP	Q8PBW5 xanthomonas
67	75	16.1	387	2	Q4NTN3_9DELT	Q4NTN3 anaeromyxob
68	73.5	15.8	507	2	Q9HW68_PSEAB	Q9HW68 pseudomonas
69	73	15.7	1982	2	Q4SFX7_TETNG	Q4SFX7 tetradodon n
70	72.5	15.6	306	2	Q6FOQ2_CANGA	Q6FGQ2 candida gla
71	72.5	15.6	313	1	YCEB_BACSU	Q34504 bacillus su
72	72.5	15.6	917	2	Q5VVB3_HUMAN	Q5VVB3 homo sapien
73	72	15.5	333	2	Q8JFX0_BRARE	Q8JFX0 brachydanio
74	71.5	15.3	294	2	Q8KPI2_BAROU	Q8KPI2 bartonella
75	71.5	15.3	491	2	Q5AM51_CANAL	Q5AM51 candida alb

ALIGNMENTS

RESULT 1
FETP_METCA
ID FETP_METCA STANDARD; PRT; 90 AA.
AC Q60AJ7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=MCA0856;
OS Methylococcus capsulatus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Methylococcales;
OC Methylococcaceae; Methylococcus.
OX NCBI_TaxID=414;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bath / NCIMB 11132;
RX PubMed=15383840; DOI=10.1371/journal.pbio.0020303;
RA Ward N.L., Larsen O., Sakwa J., Bruseck L., Khouri H.M., Durkin A.S.,
RA Dimetrov G., Jiang L., Scanlan D., Kang K.H., Lewis M.R., Nelson K.E.,
RA Methe B.A., Wu M., Heidelberg J.F., Paulsen I.T., Fouts D.E.,
RA Ravel J., Tettelin H., Ren Q., Read T.D., DeBoy R.T., Seshadri R.,
RA Salzberg S.L., Jensen H.B., Birkeland N.K., Nelson W.C., Dodson R.J.,
RA Grindhaug S.H., Holt I.E., Bidhammer I., Jonassen I., Vanaken S.,
RA Utterback T.R., Feldblyum T.V., Fraser C.M., Lilienhaug J.R.,


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RA Eisen J.A.;
RT "Genomic insights into methanotrophy: the complete genome sequence of
RT Methylococcus capsulatus (Bath).";
RL Plos Biol. 2:1616-1628(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC
CC EMBL; AE017282; AAU93044.1; -; Genomic_DNA.
CC
CC TIGR; MCA0856; -; 1.
CC
CC HAMAP; MF_00686; -; 1.
CC
CC InterPro; IPR007457; YggX.
CC
CC Pfam; PF04362; DUF495; 1.
CC
CC PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC
CC ProDom; PD029191; DUF495; 1.
CC
CC Complete proteome; Iron.
CC
CC SEQUENCE 90 AA; 10225 MW; 867B7FC9B21CBD01 CRC64;
SQ
-----
Query Match 100.0%; Score 466; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 5.5e-46;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARRIICAKLGIEADGLDAPPPPGQGRIFEHVSKKAMQDWLKLQTMLINEHRLTPPEA 60
   |||||||
Db 1 MARRIICAKLGIEADGLDAPPPPGQGRIFEHVSKKAMQDWLKLQTMLINEHRLTPPEA 60

Oy 61 SARKFLEQEREKFLFGGGSSTPGGYVP 87
   |||||||
Db 61 SARKFLEQEREKFLFGGGSSTPGGYVP 87

RESULT 2
PETP_BURMA
ID PETP_BURMA STANDARD; PRT; 91 AA.
AC Q62IU9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BMA1752;
OS Burkholderia mallei (Pseudomonas mallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=13373;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 23344;
RX PubMed=15377793; DOI=10.1073/pnas.0403306101;
RA Niernan W.C., Deshazer D., Kim H.S., Tettelin H., Nelson K.E.,
RA Feldblyum T.V., Ulrich R.L., Ronning C.M., Brinkac L.M.,
RA Daugherty S.C., Davidsen T.D., DeBoy R.T., Dimitrov G., Dodson R.J.,
RA Durkin A.S., Gwinn M.L., Haft D.H., Khouri H.M., Kolonay J.F.,
RA Madupu R., Mohammed Y., Nelson W.C., Radune D., Romero C.M.,
RA Sarría S., Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y.,
RA Zafar N., Zhou L., Fraser C.M.;
RT "Structural flexibility in the Burkholderia mallei genome.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14246-14251(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC use as long as its content is in no way modified and this statement is not

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CC removed.-----
CC EMBL; CP000010; AAU48201.1; -; Genomic_DNA.-----
DR TIGR; BMA1752; -.-----
DR HAMAP; MF_00686; -; 1.-----
DR InterPro; IPR007457; YgX.-----
DR Pfam; PF04362; DUF495; 1.-----
DR PIRSF; PIRSF029827; Fe traffic_YgX; 1.-----
DR ProDom; PD029191; DUF495; 1.-----
KW Complete proteome; Iron.-----
SQ SEQUENCE 91 AA; 10376 MW; 2CA3A83A67D5C8F0 CRC64;-----

Query Match 59.2%; Score 276; DB 1; Length 91;
Best Local Similarity 59.8%; Pred. No. 6.2e-24;
Matches 52; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

QY 1 MARRITCAKLGTEADGLDAPPPPGQGRIFEHVSKAQMOWLKLQTMLINEHRLTPFEA 60
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 MARMIHCAKLGKEALGLDPPLPGLGKRLYESVSKQAMOWMLKQQTMLINENRLMADP 60

QY 61 SARKFLEQERERKFLFGGCTSTPGYVP 87
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 RARQYLMKQTEKYFEGGADQASGYVP 87

RESULT 3
FETP_BURPS
ID_FETP_BURPS STANDARD; PRT; 91 AA.
AC 063614;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=BPSL2326;
GN Burkholderia pseudomallei (Pseudomonas pseudomallei).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia; pseudomallei group.
OX NCBI_TaxID=28450;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K96243;
RX PubMed=15377794; DOI=10.1073/pnas.0403302101;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.-M.,
RA Atkins T., Crossman I.C., Pitt T., Churcher C., Mungall K.L.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosssett B., Davis P., Deshazer D.,
RA Felwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.B., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchaveit M.,
RA Whitehead S., Yeats C., Barrett B.G., Oyston P.C.F., Parkhill J.;
RA "Genomic plasticity of the causative agent of melioidosis,
RT Burkholderia pseudomallei.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.-----
CC EMBL; BX571965; CAH36329.1; -; Genomic_DNA.-----
DR HAMAP; MF_00686; -; 1.-----
DR InterPro; IPR007457; YgX.-----
DR Pfam; PF04362; DUF495; 1.-----
DR PIRSF; PIRSF029827; Fe traffic_YgX; 1.-----
DR ProDom; PD029191; DUF495; 1.-----
KW Complete proteome; Iron.-----

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.4589 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-32

Perfect score: 466
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	235.5	50.5	92	US-09-328-352-5456	Sequence 5456, Ap
2	235	50.4	122	US-09-252-991A-23355	Sequence 23355, A
3	214	45.9	93	US-09-543-681A-5443	Sequence 5443, Ap
4	201	43.1	107	US-09-489-039A-11962	Sequence 11962, A
5	193	41.4	110	US-09-540-236-2859	Sequence 2859, Ap
6	73.5	15.8	474	US-09-252-991A-24473	Sequence 24473, A
7	73	15.7	582	US-09-902-540-11161	Sequence 11161, A
8	68.5	14.7	393	US-09-634-238-274	Sequence 274, App
9	67.5	14.5	287	US-09-585-858-48	Sequence 48, Appl
10	67.5	14.5	287	US-10-270-878-48	Sequence 48, Appl
11	66	14.2	196	US-08-900-407-1	Sequence 1, Appli
12	65	13.9	591	US-09-370-368-8	Sequence 8, Appli
13	64.5	13.8	1475	US-09-538-092-1160	Sequence 1160, Ap
14	63.5	13.6	261	US-09-489-039A-8618	Sequence 8618, Ap
15	63	13.5	586	US-08-964-268-3	Sequence 3, Appli
16	63	13.5	586	US-09-105-254-3	Sequence 3, Appli
17	63	13.5	586	US-10-413-536-3	Sequence 3, Appli
18	63	13.5	606	US-09-618-425-5	Sequence 5, Appli
19	62.5	13.4	482	US-09-135-639-2	Sequence 2, Appli
20	62.5	13.4	795	US-09-328-352-6143	Sequence 6143, Ap
21	62	13.3	623	US-09-252-991A-22906	Sequence 22906, A
22	62	13.3	1130	US-09-976-594-280	Sequence 280, App
23	61.5	13.2	395	US-09-949-016-7011	Sequence 7011, Ap
24	61.5	13.2	395	US-09-593-828-13	Sequence 13, Appl
25	61	13.1	343	US-09-252-991A-22307	Sequence 22307, A
26	61	13.1	586	US-09-252-991A-27398	Sequence 27398, A
27	61	13.1	908	US-09-623-326-9	Sequence 9, Appli

28	61	13.1	908	US-09-623-326-10	Sequence 10, Appl
29	60.5	13.0	632	US-09-902-540-11147	Sequence 11147, A
30	60	12.9	329	US-09-602-787A-306	Sequence 306, App
31	60	12.9	459	US-09-602-787A-302	Sequence 302, App
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33	60	12.9	601	US-09-033-153-2	Sequence 2, Appli
34	60	12.9	601	US-09-325-430B-2	Sequence 2, Appli
35	59.5	12.8	358	US-09-252-991A-31333	Sequence 31333, A
36	59.5	12.8	705	US-08-456-647B-4	Sequence 4, Appli
37	59.5	12.8	705	US-08-237-401A-4	Sequence 4, Appli
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39	59.5	12.8	839	US-09-577-304A-232	Sequence 232, App
40	59	12.7	223	US-09-248-796A-17759	Sequence 17759, A
41	59	12.7	390	US-09-949-016-6813	Sequence 6813, Ap
42	59	12.7	390	US-09-593-828-8	Sequence 8, Appli
43	59	12.7	431	US-09-949-016-8893	Sequence 8893, Ap
44	59	12.7	519	US-10-113-794A-2	Sequence 2, Appli
45	59	12.7	520	US-09-949-016-9918	Sequence 9918, Ap
46	59	12.7	618	US-09-252-991A-22418	Sequence 22418, A
47	59	12.7	1455	US-08-726-012B-2	Sequence 2, Appli
48	58.5	12.6	170	US-09-270-767-60691	Sequence 60691, A
49	58.5	12.6	204	US-09-270-767-45195	Sequence 45195, A
50	58.5	12.6	254	US-09-270-767-41684	Sequence 41684, A
51	58.5	12.6	1493	US-09-538-092-1263	Sequence 1263, Ap
52	58.5	12.6	2867	US-09-902-540-12593	Sequence 12593, A
53	58	12.4	561	US-09-489-039A-11625	Sequence 11625, A
54	57.5	12.3	289	US-09-105-697-2	Sequence 2, Appli
55	57.5	12.3	300	US-09-585-858-42	Sequence 42, Appl
56	57.5	12.3	300	US-10-270-878-42	Sequence 88, Appl
57	57.5	12.3	310	US-08-484-956-88	Sequence 88, Appl
58	57.5	12.3	310	US-08-757-653-88	Sequence 88, Appl
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61	57.5	12.3	315	US-08-484-956-91	Sequence 91, Appl
62	57.5	12.3	315	US-08-757-653-91	Sequence 91, Appl
63	57.5	12.3	315	US-08-520-946-91	Sequence 91, Appl
64	57.5	12.3	315	US-09-655-378A-91	Sequence 91, Appl
65	57.5	12.3	320	US-08-757-653-163	Sequence 163, App
66	57.5	12.3	320	US-08-823-516-61	Sequence 61, Appl
67	57.5	12.3	320	US-08-759-038-102	Sequence 102, App
68	57.5	12.3	320	US-08-758-314-102	Sequence 102, App
69	57.5	12.3	320	US-09-684-938-102	Sequence 102, App
70	57.5	12.3	320	US-09-308-825A-102	Sequence 102, App
71	57.5	12.3	320	US-09-940-244-61	Sequence 61, Appl
72	57.5	12.3	320	US-09-381-212-61	Sequence 61, Appl
73	57.5	12.3	320	US-09-713-601A-61	Sequence 61, Appl
74	57.5	12.3	322	US-08-484-956-89	Sequence 89, Appl
75	57.5	12.3	322	US-08-757-653-89	Sequence 89, Appl

ALIGNMENTS

RESULT 1
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 50.5%; Score 235.5; DB 2; Length 92;
Best Local Similarity 52.8%; Pred. No. 1.9e-22;

Matches	47;	Conservative	14;	Mismatches	25;	Indels	3;	Gaps	2;
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RESULT 2
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Query Match	50.4%;	Score 235;	DB 2;	Length 122;
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Oy      61 SARKELEEREKEKFLFGGGTSTPGGYVP 87
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RESULT 3
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
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; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Query Match	45.9%	Score 214;	DB 2;	Length 93;
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Db      4 MSRTI FCTPLNKEADGLDFQLYPGELGKRIFNEISKEAWGOMAKQTMLINEKCLNTMNP 63

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QY 61 SARKLEQEREKFLFGGSGTSPQGYVP 87
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DB 64 DDKLLEQEMVRFLEFGHDVHIDGYTP 90

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RESULT 4
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PR1
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity	48.3%;	Pred. No. 6.1e-18;		
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QY 61 SARKFLQEREKFLPGGTSIPQGYVP 87
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Db 77 EHRKLLQEQMVQFLFEKGDVHLEGYTP 103

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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
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; LENGTH: 110
; TYPE: PR1
; ORGANISM: M.catarhalis
US-09-540-236-2859

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Query Match	41.4%;	Score 193;	DB 2;	Length 110;
Best Local Similarity	44.6%;	Pred. No. 6.6e-17;		
Matches	37;	Conservative	12;	Mismatches 34;
			Indels	0;
			Gaps	0;

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DB     25 VFCRKYYQGNLPKLEPNPPFPNAKGQEIQDPTISAKAWNAWLELQTMLINEKHLMSMDQAKK 84

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QY 65 FLEOEREKFLPGGSTPQGYP 87
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Db 85 YLNEQREKFELDNGDYEKPAGYKP 107

RESULT 6
US-09-252-991A-24473
; Sequence 24473, Application US/09252991A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 54.4363 Seconds
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Title: US-09-955-502A-32

Perfect score: 466
Sequence: 1 MARRICAKLGIEADGLDAP.....QEREKFLFGGTSTPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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4	276	59.2	87	3	US-09-955-502-30
5	268	57.5	88	3	US-09-955-502-33
6	260	55.8	87	3	US-09-955-502-2
7	260	55.8	87	3	US-09-955-502-3
8	243	52.1	88	3	US-09-955-502-26
9	243	52.1	88	3	US-09-955-502-27
10	243	52.1	88	3	US-09-955-502-28
11	242.5	52.0	86	3	US-09-955-502-4
12	239	51.3	87	3	US-09-955-502-24
13	235	50.4	87	3	US-09-955-502-25
14	226	48.5	90	3	US-09-955-502-23
15	224	48.1	87	3	US-09-955-502-7
16	223	47.9	91	3	US-09-955-502-5
17	219	47.0	87	3	US-09-955-502-6
18	215	46.1	88	3	US-09-955-502-9
19	215	46.1	90	3	US-09-955-502-10
20	205	44.0	87	3	US-09-955-502-8
21	201	43.1	89	3	US-09-955-502-22
22	200	42.9	91	3	US-09-955-502-11
23	200	42.9	91	3	US-09-955-502-12
24	200	42.9	91	3	US-09-955-502-13
25	195	41.8	88	3	US-09-955-502-15
26	195	41.8	91	3	US-09-955-502-14
27	195	41.8	91	3	US-09-955-502-16

28	195	41.8	91	3	US-09-955-502-17	Sequence 17, Appl
29	189	40.6	78	3	US-09-955-502-19	Sequence 19, Appl
30	188	40.3	91	3	US-09-955-502-18	Sequence 18, Appl
31	186	39.9	90	3	US-09-955-502-20	Sequence 20, Appl
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33	75	16.1	597	4	US-10-424-599-188712	Sequence 188712,
34	74	15.9	603	4	US-10-425-114-54582	Sequence 54582, A
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37	71.5	15.3	268	4	US-10-425-114-57814	Sequence 57814, A
38	71.5	15.3	621	4	US-10-437-963-132015	Sequence 132015,
39	71.5	15.3	683	4	US-10-425-114-58832	Sequence 58832, A
40	71	15.2	329	3	US-09-925-301-927	Sequence 927, App
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43	70.5	15.1	491	3	US-09-820-893-56	Sequence 56, Appl
44	70.5	15.1	491	4	US-10-607-565-56	Sequence 56, Appl
45	70.5	15.1	840	4	US-10-112-944-415	Sequence 415, App
46	69.5	14.9	438	3	US-09-974-879-570	Sequence 570, App
47	69.5	14.9	438	3	US-09-305-736-553	Sequence 553, App
48	69.5	14.9	438	3	US-09-818-683-553	Sequence 553, App
49	69.5	14.9	438	3	US-09-818-683-553	Sequence 553, App
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51	69.5	14.9	507	4	US-10-282-122A-69897	Sequence 69897, A
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54	69.5	14.9	659	4	US-10-437-963-107737	Sequence 107737,
55	69.5	14.9	818	4	US-10-437-963-156121	Sequence 156121,
56	69.5	14.9	890	4	US-10-437-963-156221	Sequence 156221,
57	69.5	14.9	972	6	US-11-097-143-37266	Sequence 37266, A
58	69	14.8	328	4	US-10-437-963-174979	Sequence 174979,
59	68.5	14.7	360	4	US-10-437-963-132016	Sequence 132016,
60	68.5	14.7	393	4	US-10-264-213-177	Sequence 177, App
61	68.5	14.7	507	4	US-10-282-122A-68134	Sequence 68134, A
62	68.5	14.7	646	5	US-10-739-930-10344	Sequence 10344, A
63	68.5	14.7	829	4	US-10-437-963-156165	Sequence 156165,
64	68.5	14.7	1141	5	US-10-732-923-18071	Sequence 18071, A
65	67.5	14.5	287	4	US-10-270-875-48	Sequence 48, Appl
66	67.5	14.5	287	4	US-10-270-878-48	Sequence 48, Appl
67	67.5	14.5	287	4	US-10-270-786-48	Sequence 48, Appl
68	67.5	14.5	287	4	US-10-270-710-48	Sequence 48, Appl
69	67.5	14.5	287	4	US-10-270-859-48	Sequence 48, Appl
70	67.5	14.5	287	4	US-10-270-846-48	Sequence 48, Appl
71	67.5	14.5	365	4	US-10-437-963-107715	Sequence 107715,
72	67.5	14.5	472	4	US-10-282-122A-55283	Sequence 55283, A
73	67.5	14.5	526	4	US-10-437-963-156176	Sequence 156176,
74	67.5	14.5	4498	5	US-10-732-923-15008	Sequence 15008, A
75	67	14.4	151	4	US-10-767-701-44295	Sequence 44295, A

ALIGNMENTS

RESULT 1
US-09-955-502-32
; Sequence 32, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 32
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Methylococcus capsulatus

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.60992 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-32
Perfect score: 466
Sequence: 1 MARRIICAKLGIBADGLDAP.....QERKKFLFGGCTSTPGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	52.1	88	6	US-10-467-657-968 Sequence 968, App
2	66	14.2	199	6	US-10-821-234-950 Sequence 950, App
3	65	13.9	3803	6	US-10-995-561-773 Sequence 773, App
4	65	13.9	3960	6	US-10-995-561-771 Sequence 771, App
5	65	13.9	5335	6	US-10-995-561-777 Sequence 777, App
6	65	13.9	5406	6	US-10-995-561-774 Sequence 774, App
7	65	13.9	5415	6	US-10-995-561-779 Sequence 779, App
8	65	13.9	5464	6	US-10-995-561-775 Sequence 775, App
9	61.5	13.2	395	7	US-11-072-175-159 Sequence 159, App
10	60.5	13.0	619	7	US-11-156-953-5 Sequence 5, Appli
11	59.5	12.8	549	7	US-11-085-185-2 Sequence 2, Appli
12	57.5	12.3	177	5	US-09-995-493-124 Sequence 124, App
13	57.5	12.3	310	7	US-11-198-746-88 Sequence 88, Appl
14	57.5	12.3	310	7	US-11-198-794-88 Sequence 88, Appl
15	57.5	12.3	315	7	US-11-198-746-91 Sequence 91, Appl
16	57.5	12.3	315	7	US-11-198-794-91 Sequence 91, Appl
17	57.5	12.3	322	7	US-11-198-746-89 Sequence 89, Appl
18	57.5	12.3	322	7	US-11-198-794-89 Sequence 89, Appl
19	57.5	12.3	528	7	US-11-198-746-90 Sequence 90, Appl
20	57.5	12.3	528	7	US-11-198-794-90 Sequence 90, Appl
21	57.5	12.3	548	7	US-11-198-746-86 Sequence 86, Appl
22	57.5	12.3	548	7	US-11-198-794-86 Sequence 86, Appl
23	57.5	12.3	695	7	US-11-198-746-87 Sequence 87, Appl
24	57.5	12.3	695	7	US-11-198-794-87 Sequence 87, Appl
25	57.5	12.3	832	7	US-11-065-943-100 Sequence 100, App

26	57.5	12.3	832	7	US-11-007-797A-11	Sequence 11, Appl
27	57.5	12.3	832	7	US-11-007-642B-11	Sequence 11, Appl
28	57.5	12.3	832	7	US-11-198-746-4	Sequence 4, Appli
29	57.5	12.3	832	7	US-11-198-794-4	Sequence 1, Appli
30	57.5	12.3	832	7	US-11-242-730-1	Sequence 85, Appl
31	57.5	12.3	833	7	US-11-198-746-85	Sequence 85, Appl
32	57.5	12.3	833	7	US-11-198-794-85	Sequence 85, Appl
33	57	12.2	264	7	US-11-072-512-3606	Sequence 3606, Ap
34	56	12.0	418	6	US-10-512-325-3	Sequence 3, Appli
35	56	12.0	418	7	US-11-196-919-2	Sequence 2, Appli
36	56	12.0	776	7	US-11-072-512-3117	Sequence 3117, Ap
37	56	12.0	833	7	US-11-076-187-5	Sequence 5, Appli
38	55.5	11.9	264	7	US-11-214-199-46	Sequence 46, Appl
39	55.5	11.9	893	7	US-11-072-512-3504	Sequence 3504, Ap
40	55	11.8	449	7	US-11-010-239-65	Sequence 65, Appl
41	55	11.8	2455	7	US-11-186-999-14	Sequence 14, Appl
42	55	11.8	2455	7	US-11-186-999-16	Sequence 16, Appl
43	54	11.6	532	7	US-11-147-915-24	Sequence 24, Appl
44	54	11.6	532	7	US-11-147-915-26	Sequence 26, Appl
45	54	11.6	674	7	US-11-167-048-1	Sequence 1, Appli
46	54	11.6	832	7	US-11-098-686-10182	Sequence 10182, A
47	53.5	11.5	285	6	US-10-467-657-222	Sequence 222, App
48	53.5	11.5	285	6	US-10-467-657-8230	Sequence 8230, App
49	53.5	11.5	447	7	US-11-072-512-2123	Sequence 2123, Ap
50	53.5	11.5	636	6	US-10-516-587-2	Sequence 2, Appli
51	53	11.4	256	6	US-10-877-346-72	Sequence 72, Appl
52	53	11.4	256	7	US-11-113-424-183	Sequence 183, App
53	53	11.4	446	7	US-11-055-822-96	Sequence 96, Appl
54	53	11.4	593	7	US-11-194-246-317	Sequence 317, App
55	52.5	11.3	521	6	US-10-467-657-1344	Sequence 1344, Ap
56	52.5	11.3	635	7	US-11-098-686-10433	Sequence 10433, A
57	52	11.2	181	6	US-10-467-657-6074	Sequence 6074, Ap
58	52	11.2	333	6	US-10-131-826A-132	Sequence 132, App
59	52	11.2	361	7	US-11-186-284-173	Sequence 173, App
60	52	11.2	371	7	US-11-198-685-8	Sequence 8, Appli
61	52	11.2	371	7	US-11-198-069-8	Sequence 8, Appli
62	52	11.2	462	6	US-10-454-437-212	Sequence 212, App
63	52	11.2	498	7	US-11-124-368A-254	Sequence 254, App
64	52	11.2	558	7	US-11-072-512-2054	Sequence 2054, Ap
65	52	11.2	963	6	US-10-467-962B-2	Sequence 2, Appli
66	51.5	11.1	191	7	US-11-098-686-10672	Sequence 10672, A
67	51.5	11.1	379	7	US-11-144-833-11	Sequence 11, Appl
68	51.5	11.1	462	7	US-11-055-822-956	Sequence 956, App
69	51.5	11.1	523	7	US-11-055-822-954	Sequence 954, App
70	51.5	11.1	766	6	US-10-821-234-1691	Sequence 1691, Ap
71	51.5	11.1	1315	6	US-10-453-372-1034	Sequence 1034, Ap
72	51.5	11.1	1335	6	US-10-453-372-1030	Sequence 1030, Ap
73	51	10.9	190	6	US-10-467-657-1426	Sequence 1426, Ap
74	51	10.9	246	6	US-10-523-503-18	Sequence 18, Appl
75	51	10.9	289	7	US-11-010-239-59	Sequence 59, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 71.531 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467
Sequence: 1 MTRRIICQKLGKADALNYS.....EMINPLFGTSGKPAGYTSE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78178 Amino aci
2	295	63.2	89	9	AEB41576 L. pneumo
3	295	63.2	95	9	AEB38294 L. pneumo
4	286	61.2	87	5	ABB78176 Amino aci
5	268	57.4	87	5	ABB78177 Amino aci
6	263	56.3	87	5	ABB78175 Amino aci
7	258	55.2	88	5	ABB78171 Amino aci
8	258	55.2	88	5	ABB78172 Amino aci
9	258	55.2	88	5	ABB78173 Amino aci
10	258	55.2	88	6	ABP77219 N. gonorr
11	257	55.0	87	5	ABB78174 Amino aci
12	241	51.6	90	5	ABB78155 Amino aci
13	237	50.7	87	5	ABB78153 Amino aci
14	235	50.3	93	7	ADF05158 Bacterial
15	233	49.9	90	5	ABB78165 Amino aci
16	232	49.7	107	7	ABO65445 Klebsiell
17	230	49.3	87	5	ABB78148 Amino aci
18	230	49.3	87	5	ABB78147 Amino aci
19	230	49.3	91	5	ABB78150 Amino aci
20	227	48.6	78	5	ABB78164 Amino aci
21	227	48.6	91	5	ABB78158 Amino aci
22	227	48.6	91	5	ABB78157 Amino aci
23	227	48.6	91	5	ABB78156 Amino aci
24	224	48.0	87	5	ABB78152 Amino aci

25	223	47.8	86	5	ABB78149	Abb78149 Amino aci
26	223	47.8	87	5	ABB78151	Abb78151 Amino aci
27	220	47.1	87	5	ABB78170	Abb78170 Amino aci
28	220	47.1	122	7	ABO74609	ABO74609 Pseudomon
29	218	46.7	88	5	ABB78160	Abb78160 Amino aci
30	218	46.7	91	5	ABB78161	Abb78161 Amino aci
31	218	46.7	91	5	ABB78159	Abb78159 Amino aci
32	218	46.7	91	5	ABB78162	Abb78162 Amino aci
33	215.5	46.1	92	6	ADA34169	Ada34169 Acinetoba
34	215	46.0	90	5	ABB78168	Abb78168 Amino aci
35	214	45.8	91	5	ABB78163	Abb78163 Amino aci
36	205.5	44.0	90	5	ABB78167	Abb78167 Amino aci
37	205	43.9	88	5	ABB78154	Abb78154 Amino aci
38	204	43.7	87	5	ABB78169	Abb78169 Amino aci
39	185	39.6	110	8	ADL05173	Adl05173 M. catarr
40	164	35.1	76	5	ABB78166	Abb78166 Amino aci
41	81	17.3	451	7	ADF07116	Adf07116 Bacterial
42	68	14.6	461	2	AAW10210	Aaw10210 Mature en
43	68	14.6	490	2	AAW10209	Aaw10209 Full leng
44	67.5	14.5	369	2	AAV35630	Aay35630 Chlamydia
45	67.5	14.5	375	8	ADS44184	Ades44184 Bacterial
46	67	14.3	283	5	ABB55069	Abb55069 Lactococc
47	66.5	14.2	495	6	ADA36816	Ada36816 Protein e
48	66.5	14.2	529	5	ABG71896	Abg71896 Human mac
49	66.5	14.2	529	5	AAV95255	Aab95255 Human pro
50	66.5	14.2	719	4	ADM87275	Adm87275 Human pro
51	66.5	14.2	934	8	ADM87275	Adm87275 Human pro
52	66.5	14.2	2285	4	ABB63057	Abb63057 Drosophil
53	66	14.1	415	4	AAV30842	Aab30842 Amino aci
54	66	14.1	430	4	AAV30831	Aab30831 Amino aci
55	66	14.1	532	4	AAV30841	Aab30841 Amino aci
56	66	14.1	547	4	AAV30830	Aab30830 Amino aci
57	66	14.1	578	4	AAV30840	Aab30840 Amino aci
58	66	14.1	593	4	AAV30829	Aab30829 Amino aci
59	66	14.1	678	4	AAV30851	Aab30851 Amino aci
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63	65.5	14.0	352	4	ABB64200	Abb64200 Drosophil
64	65.5	14.0	457	8	ADQ67016	Adq67016 Novel hum
65	65.5	14.0	1797	8	ADN17774	Adn17774 Bacterial
66	65	13.9	170	6	ABU28434	Abu28434 Protein e
67	65	13.9	1085	8	ADS43754	Ades43754 Bacterial
68	64.5	13.8	56	4	AAU46284	Aau46284 Propionib
69	64.5	13.8	56	6	ABM42803	Abm42803 Propionib
70	64.5	13.8	287	4	AAV46739	AAV46739 C. tracho
71	64.5	13.8	310	6	ABU40274	Abu40274 Protein e
72	64.5	13.8	472	2	AAV37727	AAV37727 Protein i
73	64.5	13.8	472	6	ABU27359	Abu27359 Protein e
74	64.5	13.8	898	9	AEB90973	Aeb90973 Lantibiot
75	64	13.7	175	4	AAV30838	Aab30838 Amino aci

ALIGNMENTS

RESULT 1
ABB78178
ID ABB78178 standard; protein; 88 AA.
XX ABB78178;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS
XX
XX Coriella burnetii.
XX
XX US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
XX (GRAL/) GRALNICK J A.
PI
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgxB protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgxB protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgxB reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgxB homologues
XX
SQ Sequence 88 AA;

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Query Match          100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      1 MTRRIICQKLGKEADALNYSYPGELGERIYNHISEQAWQAWLSHQTMLINERYLSLIDP 60

OY      61 KARQFLEQEMINFLFGTSEKPGAGYTSE 88
        |||||||
DB      61 KARQFLEQEMINFLFGTSEKPGAGYTSE 88

RESULT 2
AEB41576
ID      AEB41576 standard; protein; 89 AA.
XX
XX      AC      AEB41576;
XX
XX      DT      08-SEP-2005 (first entry)
XX
XX      DE      L. pneumophila protein SEQ ID NO 5908.
XX
XX      KM      detection; infection; Antibacterial; Vaccine.
XX
XX      OS      Legionella pneumophila.
XX
XX      PN      WO2005049642-A2.
XX
XX      PD      02-JUN-2005.
XX
XX      PF      23-SEP-2004; 2004WO-IB003578.
XX
XX      PR      21-NOV-2003; 2003FR-00013687.
XX
XX      PA      (INSP ) INST PASTEUR.
XX      PA      (INRM ) INSERM INST NAT SANTE & RECH MEDICALE.
XX      PA      (UYLY-) UNIV LYON 1 BERNARD CLAUDE.
XX      PA      (CNRS ) CNRS CENT NAT RECH SCI.
XX
PI      Buchrieser C, Tichit M, Etienne J, Ma L, Cazalec C, Glaser P;

```

PI Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F;
PI Jarraud S;
XX
DR WPI; 2005-388305/40.
XX
PT New genome of Legionella pneumophila Paris strain and derived
PT polypeptides, useful for detection or identification of the strain and
PT for treatment and prevention of infections.
XX
XX
PS Claim 3; SEQ ID NO 5908; 660pp; English.
XX
CC The invention relates to an isolated or purified nucleotide sequences (I)
CC from Legionella pneumophila Paris strain. (I), and their related
CC sequences or fragments, are useful as primers and probes for detection
CC and amplification, including differentiation between the Paris and
CC Philadelphia strains of Legionella pneumophila and to prepare recombinant
CC (hybrid) polypeptides (II). (II) are also useful for preparation of
CC specific antibodies (Ab), also used for detection/identification of
CC Legionella, and some (I), specifically those involved in synthesis of
CC surface proteins, are targets for identification of inhibitors. (II), or
CC vectors that contain (I), are useful as vaccines and immunogenic
CC compositions, for treatment and prevention of infections by L.
CC pneumophila. The present sequence represents the amino acid sequence of a
XX L. pneumophila protein.
SQ Sequence 89 AA;

Query Match	63.2%	Score 295;	DB 9;	Length 89;
Best Local Similarity	58.8%	Pred. No. 1.1e-28;		
Matches 50;	Conservative 19;	Mismatches 16;	Indels 0;	Gaps 0;

[illegible]

XX	RESULT 3
XX	AEFB38294
ID	AEFB38294 standard; protein; 95 AA.
XX	
AC	AEFB38294;
XX	
DT	08-SEP-2005 (first entry)
XX	
DE	L. pneumophila protein SEQ ID NO 2626.
XX	
KM	detection; infection; Antibacterial; Vaccine.
XX	
OS	Legionella pneumophila.
XX	
PN	WO2005049642-A2.
XX	
PD	02-JUN-2005.
XX	
PF	23-SEP-2004; 2004WO-IB003578.
XX	
PR	21-NOV-2003; 2003FR-00013687.
XX	
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PA	(INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA	(UYLY-) UNIV LYON 1 BERNARD CLAUDE.
PA	(CNRS) CNRS CENT NAT RECH SCI.
XX	
PI	Buchrieser C, Tichit M, Etienne J, Ma L, Cazalet C, Glaser P,
PI	Rusniok C, Bouchier C, Zidane N, Magnier A, Kunst F, Vandenesch F,
PI	Jarraud S;
DR	WPI; 2005-388305/40.
XX	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.52424 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-33
Perfect score: 467
Sequence: 1 MTRRIICQKLGRKADALNYS.....EMINFLFGTSGSEKPGYTSR 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	55.2	88	2	H81014 conserved hypothet
2	241	51.6	90	2	C82320 conserved hypothet
3	233	49.9	90	2	A10116 conserved hypothet
4	227	48.6	91	2	A85954 hypothetrical prote
5	227	48.6	91	2	A65082 hypothetrical prote
6	227	48.6	91	2	F91108 hypothetrical prote
7	224	48.0	90	2	C64013 hypothetrical prote
8	220	47.1	90	2	H83003 conserved hypothet
9	218	46.7	91	2	AH0879 conserved hypothet
10	214	45.8	105	2	C82624 conserved hypothet
11	164	35.1	93	2	B84994 hypothetrical prote
12	67.5	14.5	367	2	G81526 hypothetrical prote
13	67.5	14.5	368	2	D72011 hypothetrical prote
14	67.5	14.5	368	2	B86612 hypothetrical prote
15	67.5	14.5	375	2	T39364 probable galactosy
16	67	14.3	283	2	H86839 hypothetrical prote
17	67	14.3	329	2	T29862 hypothetrical prote
18	66.5	14.2	973	2	T50449 DNA repair and rec
19	65	13.9	1085	2	JC2227 probable helicase
20	64.5	13.8	472	2	H81665 replicative DNA he
21	64.5	13.8	472	2	G71503 probable replicati
22	64.5	13.8	554	2	G82272 DNA repair protein
23	64.5	13.8	701	2	S35313 TTP1 protein - yea
24	64	13.7	609	2	S36569 B1 protein - human
25	63.5	13.6	115	2	B86771 hypothetrical prote
26	63.5	13.6	243	2	A95064 conserved hypothet
27	63.5	13.6	264	2	C97931 conserved hypothet
28	63.5	13.6	312	2	D83539 conserved hypothet
29	63	13.5	419	2	AD2741 N-acetylmuramoyl-L

30	63	13.5	580	2	F75142 abc transporter AT
31	63	13.5	582	2	B71182 probable ABC trans
32	63	13.5	913	2	T35718 hypothetrical prote
33	62.5	13.4	841	2	B90244 ribonucleotide red
34	62	13.3	514	1	HODVLB cytochrome-c3 hydr
35	62	13.3	644	2	AD0712 conserved hypothet
36	62	13.3	644	2	D90940 hypothetrical prote
37	62	13.3	644	2	G64938 hypothetrical prote
38	62	13.3	644	2	H85788 DNA polymerase I
39	62	13.3	967	2	F87678 probable membrane
40	62	13.3	997	2	S67697 hypothetrical prote
41	61.5	13.2	260	2	AH1639 oxoglutarate dehyd
42	61.5	13.2	909	2	C84965 glutamate receptor
43	61.5	13.2	918	2	I58178 alpha-aminoadipyl-
44	61.5	13.2	3746	1	YGPLV3 delta-(L-alpha-ami
45	61.5	13.2	3770	2	A40889 alpha-aminoadipyl-
46	61.5	13.2	3791	1	YGPLV8 carboxylesterase
47	61	13.1	215	2	S14287 phosphatidylglycer
48	61	13.1	253	2	AB0271 glycosyltransferas
49	61	13.1	263	2	E97189 hypothetrical prote
50	61	13.1	269	2	A69997 circular genome pr
51	61	13.1	407	2	S11479 carboxylesterase
52	61	13.1	540	2	S53370 esterase B1 - sout
53	61	13.1	540	2	A35986 hypothetrical prote
54	61	13.1	703	2	B82355 ATP-dependent heli
55	61	13.1	703	2	B82148 nitrate reductase
56	61	13.1	830	2	AE0369 two-component sens
57	61	13.1	1131	2	AD2166 peptide synthetase
58	61	13.1	2459	2	AF2136 beta-lactamase (EC
59	60.5	13.0	249	2	A35263 conserved modificat
60	60.5	13.0	309	2	D71173 probable beta-lact
61	60.5	13.0	327	2	G70402 hypothetrical prote
62	60.5	13.0	498	2	A72725 secretory protein
63	60.5	13.0	591	2	E71651 hypothetrical prote
64	60.5	13.0	3649	1	S18268 leucine aminopepti
65	60.5	13.0	3712	1	YGCEVC cytochrome P450 1A
66	60	12.8	167	2	C72763 hypothetrical prote
67	60	12.8	234	2	JH0483 xpsB protein - Xan
68	60	12.8	413	2	B70573 xpsB protein - Xan
69	60	12.8	468	2	F87359 conserved hypothet
70	60	12.8	518	2	A27821
71	60	12.8	528	2	T22941
72	60	12.8	531	2	T12056
73	60	12.8	531	2	S17937
74	60	12.8	591	1	FOMVMM
75	60	12.8	644	2	AF0262

ALIGNMENTS

RESULT 1
H81014
conserved hypothetrical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, B.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, B.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEXT>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AB002552; GB:AE002098; NID:G7227279; PIDN:;
A/Experimental source: serogroup B, strain MC58
R/Parhill, J.; Achtmann, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagers, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: F81958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB2021; NMA0419
C;Superfamily: fe(II) trafficking protein YgX

Query Match 55.2%; Score 258; DB 2; Length 88;
Best Local Similarity 50.0%; Pred. No. 7.6e-22;
Matches 44; Conservative 18; Mismatches 26; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSPPYGGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |
DB 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSQEAWAAWTRHQTMLINENRLSLADP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |

QY 61 KARQFLQEMINFLFGTGSEKPAGYTSE 88
: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82320
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein YgX

Query Match 51.6%; Score 241; DB 2; Length 90;
Best Local Similarity 51.2%; Pred. No. 6.3e-20;
Matches 44; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSPPYGGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |
DB 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWQTKQTMLINEKKLMMMDP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |

QY 61 KARQFLQEMINFLFGTGSEKPAGYT 86
: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 61 EHRKLEQEMVNFLFEGKEVHIIEGYT 86

RESULT 3
AI0116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C;Accession: AI0116
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarrega, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360

A;Accession: AI0116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <KUR>
A;Cross-references: UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022; C
C;Genetics:
A;Gene: YPO0953
C;Superfamily: fe(II) trafficking protein YgX

Query Match 49.9%; Score 233; DB 2; Length 90;
Best Local Similarity 51.2%; Pred. No. 5e-19;
Matches 44; Conservative 18; Mismatches 24; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSPPYGGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |
DB 1 MSRTIFCTPFLKDAERQDFQLYPGELGKRITYNEISKEAWSQWITKQTMLINEKKLMMNI 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |

QY 61 KARQFLQEMINFLFGTGSEKPAGYT 86
: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 61 EDRKLEQEMVNFLFEGQDVHIAGYT 86

RESULT 4
A85954
hypothetical protein ygX [imported] - Escherichia coli (strain O157:H7, substrain EDL93:
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: ygX
C;Superfamily: fe(II) trafficking protein YgX

Query Match 48.6%; Score 227; DB 2; Length 91;
Best Local Similarity 50.0%; Pred. No. 2.4e-18;
Matches 44; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSPPYGGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |
DB 1 MSRTIFCTPFLQREAEQDFQLYPGELGKRITYNEISKEAWAQWQHKQTMLINEKKLMMNA 60
| | : | | | | : : | | | | : : | | | | | | | | | | | |

QY 61 KARQFLQEMINFLFGTGSEKPAGYTSE 88
: | | : | | : | | : | | : | | : | | : | | : | | : | | : | | :
DB 61 EHRKLEQEMVNFLFEGKEVHIIEGYTPE 88

RESULT 5
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-91 <BLAT>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 63.991 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467
Sequence: 1 MTRRIICQKLGKADALNYS.....EMINFLGTGSEKPGAGTSE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	467	100.0	90	1	FETP_COXBU
2	295	63.2	89	1	FETP_LEGPA
3	295	63.2	89	1	FETP_LEGPH
4	292	62.5	89	1	FETP_LEGPL
5	271	58.0	90	1	FETP_CHRVO
6	268	57.4	90	1	FETP_METCA
7	266	57.0	87	1	FETP_FRATT
8	264	56.5	91	2	Q4LS19_9BURK
9	263	56.3	90	1	FETP_NITEU
10	263	56.3	91	1	FETP_BURMA
11	263	56.3	91	1	FETP_BURSA
12	261	55.9	92	1	FETP_XANOR
13	258	55.2	88	1	FETP_NEIGI
14	258	55.2	88	1	FETP_NEIMA
15	258	55.2	88	1	FETP_NEIMB
16	255	54.6	91	1	FETP_XANAC
17	250	53.5	92	1	FETP_XANCP
18	250	53.5	92	2	Q4UW14_XANCP
19	245	52.5	90	1	FETP_IDILO
20	241	51.6	90	1	FETP_VIBCH
21	241	51.6	91	1	FETP_RALSO
22	240	51.4	90	1	FETP_VIBVU
23	240	51.4	90	1	FETP_VIBVY
24	237	50.7	94	1	FETP_HABDU
25	234	50.1	90	1	FETP_YERBP
26	233	49.9	90	1	FETP_YERBP
27	232	49.7	90	1	FETP_PHOLL
28	232	49.7	92	2	Q4NMQ4_9DELT
29	231	49.5	90	1	FETP_VIBPA
30	230	49.3	90	1	FETP_BORBR
31	230	49.3	90	1	FETP_BORPA

32	230	49.3	90	1	FETP_BORPE	Q7WVC4 bordetella
33	226	48.4	90	1	FETP_VIBF1	Q5E7C0 vibrio fisc
34	224	48.0	90	1	FETP_HAEIN	P44048 haemophilus
35	224	48.0	90	2	Q4QMD9_HAEI8	Q4QMD9 haemophilus
36	223	47.8	90	1	FETP_PASMU	Q9CIB9 pasteurilla
37	222	47.5	90	1	FETP_ECO57	P0A8P4 escherichia
38	222	47.5	90	1	FETP_ECOLI	P0A8P3 escherichia
39	222	47.5	90	1	FETP_SHIFL	P0A8P5 shigella fl
40	222	47.5	90	1	FETP_XYLFT	Q87D06 xylella fas
41	220	47.1	90	1	FETP_PSEAB	Q9HU36 pseudomonas
42	218	46.7	90	1	FETP_ECOL6	Q8FEL9 escherichia
43	218	46.7	91	1	FETP_MANSM	Q65VU7 mannheimia
44	216	46.3	90	1	FETP_PHOPR	Q61MK7 photobacter
45	215.5	46.1	90	1	FETP_ACTAD	Q61FB3 acinetobact
46	215	46.0	90	1	FETP_ERWCT	Q6D8J9 erwinia car
47	215	46.0	90	1	FETP_PSESM	Q87UF5 pseudomonas
48	215	46.0	90	2	Q4ZLF3_PSESY	Q4ZLP3 pseudomonas
49	214	45.8	90	1	FETP_XYLFA	Q9PC73 xylella fas
50	214	45.8	90	2	Q4J228_AZOVI	Q4J228 azotobacter
51	213	45.6	90	1	FETP_SALCH	Q57K04 salmoneila
52	213	45.6	90	1	FETP_SALPA	Q5PMU1 salmoneila
53	213	45.6	90	1	FETP_SALTI	P67618 salmoneila
54	213	45.6	90	1	FETP_SALTY	P67617 salmoneila
55	205	43.9	92	1	FETP_SHEON	Q8EBX6 shewanella
56	204	43.7	90	1	FETP_PSEBP	Q8R499 pseudomonas
57	202	43.3	90	2	Q6T7F6_PSEPL	Q6T7F6 pseudomonas
58	201	43.0	78	1	FETP_WIGBR	Q8D3C5 wigleswort
59	195	41.8	90	2	Q4KJ22_PSEF5	Q4KJ22 pseudomonas
60	189	40.5	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
61	179	38.3	78	1	FETP_BUCAP	Q8K925 buchnera ap
62	176	37.7	87	1	FETP_BUCBP	Q89A44 buchnera ap
63	173	37.0	79	1	FETP_CANBP	Q7VR99 candidatus
64	164	35.1	77	1	FETP_BUCAI	P57618 buchnera ap
65	81	17.3	2492	2	Q8JWJ9_9CLOS	Q8JWJ9 sweet potat
66	80	17.1	458	2	Q6G0N1_BAROU	Q6G0N1 bartonella
67	79	16.9	458	2	Q6G4V6_BARHE	Q6G4V6 bartonella
68	77	16.5	282	2	Q97TL0_CLOAB	Q97TL0 clostridium
69	75.5	16.2	263	2	Q4JZX9_STRPN	Q4JZX9 streptococc
70	72	15.4	592	2	Q87IT6_NEUCR	Q87IT6 neurospora
71	72	15.4	1030	2	Q7S7N2_NEUCR	Q7S7N2 neurospora
72	71.5	15.3	339	2	Q7NXX9_CHRVO	Q7NXX9 chromobact
73	71	15.2	804	2	Q74KS1_LACJO	Q74KS1 lactobacill
74	70.5	15.1	264	2	Q4K2D9_STRPN	Q4K2D9 streptococc
75	70	15.0	186	2	Q8D923_VIBVU	Q8D923 vibrio vuln

ALIGNMENTS

RESULT 1
FETP_COXBU
ID FETP_COXBU STANDARD; PRT; 90 AA.
AC Q83D06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=CBU0941;
OS Coxiella burnetii.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Coxiellaceae; Coxiella.
OX NCBI_TaxID=777;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Nine Mile phase I / RSA 493;
RX MEDLINE=22608657; PubMed=12704232; DOI=10.1073/pnas.0931379100;
RA Seshadri R., Paulsen I.T., Bisen J.A., Read T.D., Nelson K.E.,
RA Nelson W.C., Ward N.L., Tettelin H., Davidsen T.M., Beanan M.J.,
RA DeBoy R.T., Daugherty S.C., Brinkac L.M., Madupu R., Dodson R.J.,
RA Khouri H.M., Lee K.H., Carty H.A., Scanlan D., Heinzen R.A.,
RA Thompson H.A., Samuel J.E., Fraser C.M., Heidelberg J.F.;
RT "Complete genome sequence of the Q-fever pathogen, Coxiella burnetii.";


```
RL Proc. Natl. Acad. Sci. U.S.A. 100:5455-5460(2003).
CC -!- FUNCTION: Could be a mediator in iron transacctions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB016962; AA090467.1; -; Genomic_DNA.
DR TIGR; CBU0941; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10482 MW; 70354D317942C9AB CRC64;

Query Match 100.0%; Score 467; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 5e-43;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRRIICQKLGKADALNYSYPGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60
Db 1 MTRRIICQKLGKADALNYSYPGELGERIYNHISEQAWQAWLSHOTMLINEYRLSLIDP 60

QY 61 KARQPLEQEMINFLFGTSGSEKPGAGYTS 88
Db 61 KARQPLEQEMINFLFGTSGSEKPGAGYTS 88

RESULT 2
FETP_LEGPA STANDARD; PRT; 89 AA.
AC Q5X3X9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=lp1902;
OS Legionella pneumophila (strain Paris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
OC Legionellaceae; Legionella.
OX NCBI_TaxID=297246;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15467220; DOI=10.1038/ng1447;
RA Cazalet C., Rusniok C., Brueggemann H., Zidane N., Magnier A., Ma L.,
RA Tichit M., Jarraud S., Bouchier C., Vandenesch F., Kunst F.,
RA Etienne J., Glaaser P., Buchrieser C.;
RT "Evidence in the legionella pneumophila genome for exploitation of
RT host cell functions and high genome plasticity.";
RL Nat. Genet. 36:1165-1173(2004).
CC -!- FUNCTION: Could be a mediator in iron transacctions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CR628336; CAH13054.1; -; Genomic_DNA.
DR legioli1; lp1902; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
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DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 89 AA; 10539 MW; F4BB7C711D9F5AA1 CRC64;

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Best Local Similarity 58.8%; Pred. No. 3e-24;
Matches 50; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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Db 61 RABEFLKEBQKVFEGSGSEKPSGY 85

RESULT 3
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AC Q5ZU80;
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DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
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GN OrderedLocusNames=lp1927;
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OS ATCC 33152).
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OC Legionellaceae; Legionella.
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RX PubMed=15448271; DOI=10.1126/science.1099776;
RA Chien M., Morozova I., Shi S., Sheng H., Chen J., Gomez S.M.,
RA Asamanl G., Hill K., Nuara J., Feder M., Rineer J., Greenberg J.J.,
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RA Pamou S., Georgiou A., Chou I.-C., Iannuccilli W., Ulz M.E.,
RA Kim D.H., Geringer-Sameth A., Goldsberry C., Morozov P., Fischer S.G.,
RA Segal G., Qu X., Rzhetsky A., Zhang P., Cavanis B., De Jong P.J.,
RA Ju J., Kalachikov S., Shuman H.A., Russo J.J.;
RT "The genomic sequence of the accidental pathogen Legionella
RT pneumophila.";
RL Science 305:1966-1968(2004).
CC -!- FUNCTION: Could be a mediator in iron transacctions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB017354; AAU27997.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
SQ SEQUENCE 89 AA; 10539 MW; F4BB7C711D9F5AA1 CRC64;

Query Match 63.2%; Score 295; DB 1; Length 89;
Best Local Similarity 58.8%; Pred. No. 3e-24;
Matches 50; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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Db 1 MSRTVFCCKLKQEAAGLEKQFPFGLGKVFNEVSKQAWMMMLSHOTMLINEYRLNLIEA 60
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 17.6595 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502a-33

Perfect score: 467

Sequence: 1 MTRRIICQKLGKADALNYS.....EMINFLFGTSEKPGYTSR 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	232	49.7	107	2	US-09-489-039A-11962 Sequence 11962, A
3	220	47.1	122	2	US-09-252-991A-23355 Sequence 23355, A
4	215.5	46.1	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	185	39.6	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	81	17.3	451	2	US-09-543-681A-7401 Sequence 7401, Ap
7	68	14.6	461	1	US-08-672-571A-3 Sequence 3, Appli
8	68	14.6	490	1	US-08-672-571A-1 Sequence 1, Appli
9	67.5	14.5	369	2	US-09-198-452A-1048 Sequence 1048, Ap
10	67.5	14.5	369	2	US-09-438-185A-977 Sequence 977, App
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15	63.5	13.6	220	2	US-09-583-110-2877 Sequence 2877, Ap
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17	63.5	13.6	374	2	US-09-248-796A-19920 Sequence 19920, A
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47	59.5	12.7	339	2	US-09-107-532A-7148	Sequence 7148, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIORITY FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 55.062 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-33
Perfect score: 467
Sequence: 1 MTRRIICQKLGKADALNYS.....EMINFLFGTGEKPAQYTS 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 75 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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8	258	55.2	88	3	US-09-955-502-28
9	241	51.6	90	3	US-09-955-502-10
10	237	50.7	87	3	US-09-955-502-8
11	233	49.9	90	3	US-09-955-502-20
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19	224	48.0	87	3	US-09-955-502-7
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22	220	47.1	87	3	US-09-955-502-25
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26	218	46.7	91	3	US-09-955-502-17
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31	204	43.7	88	3	US-09-955-502-24	Sequence 24, Appl
32	164	35.1	76	3	US-09-955-502-21	Sequence 21, Appl
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ALIGNMENTS

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; Sequence 33, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnicks, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 33
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Coxiella burnetii

US-09-955-502-33

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RESULT 2

US-09-955-502-31

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; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
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; SEQ ID NO 31
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US-09-955-502-32

Sequence 32, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1

```

Query Match

57.4%; Score 268; DB 3; Length 87;

Best Local Similarity 58.8%; Pred. No. 1.8e-25;
Matches 50; Conservative 12; Mismatches 23; Indels 0; Gaps 0;

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        | ||||| ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| :
Db      1 MARRITCAKLGIHADGLDAPFPFGPGQGRITFEHYSKEAQDWLKLQTMLINEHRLTPEEA   600
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QY      61 KARQFLQEMINFLFGTGSSEKPAY 85
      ||:||||| |||: |||
DB      61 SARQFLQERERKFLFGGGSTSPQY 85

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RESULT 4

US-09-955-502-29

; Sequence 29, Application US/09955502
 ; Patent No. US20020072118A1
 : GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-09-955-502-29

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Best Local Similarity	54.1%;	Pred. No. 7.5e-25;		
Matches 46;	Conservative 18;	Mismatches 21;	Indels 0;	Gaps 0

Dy

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Dd

1 MARMIHCAGLKGAEIGDFFPLPGELGKRLYESYSKOAWQDWLKQOTMLINENRNLNMDP 600

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RESULT 5
HS-09-955-502-30

US-09-955-502-30

Sequence 30, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
;
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

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Query Match	56.3%	Score 263;	DB 3;	Length 87;
Best Local Similarity	54.1%;	Pred. No. 7.5e-25;		
Matches 46;	Conservative 18;	Mismatches 21;	Indels 0;	Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.66291 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-33

Perfect score: 467

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	258	55.2	88	6	US-10-467-657-968
2	61.5	13.2	521	7	US-11-152-366-49
3	61.5	13.2	938	7	US-11-072-512-3855
4	61.5	13.2	7968	7	US-11-186-731-5
5	58.5	12.5	329	6	US-10-981-873-29
6	58	12.4	375	6	US-10-517-939-272
7	57.5	12.3	338	6	US-10-914-165-37
8	56	12.0	1046	7	US-11-120-308-186
9	56	12.0	1176	6	US-10-821-234-897
10	55.5	11.9	210	7	US-11-194-246-441
11	55.5	11.9	335	7	US-11-072-175-245
12	55.5	11.9	1579	7	US-11-052-554A-9
13	55.5	11.9	4868	7	US-11-044-111-24
14	55	11.8	318	7	US-11-234-786-339
15	55	11.8	626	7	US-11-098-686-10124
16	55	11.8	1560	7	US-11-059-982-1
17	55	11.8	1841	7	US-11-057-058-63
18	54.5	11.7	360	6	US-10-467-657-5376
19	54.5	11.7	638	6	US-10-995-561-1025
20	54.5	11.7	1160	6	US-10-995-561-1019
21	54.5	11.7	1302	6	US-10-995-561-1024
22	54.5	11.7	1306	6	US-10-995-561-1027
23	54	11.6	739	7	US-11-078-189-12
24	53.5	11.5	350	5	US-09-978-360A-486
25	53.5	11.5	388	6	US-10-467-657-786

26	53	11.3	368	6	US-10-689-742-100	Sequence 100, App
27	53	11.3	382	7	US-11-134-795-19	Sequence 19, Appl
28	52.5	11.2	268	7	US-11-098-686-10958	Sequence 10958, A
29	52.5	11.2	381	7	US-11-143-984A-111	Sequence 111, App
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31	52.5	11.2	406	6	US-10-995-561-749	Sequence 749, App
32	52.5	11.2	406	6	US-10-995-561-750	Sequence 750, App
33	52.5	11.2	406	6	US-10-995-561-751	Sequence 751, App
34	52.5	11.2	406	6	US-10-995-561-752	Sequence 752, App
35	52.5	11.2	479	7	US-11-152-366-48	Sequence 48, Appl
36	52.5	11.2	492	6	US-10-821-234-1108	Sequence 1108, Ap
37	52.5	11.2	522	7	US-11-152-366-51	Sequence 51, Appl
38	52.5	11.2	644	7	US-11-072-512-2945	Sequence 2945, Ap
39	52	11.1	163	6	US-10-467-657-2662	Sequence 2662, Ap
40	52	11.1	194	5	US-09-978-360A-608	Sequence 608, App
41	52	11.1	247	6	US-10-838-616-46	Sequence 46, Appl
42	52	11.1	380	6	US-10-525-674-28	Sequence 28, Appl
43	52	11.1	638	7	US-11-072-512-2626	Sequence 2626, Ap
44	52	11.1	856	6	US-10-510-947-8	Sequence 8, Appli
45	52	11.1	856	7	US-11-042-988-13	Sequence 13, Appl
46	52	11.1	856	7	US-11-135-235-1	Sequence 1, Appli
47	52	11.1	898	7	US-11-174-150-43	Sequence 43, Appl
48	51.5	11.0	277	6	US-10-821-234-1435	Sequence 1435, Ap
49	51.5	11.0	318	6	US-10-793-626-1600	Sequence 1600, Ap
50	51.5	11.0	462	7	US-11-072-512-3571	Sequence 3571, Ap
51	51.5	11.0	574	7	US-11-098-686-11000	Sequence 11000, A
52	51.5	11.0	923	7	US-11-057-058-66	Sequence 66, Appl
53	51	10.9	196	7	US-11-098-686-10972	Sequence 10972, A
54	51	10.9	200	6	US-10-793-626-1186	Sequence 1186, Ap
55	51	10.9	200	6	US-10-793-626-2390	Sequence 2390, Ap
56	51	10.9	209	5	US-09-995-493-94	Sequence 94, Appl
57	51	10.9	351	6	US-10-981-873-27	Sequence 27, Appl
58	51	10.9	383	6	US-10-513-759-4	Sequence 4, Appli
59	51	10.9	383	7	US-11-129-143-76	Sequence 76, Appl
60	51	10.9	871	6	US-10-933-025-3	Sequence 3, Appli
61	51	10.9	3011	6	US-10-985-205-3	Sequence 3, Appli
62	50.5	10.8	268	7	US-11-098-686-110697	Sequence 10697, A
63	50.5	10.8	456	6	US-10-793-626-1190	Sequence 1190, Ap
64	50.5	10.8	724	6	US-10-665-455-8	Sequence 968, App
65	50	10.7	180	6	US-11-065-455-8	Sequence 8, Appli
66	50	10.7	244	7	US-10-467-657-5848	Sequence 5848, Ap
67	50	10.7	336	6	US-10-467-657-5848	Sequence 2, Appli
68	50	10.7	421	6	US-10-858-730-2	Sequence 2186, Ap
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70	50	10.7	561	7	US-11-031-206-138	Sequence 67, Appl
71	50	10.7	651	6	US-10-770-726-67	Sequence 10, Appl
72	50	10.7	651	7	US-11-177-138-10	Sequence 103, App
73	50	10.7	786	6	US-10-467-962B-103	Sequence 48, Appl
74	50	10.7	870	7	US-11-165-211-48	Sequence 58, Appl
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ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.9696 Seconds
(without alignments)
540.539 Million cell updates/sec

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Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	5	ABB78161
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5	472	96.7	88	5	ABB78160
6	469	96.1	91	5	ABB78158
7	469	96.1	91	5	ABB78157
8	469	96.1	91	5	ABB78156
9	445	91.2	107	7	ABO65445
10	393	80.5	90	5	ABB78165
11	389	79.7	90	5	ABB78155
12	386	79.1	78	5	ABB78164
13	385	78.9	87	5	ABB78152
14	383	78.5	91	5	ABB78150
15	383	78.5	93	7	ADFO5158
16	377	77.3	87	5	ABB78151
17	371	76.0	87	5	ABB78153
18	336	68.9	88	5	ABB78154
19	259	53.1	76	5	ABB78166
20	249	51.0	87	5	ABB78148
21	249	51.0	87	5	ABB78147
22	235	48.2	86	5	ABB78149
23	228	46.7	87	5	ABB78170
24	228	46.7	122	7	ABO74609

25	224.5	46.0	89	9	AEB41576	Aeb41576 L. pneumo
26	224.5	46.0	95	9	AEB38294	Aeb38294 L. pneumo
27	222.5	45.6	90	5	ABB78167	Abb78167 Amino aci
28	222	45.5	90	5	ABB78168	Abb78168 Amino aci
29	218	44.7	87	5	ABB78169	Abb78169 Amino aci
30	218	44.7	88	5	ABB78178	Abb78178 Amino aci
31	211	43.2	88	5	ABB78171	Abb78171 Amino aci
32	211	43.2	88	5	ABB78172	Abb78172 Amino aci
33	211	43.2	88	5	ABB78173	Abb78173 Amino aci
34	211	43.2	88	6	ABP77219	Abp77219 N. gonorr
35	206	42.2	87	5	ABB78175	Abb78175 Amino aci
36	200	41.0	87	5	ABB78176	Abb78176 Amino aci
37	197	40.4	87	5	ABB78174	Abb78174 Amino aci
38	195.5	40.1	92	6	ADA34169	Ada34169 Acinetoba
39	195	40.0	87	5	ABB78177	Abb78177 Amino aci
40	130	26.6	110	8	ADL05173	Adl05173 M. catarr
41	77	15.8	1647	4	ABG10750	Abg10750 Novel hum
42	72	14.8	309	8	ADN46828	Adn46828 Thermococ
43	72	14.8	506	3	AAV74371	Aay74371 Neisseria
44	72	14.8	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.7	184	3	AAI16290	Aai16290 Pinus rad
46	71	14.5	447	2	AAI52657	Aai52657 Rat N-ace
47	71	14.5	447	7	ADE55944	Ades55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aay74372 Neisseria
49	71	14.5	507	6	AAV74373	Aay74373 Neisseria
50	71	14.5	546	3	ABU38097	Abu38097 Protein e
51	71	14.5	548	4	AAE04737	Aae04737 Brugia ma
52	70.5	14.4	184	3	AAI16325	Aai16325 Pinus rad
53	70.5	14.4	184	4	AAI65734	Aai65734 Annexin-1
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59	70	14.3	758	3	ADW71760	Adw71760 Salmonell
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62	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
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68	68	13.9	239	3	ADT07537	Adt07537 Human col
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70	68	13.9	280	5	ABG93905	Abg93905 Lactuca s
71	68	13.9	280	8	ADJ50292	Adj50292 Oil-assoc
72	68	13.9	285	4	AAI92683	Aai92683 Human pro
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ALIGNMENTS

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AC	ABB78161;
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DT	05-NOV-2002 (first entry)
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DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	
OS	hydroxyl radical; DNA damage; YggX homologue.
XX	
PN	Unidentified.
XX	
XX	US2002072118-A1.
XX	

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent Yggx homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 2
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ID ABB78159 standard; protein; 91 AA.
XX
AC ABB78159;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a Yggx homologue.
XX
KW Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; Yggx homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent Yggx homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3
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ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a Yggx homologue.
XX
KW Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; Yggx homologue.
XX
OS Salmonella typhi.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.84893 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-34
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGDFO.....SPLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	488	100.0	91	2	AH0879	conserved hypothet
2	469	96.1	91	2	A85954	hypothetical prote
3	469	96.1	91	2	A65082	hypothetical prote
4	469	96.1	91	2	F91108	hypothetical prote
5	393	80.5	90	2	A10116	conserved hypothet
6	389	79.7	90	2	C82320	conserved hypothet
7	385	78.9	90	2	C64013	hypothetical prote
8	259	53.1	93	2	B84994	hypothetical prote
9	232	47.5	105	2	C82624	conserved hypothet
10	228	46.7	90	2	H83003	conserved hypothet
11	211	43.2	88	2	H81014	conserved hypothet
12	79.5	16.3	1638	2	D87749	protein unc-73b li
13	79.5	16.3	2488	2	T42739	guanine nucleotide
14	78	16.0	1260	2	T04440	hypothetical prote
15	73.5	15.1	495	2	AH0985	probable zinc-prot
16	71.5	14.7	209	2	I64172	hypothetical prote
17	71	14.5	447	2	JC2076	alpha-1,3-mannosyl
18	71	14.5	507	2	C81063	fumarate hydratase
19	71	14.5	546	2	A81807	fumarate hydratase
20	71	14.5	548	2	A54510	63K antigen - nema
21	70	14.3	324	2	T05429	hypothetical prote
22	70	14.3	758	2	AD0763	thiosulfate reduct
23	70	14.3	758	2	A57143	thiosulfate-dithio
24	69.5	14.2	859	2	T29630	hypothetical prote
25	69	14.1	265	2	T46013	hypothetical prote
26	69	14.1	447	2	T16527	hypothetical prote
27	68.5	14.0	683	2	AC2256	hypothetical prote
28	68	13.9	445	1	XUHUMB	alpha-1,3-mannosyl
29	68	13.9	689	2	F83902	beta-galactosidase

30	67.5	13.8	166	2	F70562	hypothetical prote
31	67	13.7	447	1	A38561	alpha-1,3-mannosyl
32	67	13.7	1111	1	T23047	hypothetical prote
33	66.5	13.6	410	1	KHMSD	cathepsin D (EC 3.
34	66	13.5	447	1	A42500	alpha-1,3-mannosyl
35	66	13.5	703	2	B82148	Arp-dependent heli
36	66	13.5	1085	2	S62516	hypothetical coile
37	65.5	13.4	287	2	F82265	conserved hypothet
38	65.5	13.4	365	2	B54128	Rc-binding protein
39	65	13.3	433	2	A70465	probable GTP bindi
40	65	13.3	507	2	A83105	probable fumarase
41	65	13.3	511	2	A99574	ABC transporter at
42	65	13.3	593	2	C64097	probable soluble 1
43	65	13.3	1230	2	S56850	SMC1 protein homol
44	64.5	13.2	327	2	AD2129	transcription regu
45	64.5	13.2	385	2	D87723	protein R06A10.2 l
46	64.5	13.2	401	2	AB1978	hypothetical prote
47	64.5	13.2	544	2	T40058	probable chromatin
48	64.5	13.2	1197	2	S26947	DNA-directed DNA p
49	64	13.1	251	2	B90428	hypothetical prote
50	64	13.1	548	2	A28209	60K filarial antig
51	64	13.1	643	2	A43647	parasporeal crystal
52	63.5	13.0	379	2	S70709	type II site-speci
53	63.5	13.0	438	2	T37786	probable RNA-bindi
54	63.5	13.0	2672	2	A48126	translation activa
55	63	12.9	205	2	C26135	keratin, 50K type
56	63	12.9	235	2	G65212	hypothetical 26.7K
57	63	12.9	258	2	A97991	hypothetical prote
58	63	12.9	258	2	B95121	phosphoesterase, p
59	63	12.9	483	2	G64799	ybeV protein - Bsc
60	63	12.9	543	2	T16015	hypothetical prote
61	63	12.9	549	2	T16016	hypothetical prote
62	63	12.9	1119	2	T15842	hypothetical prote
63	63	12.9	1166	2	H71609	hypothetical prote
64	63	12.9	1209	2	T46027	hypothetical prote
65	63	12.9	1327	2	T14594	guanine nucleoti
66	63	12.9	1572	2	S45251	SNF2alpha protein
67	63	12.9	1586	2	S39580	HBRM protein - hum
68	62.5	12.8	165	2	A81382	shikimate kinase (
69	62.5	12.8	259	2	G83203	conserved hypothet
70	62.5	12.8	305	2	A75211	asparaginase (EC 3
71	62.5	12.8	375	2	T37245	GTP-binding regula
72	62.5	12.8	498	2	G91179	hypothetical prote
73	62.5	12.8	498	2	H86025	hypothetical prote
74	62.5	12.8	498	2	S47748	53.1K protein prec
75	62.5	12.8	629	2	B83107	chemotactic transd

ALIGNMENTS

RESULT 1

AH0879

conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi

A/Note: this species has also been called Salmonella typhi

C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004

C/Accession: AH0879

R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;

A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov

A/Reference number: AB0502; MUID:21534947; PMID:11677608

A/Accession: AH0879

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <PAR>

A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;

C/Genetics:

A/Gene: STY3266

C/Superfamily: Fe(II) trafficking protein YggX

OY	Query Match	100.0%;	Score 488;	DB 2;	Length 91;
	Best Local Similarity	100.0%;	Pred. No. 2.1e-42;		
	Matches	91;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60			
Db	1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60			
OY	61 EHRKLEQEMVSVFLFEGKDVHIEGYTPEDKK	91			
Db	61 EHRKLEQEMVSVFLFEGKDVHIEGYTPEDKK	91			

RESULT 2

A85954

hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004

C;Accession: A85954

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: A85954

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-91 <STO>

A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: y9gx

C;Superfamily: fe(II) trafficking protein Y9GX

OY	Query Match	96.1%;	Score 469;	DB 2;	Length 91;
	Best Local Similarity	94.5%;	Pred. No. 1.8e-40;		
	Matches	86;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60			
Db	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60			
OY	61 EHRKLEQEMVSVFLFEGKDVHIEGYTPEDKK	91			
Db	61 EHRKLEQEMVSVFLFEGKEVHIEGYTPEDKK	91			

RESULT 3

A65082

hypothetical protein b2962 - Escherichia coli (strain K-12)

C;Species: Escherichia coli

C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004

C;Accession: A65082

R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.

A;Reference number: A64720; MUID:97426617; PMID:9278503

A;Accession: A65082

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-91 <BLAT>

A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G

A;Experimental source: strain K-12, substrain MG1655

C;Superfamily: fe(II) trafficking protein Y9GX

OY	Query Match	96.1%;	Score 469;	DB 2;	Length 91;
	Best Local Similarity	94.5%;	Pred. No. 1.8e-40;		
	Matches	86;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60			

Db	1	MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60
OY	61	EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK	91
Db	61	EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK	91
RESULT 4			
F91108		hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RIM	
C;Species: Escherichia coli			
C;Date: 18-Jul-2001		#sequence_revision 18-Jul-2001 #text_change 05-Oct-2004	
C;Accession: F91108			
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.		gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.	
DNA Res. 8, 11-22, 2001			
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno			
A;Reference number: A99629; MUID:21156231; PMID:11258796			
A;Accession: F91108			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-91 <HAY>			
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;			
A;Experimental source: strain O157:H7, substrain RIMD 0509952			
C;Genetics:			
A;Gene: ECs3838			
C;Superfamily: fe(II) trafficking protein Y9GX			
Query Match		96.1%;	Score 469; DB 2; Length 91;
Best Local Similarity		94.5%;	Pred. No. 1.8e-40;
Matches		86; Conservative	5; Mismatches 0; Indels 0; Gaps 0;
OY	1	MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60
Db	1	MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60
OY	61	EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK	91
Db	61	EHRKLEQEMVNFLFEGKEVHIEGYTPEDKK	91
RESULT 5			
A10116		conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)	
C;Species: Yersinia pestis			
C;Date: 02-Nov-2001		#sequence_revision 02-Nov-2001 #text_change 05-Oct-2004	
C;Accession: A10116			
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.		deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;	
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,		Nature 413, 523-527, 2001	
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.			
A;Reference number: AB0001; MUID:21470413; PMID:11586360			
A;Accession: A10116			
A;Status: preliminary			
A;Molecule type: DNA			
A;Residues: 1-90 <KUR>			
A;Cross-references: UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;			
C;Genetics:			
A;Gene: YPO0953			
C;Superfamily: fe(II) trafficking protein Y9GX			
Query Match		80.5%;	Score 393; DB 2; Length 90;
Best Local Similarity		81.1%;	Pred. No. 8.1e-33;
Matches		73; Conservative	9; Mismatches 8; Indels 0; Gaps 0;
OY	1	MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKKLNMNNA	60
Db	1	MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKDAMSQWITKQTMLINEKLSMNNI	60
OY	61	EHRKLEQEMVSFLFEGKDVHIEGYTPEDK	90
Db	61	EDRKLEQEMVNFLFEGQDVHIAGYTPPSK	90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-34

Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SPLFEGKDVHIEGYTPEDKK 91

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	483	99.0	90	1	FETP_SALCH
2	483	99.0	90	1	FETP_SALPA
3	483	99.0	90	1	FETP_SALTI
4	483	99.0	90	1	FETP_SALTY
5	464	95.1	90	1	FETP_ECO57
6	464	95.1	90	1	FETP_ECO57
7	464	95.1	90	1	FETP_ECOLI
8	460	94.3	90	1	FETP_SHIFL
9	416	85.2	90	1	FETP_ERMCT
10	401	82.2	90	1	FETP_YERPS
11	393	80.5	90	1	FETP_YERPA
12	393	80.5	90	1	FETP_YERPE
13	389	79.7	90	1	FETP_VIBCH
14	389	79.7	90	1	FETP_VIBVU
15	389	79.7	90	1	FETP_VIBVY
16	387	79.3	91	1	FETP_MANSM
17	385	78.9	90	1	FETP_HABIN
18	385	78.9	90	2	Q4QMD9_HAE18
19	383	78.5	90	1	FETP_PHOPR
20	377	77.3	90	1	FETP_PASMU
21	376	77.0	94	1	FETP_PHOBL
22	371	76.0	94	1	FETP_HAEDU
23	365	74.8	90	1	FETP_VIBF1
24	341	69.9	90	1	FETP_IDILO
25	336	68.9	92	1	FETP_SHEON
26	259	53.1	77	1	FETP_BUCAL
27	249	51.0	90	1	FETP_BORBR
28	249	51.0	90	1	FETP_BORPA
29	249	51.0	90	1	FETP_BORPE
30	243	49.8	78	1	FETP_BUCAP
31	239	49.0	91	1	FETP_XANAC

32	232	47.5	90	1	FETP_XYLFA	Q9pc73 xylella fas
33	232	47.5	92	1	FETP_XANOR	Q5gy22 xanthomonas
34	228.5	46.8	89	1	FETP_LEGPL	Q5wvc4 legionella
35	228	46.7	90	1	FETP_PSEAB	Q9hu36 pseudomonas
36	228	46.7	90	1	FETP_XYLFT	Q87d06 xylella fas
37	228	46.7	92	1	FETP_XANCP	Q8p829 xanthomonas
38	228	46.7	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
39	225	46.1	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
40	224.5	46.0	89	1	FETP_LEGPA	Q5x3x9 legionella
41	224.5	46.0	89	1	FETP_LEGPH	Q5zu80 legionella
42	222	45.5	90	1	FETP_NITEU	Q82xf2 nitrosomona
43	222	45.5	90	1	FETP_PSESM	Q87uf5 pseudomonas
44	222	45.5	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
45	218	44.7	90	1	FETP_COXBU	Q83d06 coxiella bu
46	218	44.7	90	1	FETP_PSEPK	Q88r49 pseudomonas
47	218	44.7	90	2	Q4J228_AZOVI	Q4j228 azotobacter
48	215	44.1	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
49	213	43.6	90	1	FETP_CHRVO	Q7nsr4 chromobacte
50	212	43.4	79	1	FETP_CANBF	Q7vr99 candidatus
51	211	43.2	88	1	FETP_NEIG1	Q5f553 neisseria g
52	211	43.2	88	1	FETP_NEIMA	Q67615 neisseria m
53	211	43.2	88	1	FETP_NEIMB	Q67616 neisseria m
54	207	42.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
55	206	42.2	91	1	FETP_BURMA	Q62iu9 burkholderi
56	206	42.2	91	1	FETP_BURPS	Q63sj4 burkholderi
57	205	42.0	90	2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
58	205	42.0	91	1	FETP_RALSO	Q8y010 ralstonia s
59	203	41.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
60	195	40.0	90	1	FETP_METCA	Q60aj7 methylococc
61	192	39.3	87	1	FETP_FRATT	Q5nhj8 francisella
62	190.5	39.0	90	1	FETP_AC1AD	Q6ffh3 acinetobact
63	146	29.9	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	145	29.7	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	82.5	16.9	482	2	Q5NUY1_9BURK	Q5nuyl ralstonia m
66	82.5	16.9	514	2	Q6A1Z9_DSPPS	Q6aiz9 desulfofale
67	79.5	16.3	1638	2	Q7KPP4_CAEBL	Q7kpp4 caenorhabdi
68	79.5	16.3	2140	2	Q6BEW2_CAEBL	Q6bew2 caenorhabdi
69	79.5	16.3	2488	2	Q61528_CAEBL	Q61528 caenorhabdi
70	78.5	16.1	337	2	Q81AR8_BACCR	Q81ar8 bacillus ce
71	78	16.0	1260	2	Q49677_ARATH	Q49677 arabidopsis
72	77.5	15.9	1047	2	Q5CJ53_CRYHO	Q5cj53 cryptospori
73	76.5	15.7	486	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
74	75.5	15.5	1278	2	Q5CYM7_CRYPV	Q5cym7 cryptospori
75	75	15.4	385	2	Q734A2_BACCI	Q734a2 bacillus ce

ALIGNMENTS

RESULT 1
FETP_SALCH STANDARD; PRT; 90 AA.
ID FETP_SALCH
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RT Wang H.-S., Lee Y.-S.;
RL "The genome sequence of Salmonella enterica serovar Choleraesuis, a highly invasive and resistant zoonotic pathogen.";
CC Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron acquisition and iron-regulating processes, such as synthesis and/or


```
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
DR      HAMAP; MF_00686; -; 1.
DR      InterPro; IPR007457; Y9GX.
DR      Prodom; PD029191; DUF495; 1.
KW      Complete proteome; Iron.
FT      INIT_MET 0
SQ      SEQUENCE 90 AA; 10768 MW; B3B6A1EE2255E3C CRC64;

Query Match          99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 SRTIFCTYLQDAEGQDFQLYPGBLGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 61
        |||
Db       1 SRTIFCTYLQDAEGQDFQLYPGBLGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60

QY      62 HRKLLBQEMVSFLFEGKDVHIEGYTPEDKK 91
        |||
Db       61 HRKLLBQEMVSFLFEGKDVHIEGYTPEDKK 90

RESULT 2
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ID _FETP_SALPA STANDARD; PRT; 90 AA.
AC Q5PMM1;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y9GX; OrderedLocustNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=543388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P., Mclellan M.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozerisky P., Mclellan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR      SMR; Q5PMM1; 1-91.
DR      HAMAP; MF_00686; -; 1.
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DR      InterPro; IPR007457; Y9GX.
DR      Prodom; PD029191; DUF495; 1.
KW      Complete proteome; Iron.
FT      INIT_MET 0
SQ      SEQUENCE 90 AA; 10768 MW; B3B6A1EE2255E3C CRC64;

Query Match          99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db       1 SRTIFCTYLQDAEGQDFQLYPGBLGKRIYNEISKDAWAQWQHKTMLINEKLNMMNAE 60

QY      62 HRKLLBQEMVSFLFEGKDVHIEGYTPEDKK 91
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RESULT 3
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ID _FETP_SALTI STANDARD; PRT; 90 AA.
AC P67618; O8XFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y9GX; OrderedLocustNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
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RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Felwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR      EMBL; AE016844; AAO70576.1; -; Genomic_DNA.
DR      SMR; P67618; 1-90.
DR      HAMAP; MF_00686; -; 1.
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.2616 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-34
Perfect score: 488
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	228	46.7	122	2	US-09-252-991A-23355
4	195.5	40.1	92	2	US-09-328-352-5456
5	130	26.6	110	2	US-09-540-236-2859
6	71	14.5	548	2	US-09-167-299-3
7	70.5	14.4	184	2	US-09-325-932A-66
8	68.5	14.0	544	2	US-09-248-796A-18911
9	68	13.9	280	2	US-09-323-998E-37
10	68	13.9	337	2	US-09-270-767-41746
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ALIGNMENTS

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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

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667.774 Million cell updates/sec

Title: US-09-955-502A-34

Perfect score: 488
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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6	469	96.1	91	3	US-09-955-502-11	Sequence 11, Appl
7	469	96.1	91	3	US-09-955-502-12	Sequence 12, Appl
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21	232	47.5	89	3	US-09-955-502-22	Sequence 22, Appl
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27	211	43.2	88	3	US-09-955-502-27	Sequence 27, Appl

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31	197	40.4	87	3	US-09-955-502-31	Sequence 31, Appl
32	195	40.0	87	3	US-09-955-502-32	Sequence 32, Appl
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75	65.5	13.4	546	4	US-10-098-732A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnicks, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: Oxygen-Labile Proteins
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi

US-09-955-502-14

Query Match 100.0%; Score 488; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2

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; Sequence 16, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 16

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella dublin

US-09-955-502-16

Query Match 100.0%; Score 488; DB 3; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60
|||||
Db 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3

US-09-955-502-17
; Sequence 17, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 17

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhi CT18

US-09-955-502-17

Query Match 100.0%; Score 488; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 6.8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60
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Db 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 4

US-09-955-502-18
; Sequence 18, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 18

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhimurium

US-09-955-502-18

Query Match 97.1%; Score 474; DB 3; Length 91;
Best Local Similarity 97.8%; Pred. No. 2.9e-47;
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60
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Db 1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA 60

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 5

US-09-955-502-15
; Sequence 15, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentln Ver. 2.1

; SEQ ID NO 15

; LENGTH: 88

; TYPE: PRT

; ORGANISM: Salmonella enteritidis

US-09-955-502-15

Query Match 96.7%; Score 472; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.8e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.82187 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-34

Perfect score: 488

Sequence: 1 MSRTFCTYLQDAEGQDFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table:

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Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Published Applications AA_New:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	43.2	88	US-10-467-657-968	Sequence 968, App
2	68	13.9	478	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	62	12.7	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-4	Sequence 4, Appli
8	62	12.7	1167	US-10-942-072-6	Sequence 6, Appli
9	60.5	12.4	504	US-11-072-512-3467	Sequence 3467, App
10	59.5	12.2	264	US-10-821-234-1555	Sequence 1555, App
11	59.5	12.2	285	US-10-467-657-222	Sequence 222, App
12	59.5	12.2	285	US-10-467-657-8230	Sequence 8230, App
13	59.5	12.2	650	US-10-467-657-1948	Sequence 1948, App
14	59.5	12.2	834	US-10-453-372-658	Sequence 658, App
15	59.5	12.2	1995	US-11-069-834-60	Sequence 60, Appli
16	59	12.1	257	US-11-054-515-1710	Sequence 1710, App
17	59	12.1	697	US-10-485-517-202	Sequence 202, App
18	59	12.1	1168	US-10-485-517-11	Sequence 11, Appli
19	59	12.1	1450	US-10-485-517-152	Sequence 648, App
20	58.5	12.0	695	US-10-453-372-648	Sequence 922, App
21	58.5	12.0	700	US-10-995-561-922	Sequence 924, App
22	58.5	12.0	700	US-10-995-561-924	Sequence 10505, A
23	58.5	12.0	749	US-11-098-686-10505	Sequence 2352, App
24	58.5	12.0	782	US-10-793-626-2352	Sequence 25, Appli
25	58	11.9	448	US-10-618-320A-25	

26	58	11.9	480	US-10-510-386-12	Sequence 12, Appli
27	58	11.9	1501	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	US-10-453-372-638	Sequence 638, App
38	57.5	11.8	905	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	US-10-453-372-664	Sequence 664, App
40	57.5	11.8	963	US-10-995-561-923	Sequence 923, App
41	57.5	11.8	963	US-10-453-372-660	Sequence 660, App
42	57.5	11.8	1012	US-10-453-372-646	Sequence 646, App
43	57.5	11.8	3803	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	US-10-995-561-777	Sequence 777, App
46	57.5	11.8	5406	US-10-995-561-774	Sequence 774, App
47	57.5	11.8	5415	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	US-10-995-561-775	Sequence 775, App
49	57.5	11.8	5935	US-10-995-561-776	Sequence 776, App
50	57	11.7	234	US-10-524-647-120	Sequence 120, App
51	57	11.7	234	US-10-524-972-108	Sequence 108, App
52	57	11.7	432	US-10-821-234-1463	Sequence 1463, App
53	57	11.7	440	US-11-072-512-3856	Sequence 3856, App
54	56.5	11.6	647	US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254	US-10-821-234-147	Sequence 47, Appli
56	56.5	11.6	1897	US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907	US-11-000-463-250	Sequence 250, App
58	56.5	11.6	3433	US-10-714-781A-67	Sequence 67, Appli
59	56	11.5	206	US-11-124-367A-316	Sequence 316, App
60	55.5	11.4	136	US-10-793-626-580	Sequence 580, App
61	55.5	11.4	279	US-11-098-686-10812	Sequence 10812, A
62	55.5	11.4	1188	US-11-115-639-42	Sequence 42, Appli
63	55.5	11.4	1188	US-11-115-639-43	Sequence 43, Appli
64	55	11.3	189	US-11-071-262-1	Sequence 1, Appli
65	55	11.3	667	US-10-793-626-198	Sequence 198, App
66	55	11.3	692	US-11-038-284-33	Sequence 33, Appli
67	55	11.3	783	US-11-037-243-67	Sequence 67, Appli
68	55	11.3	873	US-11-038-284-35	Sequence 35, Appli
69	55	11.3	889	US-11-038-284-15	Sequence 15, Appli
70	55	11.3	1142	US-11-109-156-22	Sequence 22, Appli
71	55	11.3	2665	US-11-124-368A-214	Sequence 214, App
72	55	11.3	2668	US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	317	US-10-523-503-74	Sequence 74, Appli
74	54.5	11.2	450	US-10-618-320A-26	Sequence 26, Appli
75	54.5	11.2	496	US-11-069-642-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

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SEQ ID NO 968
LENGTH: 88
TYPE: prt
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

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Matches	Conservative	Mismatches		
39;	19;	29;		
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	1 MARWVFCVKLNKEAEGMKFPPLPNELGKRIFENVSQEAAMATTRHOTMLINENRLSLADP	60		
Db	1 EHRKLEQEMVSFLF-EGKDVHIEGYTPE	88		
QY	61 EHRKLEQEMVSFLF-EGKDVHIEGYTPE	88		
Db	61 RAREYLAQOMEQYFFGDGADA-VQGYVPO	88		

RESULT 2
 US-10-821-234-915
 Sequence 915, Application US/10821234
 Publication No. US2005025511A1
 GENERAL INFORMATION:
 APPLICANT: Labat, Ivan
 APPLICANT: Stache-Crain, Birgit
 APPLICANT: Andarmani, Susan
 APPLICANT: Tang, Y. Tom
 TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
 FILE REFERENCE: 821A
 CURRENT APPLICATION NUMBER: US/10/821,234
 CURRENT FILING DATE: 2004-04-07
 CURRENT APPLICATION NUMBER: US 60/462,047
 PRIOR FILING DATE: 2003-04-07
 NUMBER OF SEQ ID NOS: 1704
 SOFTWARE: pt_seq_genes Version 1.0
 SEQ ID NO 915
 LENGTH: 478

94-915
13.9%; Score 68; DB 6; Length 478;
ch Similarity 25.5%; Pred. No. 3.4; Indels 28; Gaps 5;
Conservative 20; Mismatches

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GEH :|:||::||
APLAYDRDLARVYGAPOLVEKVRTNDRKELEGEVRVOYTGRRDSFKAF-KALGVMD 438
APPPLA,SHRKLIEQMVSFLFEKDVI-----EGTTP 87
APPLICATION : ||| | : ||| |
TITLE OF INVENTION : VTFOFGRRVHLAPPPTWGYDP 475
FILE OF INVENTION
CURRENT REFERENCE:
CURRENT APPLICATION: 00592 94246
PRIOR FILING DATE: U.S.
PRIOR APPLICATION NUMBER: 2005-08-
PRIOR FILING DATE: 2002-10-21 US/10/
NUMBER OF SEQ ID NOS: 2001-10-19 US 60/345,438

GLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET

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; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
; US-11-194-246-317
13 3% Score 65; DB 7; Length 593;

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Query Match          100%      Pred No. 9.8,   23;   Indels    30;   Cof-
Best Local Similarity 24.1%;
Matches             20;   Conservative    10;   Mismatches
                                                                -----ISKDA 38
OY              9 YLOR--DAGQDFOLYPGEHLGKRIYN-----|||
                  :| | | | | | | : | :: : |
                240 FLNRFDNENTDFQKWRDEQIRQLQTDNLTERRLRMALWKTETLTSWINLLSAESKSQOE 299
Db
OY              39 MAOWQHKOQTMLINEKKLNMMNAE 61
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                300 WRYWEAKODILKNTTKKLTALESKE 322
Db
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SUIT 4
 -10-467-657-1658
 Sequence 1658, Application US/10467657
 Publication No. US20050260581A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASIGNANI Vega
 APPLICANT: MONACI Elisabetta
 APPLICANT: MONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 TITLE OF INVENTION: GONOCOCCAL
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 CURRENT FILING DATE: 2003-08-11
 CURRENT APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: Seqwin99, version 1.04
 SEQ ID NO 1658
 LENGTH: 177
 TYPE: PRT
 ORGANISM: *Neisseria gonorrhoeae*
 US-10-467-657-1658

[illegible]

RESULT 5
US-10-510-386-218
Sequence 218, Application US/10510386
Publication No. US20050244922A1
GENERAL INFORMATION:
APPLICANT: Andersen, Jens Tonne
APPLICANT: Clausen, Ib Groth
APPLICANT: Jorgensen, Sreen Troels
APPLICANT: Olsen, Peter Bjarke
APPLICANT: Rasmussen, Michael Dolberg
APPLICANT: Rasmussen, Michael Bacillus Host Cell
TITLE OF INVENTION: Improved 204-US
FILE REFERENCE: 10294.204-US
CURRENT FILING DATE: 2004-10-04
CURRENT FILING DATE: 2004

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.9696 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-35
Perfect score: 488
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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7:	geneseqp2003bs:*
8:	geneseqp20048:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	472	96.7	88	5	ABB78160	Abb78160 Amino aci
6	469	96.1	91	5	ABB78158	Abb78158 Amino aci
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10	393	80.5	90	5	ABB78165	Abb78165 Amino aci
11	389	79.7	90	5	ABB78155	Abb78155 Amino aci
12	385	79.1	78	5	ABB78164	Abb78164 Amino aci
13	385	78.9	87	5	ABB78152	Abb78152 Amino aci
14	383	78.5	91	5	ABB78150	Abb78150 Amino aci
15	383	78.5	93	7	ADF05158	Adf05158 Bacterial
16	377	77.3	87	5	ABB78151	Abb78151 Amino aci
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22	235	48.2	86	5	ABB78149	Abb78149 Amino aci
23	228	46.7	87	5	ABB78170	Abb78170 Amino aci
24	228	46.7	122	7	ABO74609	ABO74609 Pseudomon

25	224.5	46.0	89	9	ABB41576	Aeb41576 L. pneumo
26	224.5	46.0	95	9	AEB38294	Aeb38294 L. pneumo
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33	211	43.2	88	5	ABB78173	Abb78173 Amino aci
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41	77	15.8	1647	4	ADN46828	Adn46828 Thermococ
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45	71.5	14.7	184	3	AAB16290	Aar52657 Rat N-ace
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47	71	14.5	447	7	ADE55944	Aay74372 Neisseria
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49	71	14.5	507	3	AAV74373	Abu38097 Protein e
50	71	14.5	546	6	ABU38097	Aae04737 Brugia ma
51	71	14.5	548	4	AAE04737	Aab16325 Ptnus rad
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53	70.5	14.4	184	4	AAB65734	Adb94702 Programme
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57	70	14.3	297	3	AAG31202	Aag31201 Arabidops
58	70	14.3	324	3	AAG31201	Adw71760 Salmonell
59	70	14.3	758	9	ADW71760	Aag38052 Arabidops
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63	69.5	14.2	1387	8	ADV79687	Abg16577 Novel hum
64	69	14.1	503	4	ABG16577	Adz85056 Partial F
65	69	14.1	679	9	ADZ85056	Abp73745 Candida a
66	68.5	14.0	608	5	ABP73745	Adz829711 Bacterial
67	68.5	14.0	632	8	ADS29711	Adt07537 Human col
68	68	13.9	239	8	ADT07537	Aay54294 Amino aci
69	68	13.9	280	3	AAV54294	Abg93905 Lactuca s
70	68	13.9	280	5	ABG93905	Adj50292 Oil-assoc
71	68	13.9	280	8	ADJ50292	Aab88379 Human pro
72	68	13.9	285	4	AAB92683	Ady63123 Human clo
73	68	13.9	302	4	AAB88379	Abu11747 Human MDD
74	68	13.9	302	9	ADY63123	
75	68	13.9	414	6	ABU11747	

ALIGNMENTS

RESULT 1
ABB78161
ID ABB78161 standard; protein; 91 AA.
XX ABB78161;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YgXx homologue.
DE
XX
KW Superoxide damage; cell; YgXx; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgXx homologue.
OS
XX Unidentified.
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
PR 22-SEP-2000; 2000US-0234588P.
XX
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnicks JA;
XX
XX WPI, 2002-589476/63.
DR
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
PT
XX
XX
PS Example; Fig 1A; 16pp; English.
XX
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX
SQ Sequence 91 AA;

```

Query Match          100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MSRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKCLNMWNA 60
        |||||||
Db      1 MSRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQWQHKTMLINEKCLNMWNA 60
        |||||||

QY      61 EHRKLLQEMVSFLFEGKDVHIEGYTPEDKK 91
        |||||||
Db      61 EHRKLLQEMVSFLFEGKDVHIEGYTPEDKK 91
        |||||||

RESULT 2
ABB78159
ID      ABB78159 standard; protein; 91 AA.
XX
AC      ABB78159;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Amino acid sequence of a YggX homologue.
XX
KW      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
        hydroxyl radical; DNA damage; YggX homologue.
XX
OS      Unidentified.
XX
PN      US2002072118-A1.
XX
PD      13-JUN-2002.
XX
PF      18-SEP-2001; 2001US-00955502.
XX
PR      22-SEP-2000; 2000US-0234588P.
XX
PA      (DOWN/) DOWNS D.
XX      (GRAL/) GRALNICK J A.
XX
PI      Downs D, Gralnick JA;
XX

```

DR WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more YggX protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX

XX Example; Fig 1A; 16pp; English.

PS

XX The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the

CC native amount of YggX protein (a protein identified from *Salmonella*

CC enterica serovar typhimurium) or its homolog, where the cells are

CC rendered more resistant to superoxide damage. YggX reduces the oxidation

CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from

CC clusters. The resulting decrease in free-iron levels generates fewer

CC hydroxyl radicals and thus reduced DNA damage. The method is useful for

CC reducing superoxide damage in a bacterial, yeast, mammalian or plant

CC cell. ABB78147-78 represent YggX homologues

XX

XX

SQ Sequence 91 AA;

Query Match	100.0%;	Score 488;	DB 5;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 2.3e-49;		
Matches	91;	Conservative 0;	Mismatches 0;	Indels 0;
QY	1 MSRTIFCTYLQRDAEGODFQLYPGELGKRIYNEISKDAMAQWOHKQMTL INEKKLNWNA	60		
Db	1 MSRTIFCTYLQRDAEGODFQLYPGELGKRIYNEISKDAMAQWOHKQMTL INEKKLNWNA	60		
QY	61 EHRKLLQEMVSFLFEGKDVHIEGYTPEDKK	91		
Db	61 EHRKLLQEMVSFLFEGKDVHIEGYTPEDKK	91		

RESULT 3
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KM Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; yggX homologue.
XX
OS Salmonella typhi.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.84893 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-35
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAGQDFQ.....SFLPEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	488	100.0	91	2	AH0879	conserved hypothe
2	469	96.1	91	2	A85954	hypothetical prote
3	469	96.1	91	2	A65082	hypothetical prote
4	469	96.1	91	2	F91108	hypothetical prote
5	393	80.5	90	2	A10116	conserved hypothe
6	389	79.7	90	2	C82320	conserved hypothe
7	385	78.9	90	2	C64013	hypothetical prote
8	259	53.1	93	2	E84994	hypothetical prote
9	232	47.5	105	2	C82624	conserved hypothe
10	228	46.7	90	2	H83003	conserved hypothe
11	211	43.2	88	2	H81014	conserved hypothe
12	79.5	16.3	1638	2	D87749	protein unc-73b [1
13	79.5	16.3	2488	2	T42739	guanine nucleotide
14	78	16.0	1260	2	T04440	hypothetical prote
15	73.5	15.1	495	2	AH0985	probable zinc-prot
16	71.5	14.7	209	2	I64172	hypothetical prote
17	71	14.5	447	2	JC2076	alpha-1,3-mannosyl
18	71	14.5	507	2	C81063	fructurase hydratase
19	71	14.5	546	2	A81807	fructurase hydratase
20	71	14.5	548	2	A54510	63k antigen - nema
21	70	14.3	324	2	T05429	hypothetical prote
22	70	14.3	758	2	AD0763	thiosulfate reduct
23	70	14.3	758	2	A57143	thiosulfate-dithio
24	69.5	14.2	859	2	T29630	hypothetical prote
25	69	14.1	265	2	T46013	hypothetical prote
26	69	14.1	447	2	T16527	hypothetical prote
27	68.5	14.0	683	2	AC2256	hypothetical prote
28	68	13.9	445	1	XUHUMB	alpha-1,3-mannosyl
29	68	13.9	689	2	F83902	beta-galactosidase

30	67.5	13.8	166	2	F70562	hypothetical prote
31	67	13.7	447	1	A38561	alpha-1,3-mannosyl
32	66.7	13.7	1111	2	T23047	hypothetical prote
33	66.5	13.6	410	1	KHMSD	cathepsin D (EC 3.
34	66	13.5	447	1	A42500	alpha-1,3-mannosyl
35	66	13.5	703	2	B82148	ATP-dependent heil
36	66	13.5	1085	2	S62516	hypothetical coile
37	65.5	13.4	287	2	F82265	conserved hypothe
38	65.5	13.4	365	2	B54128	Fe-binding protein
39	65	13.3	433	2	A70465	probable GTP bindi
40	65	13.3	507	2	A83105	probable fumarase
41	65	13.3	511	2	A99574	ABC transporter at
42	65	13.3	593	2	C64097	probable soluble 1
43	65	13.3	1230	2	S56850	SMC1 protein homol
44	64.5	13.2	327	2	AD2129	transcription regu
45	64.5	13.2	385	2	D87723	protein R06A10.2 [
46	64.5	13.2	401	2	AE1978	hypothetical prote
47	64.5	13.2	544	2	T40058	probable chromatin
48	64.5	13.2	1197	2	S26947	DNA-directed DNA p
49	64	13.1	251	2	E90428	hypothetical prote
50	64	13.1	548	2	A28209	60k filarial antiq
51	64	13.1	643	2	A43647	paraaporal crystal
52	63.5	13.0	379	2	S70709	type II site-speci
53	63.5	13.0	438	2	T37786	probable RNA-bindi
54	63.5	13.0	2672	2	A48126	translation activa
55	63	12.9	205	2	C26135	keratin, 50K type
56	63	12.9	235	2	G65212	hypothetical 26.7K
57	63	12.9	258	2	A97991	hypothetical prote
58	63	12.9	258	2	E95121	phosphoesterase, p
59	63	12.9	483	2	G64799	ybeV protein - Bac
60	63	12.9	543	2	T16015	hypothetical prote
61	63	12.9	549	2	T16016	hypothetical prote
62	63	12.9	1119	2	T15842	hypothetical prote
63	63	12.9	1166	2	H71609	hypothetical prote
64	63	12.9	1209	2	T46027	hypothetical prote
65	63	12.9	1327	2	T14594	guanidine nucleoti
66	63	12.9	1572	2	S45251	SNF2alpha protein
67	63	12.9	1586	2	S39580	HBRM protein - hum
68	62.5	12.8	165	2	A81382	shikimate kinase (
69	62.5	12.8	259	2	G83203	conserved hypothe
70	62.5	12.8	305	2	A75211	asparaginase (EC 3
71	62.5	12.8	375	2	T37245	GTP-binding regula
72	62.5	12.8	498	2	G91179	hypothetical prote
73	62.5	12.8	498	2	H86025	hypothetical prote
74	62.5	12.8	498	2	S47748	53.1K protein prec
75	62.5	12.8	629	2	B83107	chemotactic transd

ALIGNMENTS

RESULT 1
AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C;Species: Salmonella enterica subsp. enterica serovar Typh
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AH0879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <PAR>
A;Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:G16504189;
C;Genetics:
A;Gene: STY3266
C;Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 488; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.1e-42;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60
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Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60

OY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 2

A85954
hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:g12517511; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: y9gx
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60
|||||
Db 1 MSRTIFCTFLQREABGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKCLNMNNA 60

OY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKEVHIEGYTPEDKK 91

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)

C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB000378; GB:U00096; NID:9
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60
|||||

Db 1 MSRTIFCTFLQREABGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKCLNMNNA 60
OY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKEVHIEGYTPEDKK 91

RESULT 4

F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 96.1%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 1.8e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60
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Db 1 MSRTIFCTFLQREABGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKCLNMNNA 60

OY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
Db 61 EHRKLEQEMVSFLFEGKEVHIEGYTPEDKK 91

RESULT 5
A10116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10116
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titchall, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: A10116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;
C/Genetics:
A/Gene: YPO0953
C/Superfamily: fe(II) trafficking protein Y9gx

Query Match 80.5%; Score 393; DB 2; Length 90;
Best Local Similarity 81.1%; Pred. No. 8.1e-33;
Matches 73; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

OY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAQWQHQTMLINEKCLNMNNA 60
|||||
Db 1 MSRTIFCTFLKDAERQDFQLYPGELGKRIYNEISKEAWSQWITKQTMLINEKCLNMNNA 60

OY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 90
|||||
Db 61 EDRKLEQEMVSFLFEGQDVHIEGYTPPSK 90

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-35
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB ID	Description
1	483	99.0	90	1	FETP_SALCH
2	483	99.0	90	1	FETP_SALPA
3	483	99.0	90	1	FETP_SALTI
4	483	99.0	90	1	FETP_SALTY
5	464	95.1	90	1	FETP_ECO57
6	464	95.1	90	1	FETP_ECOLI
7	464	95.1	90	1	FETP_SHIFL
8	460	94.3	90	1	FETP_ECOL6
9	416	85.2	90	1	FETP_ERWCT
10	401	82.2	90	1	FETP_YERPS
11	393	80.5	90	1	FETP_VIBPA
12	393	80.5	90	1	FETP_YERPE
13	389	79.7	90	1	FETP_VIBCH
14	389	79.7	90	1	FETP_VIBVU
15	389	79.7	90	1	FETP_VIBVY
16	387	79.3	91	1	FETP_MANSM
17	385	78.9	90	1	FETP_HAEIN
18	385	78.9	90	2	Q4QMD9_HAEI8
19	383	78.5	90	1	FETP_PHOPR
20	377	77.3	90	1	FETP_PASMU
21	376	77.0	90	1	FETP_PHOLD
22	371	76.0	94	1	FETP_HAEDU
23	365	74.8	90	1	FETP_VIBF1
24	341	69.9	90	1	FETP_IDILO
25	336	68.9	92	1	FETP_SHEON
26	259	53.1	77	1	FETP_BUCAI
27	249	51.0	90	1	FETP_BORBR
28	249	51.0	90	1	FETP_BORPA
29	249	51.0	90	1	FETP_BORPS
30	243	49.8	78	1	FETP_BUCAP
31	239	49.0	91	1	FETP_XANAC

32	232	47.5	90	1	FETP_XYLFA	Q9pc73 xylella fas
33	232	47.5	92	1	FETP_XANOR	O5gy22 xanthomonas
34	228.5	46.8	89	1	FETP_LEGPL	O5wvc4 legionella
35	228	46.7	90	1	FETP_PSEAF	O9huj6 pseudomonas
36	228	46.7	90	1	FETP_XYLFT	O87d06 xylella fas
37	228	46.7	92	1	FETP_XANCP	O8p829 xanthomonas
38	228	46.7	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
39	225	46.1	78	1	FETP_WIGBR	O8d3c5 wiggleswort
40	224.5	46.0	89	1	FETP_LEGPA	O5x3x9 legionella
41	224.5	46.0	89	1	FETP_LEGPH	O5zu80 legionella
42	222	45.5	90	1	FETP_NITEU	O82xf2 nitrosomona
43	222	45.5	90	1	FETP_PSESM	O87uf5 pseudomonas
44	222	45.5	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
45	218	44.7	90	1	FETP_COXBU	O83d06 coxiella bu
46	218	44.7	90	1	FETP_PSEBP	O88r49 pseudomonas
47	218	44.7	90	2	Q4J228_AZOVI	Q4j228 azotobacter
48	215	44.1	90	2	O6T7F6_PSEFL	O6t7f6 pseudomonas
49	213	43.6	90	1	FETP_CHRVO	O7nsr4 chromobacte
50	212	43.4	79	1	FETP_CANBF	O7vrg9 candidatus
51	211	43.2	88	1	FETP_NEIG1	O5f553 neisseria g
52	211	43.2	88	1	FETP_NEIMA	P67615 neisseria m
53	211	43.2	88	1	FETP_NEIMB	P67616 neisseria m
54	207	42.4	87	1	FETP_BUCBP	O89a44 buchnera ap
55	206	42.2	91	1	FETP_BURMA	O62iu9 burkholderi
56	206	42.2	91	1	FETP_BURPS	O63sj4 burkholderi
57	205	42.0	90	2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
58	205	42.0	91	1	FETP_RALSO	O8y010 ralsstonia s
59	203	41.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
60	195	40.0	90	1	FETP_METCA	O60aj7 methylococc
61	192	39.3	87	1	FETP_FRATT	O5nhj8 francisella
62	190.5	39.0	90	1	FETP_ACIAD	O6ffb3 acinetobact
63	146	29.9	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	145	29.7	92	2	Q4NMW4_9DELT	Q4nmw4 anaeromyxob
65	82.5	16.9	482	2	O5NUY1_9BURK	O5nuyl1 ralsstonia m
66	82.5	16.9	514	2	O6A1Z9_DESPS	O6aiz9 desulfotale
67	79.5	16.3	1638	2	Q7KPP4_CAEEL	O7kpp4 caenorhabdi
68	79.5	16.3	2140	2	Q6BEW2_CAEEL	Q6bew2 caenorhabdi
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70	78.5	16.1	337	2	O81AR8_BACCR	O81ar8 bacillus ce
71	78	16.0	1260	2	O49677_ARATH	O49677 arabidopsis
72	77.5	15.9	1047	2	O5CJ53_CRYHO	O5cj53 cryptospori
73	76.5	15.7	486	2	O7WX51_ALCEU	O7wx51 alcaligenes
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ALIGNMENTS

RESULT 1
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or


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CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
DR      HAMAP; MF_00686; -; 1.
DR      InterPro; IPR007457; YggX.
DR      ProDom; PD029191; DUF495; 1.
DR      Complete proteome; Iron.
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Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1 SRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAAWQOHKQTMLINEKLNMMNAE 60

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Db      61 HRKLEQEMVSFLFEGKDVHIEGYTPEDKK 90

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AC      Q5PMM1;
DT      13-SEP-2005 (Rel. 48, Created)
DT      13-SEP-2005 (Rel. 48, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Probable Fe(2+) trafficking protein.
GN      Name=YggX; OrderedLocustNames=SPA2974;
OS      Salmonella paratyphi-a.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmonella.
OX      NCBI_TaxID=54388;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=ATCC 9150 / SARB42;
RX      PubMed=15531882; DOI=10.1038/ng1470;
RA      McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA      Porwollik S., Sabo A., Meyer R., Bieri T., Ozeresky P., Mclellan M.,
RA      Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA      Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA      Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P., Florea L.,
RA      Delehauntz K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA      Spieth J., Wilson R.K.;
RT      "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT      restricted serovars of Salmonella enterica that cause typhoid.";
RL      Nat. Genet. 36:1268-1274(2004).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-requiring processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR      SMR; Q5PMM1; 1-91.
DR      HAMAP; MF_00686; -; 1.
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DR      InterPro; IPR007457; YggX.
DR      ProDom; PD029191; DUF495; 1.
DR      Complete proteome; Iron.
FT      INIT MET      0
SQ      SEQUENCE      90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;

Query Match      99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      2 SRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAAWQOHKQTMLINEKLNMMNAE 61
         |||||
Db      1 SRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAAWQOHKQTMLINEKLNMMNAE 60

OY      62 HRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
         |||||
Db      61 HRKLEQEMVSFLFEGKDVHIEGYTPEDKK 90

RESULT 3
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AC      P67618; Q8XFV6;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Probable Fe(2+) trafficking protein.
GN      Name=YggX; OrderedLocustNames=STRY3266, t3024;
OS      Salmonella typhi.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmonella.
OX      NCBI_TaxID=601;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=CT18;
RX      MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA      Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA      Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA      Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA      Felwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagers K.,
RA      Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA      Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA      Whitehead S., Barrell B.G.;
RT      "Complete genome sequence of a multiple drug resistant Salmonella
RT      enterica serovar Typhi CT18.";
RL      Nature 413:848-852(2001).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=Ty2 / ATCC 700931;
RX      MEDLINE=22531367; PubMed=12644504;
RX      DOI=10.1128/JB.185.7.2330-2337.2003;
RA      Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA      Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT      "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT      and CT18.";
RL      J. Bacteriol. 185:2330-2337(2003).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-requiring processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR      EMBL; AE016844; AA070576.1; -; Genomic_DNA.
DR      SMR; P67618; 1-90.
DR      HAMAP; MF_00686; -; 1.
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.2616 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-35
Perfect score: 488
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	228	46.7	122	2	US-09-252-991A-23355
4	195.5	40.1	92	2	US-09-328-352-5456
5	130	26.6	110	2	US-09-540-236-2859
6	71	14.5	548	2	US-09-167-299-3
7	70.5	14.4	184	2	US-09-325-932A-66
8	68.5	14.0	544	2	US-09-248-796A-18911
9	68	13.9	280	2	US-09-323-998E-37
10	68	13.9	337	2	US-09-270-767-41746
11	68	13.9	1214	2	US-10-164-595-24
12	66.5	13.6	325	2	US-09-134-000C-4346
13	66	13.5	292	2	US-09-328-352-5836
14	65.5	13.4	546	1	US-08-533-669A-2
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27	65.5	13.4	1427	2	US-09-565-501A-97

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35	64	13.1	98	2	US-09-270-767-41085	Sequence 41085, A
36	64	13.1	98	2	US-09-270-767-56301	Sequence 56301, A
37	64	13.1	569	2	US-09-107-532A-6689	Sequence 6689, Ap
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39	64	13.1	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
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ALIGNMENTS

RESULT 1
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; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:34:35 ; Search time 56.9391 Seconds
(without alignments)
667.774 Million cell updates/sec

Title: US-09-955-502A-35
Perfect score: 488
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Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	469	96.1	91	3	US-09-955-502-11
7	469	96.1	91	3	US-09-955-502-12
8	469	96.1	91	3	US-09-955-502-13
9	393	80.5	90	3	US-09-955-502-20
10	389	79.7	90	3	US-09-955-502-10
11	386	79.1	78	3	US-09-955-502-19
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17	259	53.1	76	3	US-09-955-502-21
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19	249	51.0	87	3	US-09-955-502-3
20	235	48.2	86	3	US-09-955-502-4
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22	228	46.7	87	3	US-09-955-502-25
23	222	45.5	90	3	US-09-955-502-23
24	218	44.7	87	3	US-09-955-502-24
25	218	44.7	88	3	US-09-955-502-33
26	211	43.2	88	3	US-09-955-502-26
27	211	43.2	88	3	US-09-955-502-27

28	211	43.2	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.2	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.2	87	3	US-09-955-502-30	Sequence 30, Appl
31	197	40.4	87	3	US-09-955-502-31	Sequence 31, Appl
32	195	40.0	87	3	US-09-955-502-32	Sequence 32, Appl
33	195	40.0	87	3	US-09-955-502-33	Sequence 33, Appl
34	72.5	14.9	786	5	US-10-732-923-4885	Sequence 41109, A
35	72	14.8	507	4	US-10-282-122A-68134	Sequence 4885, Ap
36	72	14.8	1261	4	US-10-437-963-189166	Sequence 68134, A
37	71.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
38	71	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
39	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
40	70.5	14.4	184	4	US-10-393-840-118	Sequence 118, App
41	70.5	14.4	593	5	US-10-450-763-50306	Sequence 50306, A
42	69	14.1	503	5	US-10-450-763-46936	Sequence 46936, A
43	69	14.1	479	5	US-10-805-684-105	Sequence 105, App
44	68.5	14.0	449	4	US-10-424-599-279212	Sequence 279212,
45	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, Ap
46	68.5	14.0	632	4	US-10-369-493-18744	Sequence 18744, A
47	68	13.9	280	3	US-09-323-998D-37	Sequence 37, Appl
48	68	13.9	280	4	US-10-389-566-2296	Sequence 2296, Ap
49	68	13.9	445	4	US-10-844-874-14	Sequence 14, Appl
50	68	13.9	445	5	US-10-713-970-13	Sequence 13, Appl
51	68	13.9	478	4	US-10-087-192-378	Sequence 378, App
52	68	13.9	689	4	US-10-369-493-17280	Sequence 17280, A
53	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
54	68	13.9	764	5	US-10-491-467-15	Sequence 15, Appl
55	68	13.9	1206	4	US-10-085-198-144	Sequence 144, App
56	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
57	67.5	13.8	166	5	US-10-489-706-269	Sequence 269, App
58	67	13.7	119	4	US-10-382-566-1126	Sequence 1126, Ap
59	67	13.7	167	4	US-10-437-963-158697	Sequence 158697,
60	67	13.7	306	4	US-10-424-599-241560	Sequence 241560,
61	66.5	13.6	315	4	US-10-282-122A-57222	Sequence 57222, A
62	66.5	13.6	315	5	US-10-958-216-464	Sequence 464, App
63	66.5	13.6	315	5	US-10-958-216-466	Sequence 466, App
64	66.5	13.6	561	4	US-10-437-963-169643	Sequence 169643,
65	66.5	13.6	638	5	US-10-831-070-272	Sequence 272, App
66	66.5	13.6	2910	5	US-10-732-923-3342	Sequence 3342, Ap
67	66	13.5	120	4	US-10-389-566-1079	Sequence 1079, Ap
68	66	13.5	120	4	US-10-389-566-1125	Sequence 1125, Ap
69	66	13.5	459	4	US-10-087-192-375	Sequence 375, App
70	65.5	13.4	221	4	US-10-767-701-41912	Sequence 41912, A
71	65.5	13.4	481	5	US-10-732-923-982	Sequence 982, App
72	65.5	13.4	545	5	US-10-732-923-9369	Sequence 9369, App
73	65.5	13.4	546	3	US-09-874-923-2	Sequence 2, Appli
74	65.5	13.4	546	3	US-09-991-496-2	Sequence 2, Appli
75	65.5	13.4	546	4	US-10-098-732A-71	Sequence 71, Appl

ALIGNMENTS

RESULT 1
US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234, 588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.82187 Seconds
(without alignments)
280.957 Million cell updates/sec

Title: US-09-955-502A-35

Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*

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- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	211	43.2	88	US-10-467-657-968	Sequence 968, App
2	68	13.9	478	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	62	12.7	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-4	Sequence 4, Appl
8	62	12.7	1167	US-10-942-072-6	Sequence 6, Appl
9	60.5	12.4	504	US-11-072-512-3467	Sequence 3467, App
10	59.5	12.2	264	US-10-821-234-1555	Sequence 1555, App
11	59.5	12.2	285	US-10-467-657-222	Sequence 222, App
12	59.5	12.2	285	US-10-467-657-8230	Sequence 8230, App
13	59.5	12.2	650	US-10-467-657-1948	Sequence 1948, App
14	59.5	12.2	834	US-10-453-372-658	Sequence 658, App
15	59.5	12.2	1995	US-11-069-834-60	Sequence 60, Appl
16	59	12.1	257	US-11-054-515-1710	Sequence 1710, App
17	59	12.1	697	US-10-485-517-202	Sequence 202, App
18	59	12.1	1168	US-10-942-072-11	Sequence 11, Appl
19	59	12.1	1450	US-10-485-517-152	Sequence 152, App
20	58.5	12.0	695	US-10-453-372-648	Sequence 648, App
21	58.5	12.0	700	US-10-995-561-922	Sequence 922, App
22	58.5	12.0	700	US-10-995-561-924	Sequence 924, App
23	58.5	12.0	749	US-11-098-686-10505	Sequence 10505, A
24	58.5	12.0	782	US-10-793-626-2352	Sequence 2352, App
25	58	11.9	448	US-10-618-320A-25	Sequence 25, Appl

26	58	11.9	480	6	US-10-510-386-12	Sequence 12, Appl
27	58	11.9	1501	7	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	6	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	7	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	6	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	6	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	6	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	6	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	6	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	6	US-10-453-372-638	Sequence 638, App
38	57.5	11.8	905	6	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	6	US-10-453-372-664	Sequence 664, App
40	57.5	11.8	963	6	US-10-995-561-923	Sequence 923, App
41	57.5	11.8	963	6	US-10-453-372-660	Sequence 660, App
42	57.5	11.8	1012	6	US-10-453-372-646	Sequence 646, App
43	57.5	11.8	3803	6	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	6	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	6	US-10-995-561-777	Sequence 777, App
46	57.5	11.8	5406	6	US-10-995-561-774	Sequence 774, App
47	57.5	11.8	5415	6	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	6	US-10-995-561-775	Sequence 775, App
49	57.5	11.8	5935	6	US-10-995-561-776	Sequence 776, App
50	57	11.7	234	6	US-10-524-972-120	Sequence 120, App
51	57	11.7	234	6	US-10-524-972-108	Sequence 108, App
52	57	11.7	432	6	US-10-821-234-1463	Sequence 1463, App
53	57	11.7	440	7	US-11-072-512-3856	Sequence 3856, App
54	56.5	11.6	647	7	US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254	6	US-10-821-234-147	Sequence 47, Appl
56	56.5	11.6	1897	6	US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907	7	US-11-000-463-250	Sequence 250, App
58	56.5	11.6	3433	6	US-10-714-781A-67	Sequence 67, Appl
59	56	11.5	206	7	US-11-124-367A-316	Sequence 316, App
60	55.5	11.4	136	6	US-10-793-626-580	Sequence 580, App
61	55.5	11.4	279	7	US-11-098-686-10812	Sequence 10812, A
62	55.5	11.4	1188	7	US-11-115-639-42	Sequence 42, Appl
63	55.5	11.4	1188	7	US-11-115-639-43	Sequence 43, Appl
64	55	11.3	189	7	US-11-071-262-1	Sequence 1, Appl
65	55	11.3	667	7	US-10-793-626-198	Sequence 198, App
66	55	11.3	692	7	US-11-038-284-33	Sequence 33, Appl
67	55	11.3	783	7	US-11-037-243-67	Sequence 67, Appl
68	55	11.3	873	7	US-11-038-284-35	Sequence 35, Appl
69	55	11.3	889	7	US-11-038-284-15	Sequence 15, Appl
70	55	11.3	1142	7	US-11-109-156-22	Sequence 22, Appl
71	55	11.3	2665	7	US-11-124-368A-214	Sequence 214, App
72	55	11.3	2668	7	US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	317	6	US-10-523-503-74	Sequence 74, Appl
74	54.5	11.2	450	6	US-10-618-320A-26	Sequence 26, Appl
75	54.5	11.2	496	7	US-11-069-642-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
Sequence 968, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.9696 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-36
Perfect score: 486
Sequence: 1 MSRTIFCTPLQREAGGDPQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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6	469	96.5	91	5	ABB78162
7	455	93.6	91	5	ABB78163
8	453	93.2	88	5	ABB78160
9	450	92.6	107	7	ABO65445
10	402	82.7	90	5	ABB78155
11	396	81.5	90	5	ABB78165
12	395	81.3	78	5	ABB78164
13	389	80.0	93	7	ADF05158
14	388	79.8	91	5	ABB78150
15	387	79.6	87	5	ABB78152
16	379	78.0	87	5	ABB78151
17	373	76.7	87	5	ABB78153
18	332	68.3	88	5	ABB78154
19	265	54.5	76	5	ABB78166
20	255	52.5	87	5	ABB78148
21	255	52.5	87	5	ABB78147
22	241	49.6	86	5	ABB78149
23	231.5	47.6	89	9	ABE41576
24	231.5	47.6	95	9	ABE38294

25	231	47.5	87	5	ABB78170	Abb78170 Amino aci
26	231	47.5	122	7	ABO74609	AbO74609 Pseudomon
27	227	46.7	88	5	ABB78178	Abb78178 Amino aci
28	227	46.7	90	5	ABB78168	Abb78168 Amino aci
29	225	46.3	87	5	ABB78169	Abb78169 Amino aci
30	216.5	44.5	90	5	ABB78167	Abb78167 Amino aci
31	213	43.8	88	5	ABB78171	Abb78171 Amino aci
32	213	43.8	88	5	ABB78172	Abb78172 Amino aci
33	213	43.8	88	5	ABB78173	Abb78173 Amino aci
34	213	43.8	88	6	ABP77219	Abp77219 N. gonorr
35	206	42.4	87	5	ABB78175	Abb78175 Amino aci
36	200	41.2	87	5	ABB78177	Abb78177 Amino aci
37	200	41.2	87	5	ABB78174	Abb78174 Amino aci
38	200	41.2	87	5	ABB78176	Abb78176 Amino aci
39	199.5	41.0	92	6	ADA34169	Ada34169 Acinetoba
40	131	27.0	110	8	ADL05173	Adl05173 M. catarr
41	83	17.1	506	3	AAV74371	Aay74371 Neisseria
42	83	17.1	1647	4	ABG10750	Abg10750 Novel hum
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44	78	16.0	507	3	AAV74372	Aay74372 Neisseria
45	78	16.0	507	3	AAV74373	Aay74373 Neisseria
46	78	16.0	546	6	ABU38097	Abu38097 Protein e
47	76	15.6	548	4	AAE04737	Aae04737 Brugia ma
48	75	15.4	309	8	ADN46828	Adn46828 Thermococ
49	74.5	15.3	632	8	ADS29711	Ads29711 Bacterial
50	72	14.8	474	9	ABO75727	AbO75727 Pseudomon
51	71.5	14.7	679	9	ADZ85056	Adz85056 Partial F
52	71	14.6	311	7	ADM26256	Adm26256 Hyperther
53	70.5	14.5	285	4	AAE92683	Aae92683 Human pro
54	70.5	14.5	414	6	ABU11747	Abu11747 Human MDD
55	70.5	14.5	614	9	ADX06837	Adx06837 Cyclin-de
56	70.5	14.5	614	9	ADY16108	Ady16108 PRO polyp
57	70.5	14.5	764	5	ABB77432	Abb77432 Human tum
58	70.5	14.5	764	7	ADC99062	Adc99062 Human KXP
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67	69.5	14.3	374	4	AAE39682	Aae39682 Human pol
68	69.5	14.3	389	4	AAE41468	Aae41468 Human pol
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70	69.5	14.3	481	7	ADD30148	Add30148 Plant yie
71	69.5	14.3	481	7	ADE31497	Ade31497 Plant yie
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73	69.5	14.3	485	5	ABB08477	Abb08477 Human lat
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ALIGNMENTS

RESULT 1
ABB78158 standard; protein; 91 AA.
ID ABB78158;
AC ABB78158;
XX 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of a YggX homologue.
DE
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
XX US2002072118-A1.
XX
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 EHRKLLLEQEMVNFLFEGKEVHIIEGYTPEDKK 91
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DB 61 EHRKLLLEQEMVNFLFEGKEVHIIEGYTPEDKK 91

RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX
XX ABB78157;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Unidentified.
OS
XX
PN US2002072118-A1.
XX
XX 13-JUN-2002.
PD
XX
PF 18-SEP-2001; 2001US-00955502.
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XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREABEGDFQLYPGELGKRIYNEISKEAWAQOHKQTMLINEKCLNMNNA 60
 |||||
DB 1 MSRTIFCTFLQREABEGDFQLYPGELGKRIYNEISKEAWAQOHKQTMLINEKCLNMNNA 60

QY 61 EHRKLLLEQEMVNFLFEGKEVHIIEGYTPEDKK 91
 |||||
DB 61 EHRKLLLEQEMVNFLFEGKEVHIIEGYTPEDKK 91

RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.
XX
XX ABB78156;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE
XX
XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Escherichia coli.
OS
XX
PN US2002072118-A1.
XX
XX 13-JUN-2002.
PD
XX
PF 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.84893 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502A-36
Perfect score: 486
Sequence: 1 MSRTIFCTFLQRAEGQDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	486	100.0	91	2	A85954	hypothetical prote
2	486	100.0	91	2	A65082	hypothetical prote
3	486	100.0	91	2	F91108	hypothetical prote
4	469	96.5	91	2	AH0879	conserved hypot
5	402	82.7	90	2	C82320	conserved hypot
6	396	81.5	90	2	A10116	conserved hypot
7	387	79.6	90	2	C64013	hypothetical prote
8	265	54.5	93	2	B84994	hypothetical prote
9	231	47.5	90	2	H83003	conserved hypot
10	226	46.5	105	2	C82624	conserved hypot
11	213	43.8	88	2	H81014	conserved hypot
12	78	16.0	507	2	C81063	fumarate hydratase
13	78	16.0	546	2	A81807	fumarate hydratase
14	76	15.6	548	2	A54510	63k antigen - nema
15	75.5	15.5	1638	2	D87749	protein unc-73b [i
16	75.5	15.5	2488	2	T42739	guanine nucleotide
17	74.5	15.3	683	2	AC2256	hypothetical prote
18	72	14.8	265	2	T46013	hypothetical prote
19	72	14.8	447	2	T16527	hypothetical prote
20	72	14.8	507	2	A83105	probable fumarase
21	72	14.8	511	2	A99574	ABC transporter at
22	69	14.2	258	2	A97991	hypothetical prote
23	69	14.2	258	2	E95121	phosphoesterase, p
24	69	14.2	548	2	A28209	60k filarial antig
25	69	14.2	1119	2	T15842	hypothetical prote
26	68	14.0	2672	2	A48126	translation activa
27	67.5	13.9	209	2	I64172	hypothetical prote
28	67	13.8	235	2	G65212	hypothetical prote
29	67	13.8	324	2	T05429	hypothetical prote

30	67	13.8	433	2	A70465	probable GTP bindi
31	67	13.8	447	2	UC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2	T40058	probable chromatin
33	66.5	13.7	1260	2	T04440	hypothetical prote
34	66	13.6	593	2	C64097	probable soluble 1
35	66	13.6	689	2	F83902	beta-galactosidase
36	65.5	13.5	173	2	H86869	hypothetical prote
37	65.5	13.5	305	2	A75211	asparaginase (EC 3
38	65.5	13.5	323	2	A90536	lipoprotein [impor
39	65.5	13.5	365	2	B54128	Fc-binding protein
40	65.5	13.5	821	2	A12417	hypothetical prote
41	65	13.4	251	2	E90428	regulatory protein
42	65	13.4	330	2	S74456	alpha-1,3-mannosyl
43	65	13.4	445	1	XUHUMB	hypothetical prote
44	65	13.4	456	2	G71152	hypothetical prote
45	65	13.4	1008	2	H85055	probable transposo
46	65	13.4	1141	2	T29185	hypothetical prote
47	65	13.4	1230	2	S56850	SMC1 protein homol
48	64.5	13.3	245	2	AG2300	hypothetical prote
49	64.5	13.3	305	2	A71247	probable L-asparag
50	64.5	13.3	495	2	AH0985	probable zinc-prot
51	64.5	13.3	859	2	T29630	hypothetical prote
52	64	13.2	220	2	S62410	hypothetical prote
53	64	13.2	438	2	T37786	probable RNA-bindi
54	64	13.2	447	1	A38561	alpha-1,3-mannosyl
55	64	13.2	583	2	T48365	hypothetical prote
56	64	13.2	604	2	S66993	hypothetical prote
57	64	13.2	990	2	T43445	hypothetical prote
58	64	13.2	1051	2	S27002	phospholipase C (B
59	64	13.2	1234	2	S52099	phospholipase C be
60	64	13.2	1234	2	I38994	phospholipase C-be
61	63.5	13.1	91	2	H90521	hypothetical prote
62	63.5	13.1	243	2	T29635	hypothetical prote
63	63.5	13.1	460	2	T00639	hypothetical prote
64	63.5	13.1	591	1	FOMVMM	gag polypeptide in
65	63	13.0	880	2	AE0179	probable ATPase ch
66	63	13.0	1251	2	A56677	neuronal cell cycl
67	63	13.0	1327	2	T14594	guanidine nucleoti
68	63	13.0	1611	1	WMTMPV	183k protein - pep
69	62.5	12.9	483	1	SYBSET	glutamate-tRNA lig
70	62.5	12.9	551	2	E84106	hypothetical prote
71	62.5	12.9	555	2	C96667	unknown protein, 7
72	62.5	12.9	617	2	B71071	probable prollyl en
73	62.5	12.9	964	1	T04325	probable ATP-depen
74	62.5	12.9	1417	2	T00661	hypothetical prote
75	62.	12.8	169	2	PN0560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:g12517511; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: yggx
C/Superfamily: fe(II) trafficking protein Yggx
Query Match 100.0%; Score 486; DB 2; Length 91;

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 ; Search time 66.1725 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-36
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPBGKRVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	481	99.0	90	1	FETP_ECO57	P0A8P4 escherichia
2	481	99.0	90	1	FETP_ECOLI	P0A8P3 escherichia
3	481	99.0	90	1	FETP_SHIFL	P0A8P5 shigella fl
4	477	98.1	90	1	FETP_ECOL6	Q8fe19 escherichia
5	464	95.5	90	1	FETP_SALCH	Q57K04 salmonella
6	464	95.5	90	1	FETP_SALPA	Q5pmu1 salmonella
7	464	95.5	90	1	FETP_SALTI	P67618 salmonella
8	464	95.5	90	1	FETP_SALTY	P67617 salmonella
9	411	84.6	90	1	FETP_ERWCT	Q6d8j9 erwinia car
10	404	83.1	90	1	FETP_YERPS	Q66m3 yersinia ps
11	402	82.7	90	1	FETP_VIBCH	Q9kura vibrio chol
12	402	82.7	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
13	402	82.7	90	1	FETP_VIBVY	Q7mhi4 vibrio vuln
14	399	82.1	90	1	FETP_VIBPA	Q87li5 vibrio para
15	396	81.5	90	1	FETP_YERPE	Q8zhe7 yersinia pe
16	389	80.0	91	1	FETP_MANSN	Q65vt7 mannheimia
17	387	79.6	90	1	FETP_HABIN	P44048 haemophilus
18	387	79.6	90	2	Q4QMD9_HABIS8	Q4qmd9 haemophilus
19	382	78.6	90	1	FETP_PHOPR	Q6lmk7 photobacter
20	381	78.4	90	1	FETP_PHOHL	Q7n7k1 photobacter
21	379	78.0	90	1	FETP_PASMU	Q9clb9 pasteurella
22	373	76.7	94	1	FETP_HABDU	Q7vkb6 haemophilus
23	366	75.3	90	1	FETP_VIBF1	Q5e7c0 vibrio fisc
24	335	68.9	90	1	FETP_IDILO	Q5qy58 idiomarina
25	332	68.3	92	1	FETP_SHEN	Q8ebx6 shewanella
26	265	54.5	90	1	FETP_BUCAI	P57618 buchenera ap
27	255	52.5	90	1	FETP_BORBR	Q7wh06 bordetella
28	255	52.5	90	1	FETP_BORPA	Q7w9q2 bordetella
29	255	52.5	90	1	FETP_BORPE	Q7wvc4 bordetella
30	247	50.8	78	1	FETP_BUCAP	Q8k925 buchenera ap
31	235	48.4	78	1	FETP_WIGBR	Q8d3c5 wigleswort

ALIGNMENTS

32	231.5	47.6	89	1	FETP_LEGPA	Q5x3x9 legionella
33	231.5	47.6	89	1	FETP_LEGPH	Q5zu80 legionella
34	231	47.5	90	1	FETP_PSEAB	Q9uh36 pseudomonas
35	231	47.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
36	228.5	47.0	89	1	FETP_LEGPL	Q5wvc4 legionella
37	227	46.7	90	1	FETP_COXBU	Q83d06 coxiella bu
38	227	46.7	90	1	FETP_PSESM	Q87u15 pseudomonas
39	227	46.7	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
40	226	46.5	90	1	FETP_XYLF	Q9pc73 xylella fas
41	225	46.3	90	1	FETP_PSEPK	Q88r49 pseudomonas
42	225	46.3	92	1	FETP_XANOR	Q5gy22 xanthomonas
43	223	45.9	90	2	Q4J2Z8_AZOV1	Q4j2z8 azotobacter
44	222	45.7	90	1	FETP_XYLF	Q87d06 xylella fas
45	222	45.7	92	1	FETP_XANCP	Q8p829 xanthomonas
46	222	45.7	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
47	220	45.3	90	1	FETP_NITEU	Q82xf2 nitrosomona
48	215	44.2	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
49	214	44.0	87	1	FETP_BUCBP	Q89a44 buchenera ap
50	213	43.8	88	1	FETP_NEIG1	Q5f553 neisseria g
51	213	43.8	88	1	FETP_NEIMA	P67615 neisseria m
52	213	43.8	88	1	FETP_NEIMB	P67616 neisseria m
53	212	43.6	79	1	FETP_CANBF	Q7vr99 candidatus
54	212	43.6	90	2	Q4KJ2_PSEF5	Q4kjt2 pseudomonas
55	211	43.4	90	1	FETP_CHRVO	Q7nsr4 chromobacte
56	207	42.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
57	206	42.4	91	1	FETP_BURMA	Q62ius burkholderi
58	206	42.4	91	1	FETP_BURPS	Q63sj4 burkholderi
59	206	42.4	91	1	FETP_RALSO	Q8y010 ralstonia s
60	200	41.2	90	1	FETP_METCA	Q60aj7 methylococc
61	199	40.9	87	1	FETP_FRATT	Q5nhj8 francisella
62	194.5	40.0	90	1	FETP_AC1AD	Q4fvj7 psychrobact
63	144	29.6	96	2	Q4FVJ7_9GAMM	Q4fwg4 anaeromyxob
64	142	29.2	92	2	Q4NWQ4_9DELT	Q5nuyl ralstonia m
65	90.5	18.6	482	2	Q5NUY1_9BURK	Q6aiz9 desulfotale
66	85.5	17.6	514	2	Q6AIZ9_DESPS	Q88pf3 pseudomonas
67	81	16.7	507	2	Q88PF3_PSEBK	Q7nsf0 chromobacte
68	81	16.7	508	2	Q7NSF0_CHRVO	Q7wx51 alcaligenes
69	80	16.5	486	2	Q7WX51_ALCEU	Q4yvr2 plasmodium
70	78.5	16.2	760	2	Q4YVR2_PLAIB	Q9jte3 neisseria m
71	78	16.0	507	2	Q9JYB9_NEIMB	Q9jte3 neisseria m
72	78	16.0	546	2	Q9JTB3_NEIMA	Q4ub40 theileria a
73	78	16.0	2248	2	Q4UB40_THEAN	Q8lar8 bacillus ce
74	77.5	15.9	337	2	Q8LAR8_BACCR	
75	77.5	15.9	1123	2	Q7RJL0_PLAYO	Q7rj10 plasmodium

RESULT 1

FETP_ECO57
ID FETP_ECO57 STANDARD; PRT; 90 AA.
AC P0A8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=y9gX; OrderedLocusNames=z4307, EC83838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grobeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


```
RL Nature 409:529-533 (2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Onishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22 (2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, AE005174; AAG58093.1; -; Genomic_DNA.
DR EMBL, BA000007; BAB37261.1; -; Genomic_DNA.
DR PIR, A85954; A85954.
DR PIR, F91108; F91108.
DR HAMAP, MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam, PF04362; DUF495; 1.
DR PIRSF, PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom, PD029191; DUF495; 1.
KM Complete proteome; Iron.
FT INIT MET 0 By similarity.
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREABGDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMWNAE 61
Db 1 SRTIFCTFLQREABGDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMWNAE 60

QY 62 HRKLLQEMVNFLEPGKEVHIEGYTPEDKK 91
Db 61 HRKLLQEMVNFLEPGKEVHIEGYTPEDKK 90

RESULT 2
FETP_ECOLI STANDARD; PRT; 90 AA.
ID FETP_ECOLI P52065;
AC P0A8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474 (1997).
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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313 (1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12.";
RL FEWS Microbiol. Lett. 169:375-382 (1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195 (1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the yggX gene of
RT Escherichia coli.";
RL J. Bacteriol. 185:6624-6632 (2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein YggX
RT from Escherichia coli.";
RL Protein Sci. 14:1673-1678 (2005).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -1- SUBUNIT: Monomer (Probable).
CC -1- INDUCTION: By oxidative stress and soxS.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL, U28377; AAA69129.1; -; Genomic_DNA.
DR EMBL, U00096; AAC75999.1; -; Genomic_DNA.
DR PIR, A65082; A65082.
DR PDB, 1YHD; NMR; A=1-90.
DR SWISS-2DPAGE, P0A8P3; COLI.
DR Echobase, EB2809; -.
DR EcoGene, EG12984; YggX.
DR HAMAP, MF_00686; -; 1.
DR InterPro: IPR007457; YggX.
DR Pfam, PF04362; DUF495; 1.
DR PIRSF, PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom, PD029191; DUF495; 1.
KW 3D-structure; Complete proteome; Direct protein sequencing; Iron.
FT INIT MET 0
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

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Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREABGDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMWNAE 61
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Run on: February 28, 2006, 20:25:19 ; Search time 18.2616 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-36
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGGQDFQ.....NFLFEKKEVHIHGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	199.5	41.0	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	131	27.0	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	76	15.6	548	2	US-09-167-299-3 Sequence 3, Appli
7	72	14.8	474	2	US-09-252-991A-24473 Sequence 24473, A
8	70.5	14.5	1214	2	US-10-164-595-24 Sequence 24, Appl
9	67.5	13.9	184	2	US-09-325-932A-66 Sequence 66, Appl
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ALIGNMENTS

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Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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Title: US-09-955-502A-36

Perfect score: 486
Sequence: 1 MSRTIRCTFLQRAEGQDFQ.....NFLPFGKEVHICGYTPEDKK 91

Scoring table: BLOSUM62
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and is derived by analysis of the total score distribution.

SUMMARIES

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9	402	82.7	90	3	US-09-955-502-10
10	396	81.5	90	3	US-09-955-502-20
11	395	81.3	78	3	US-09-955-502-20
12	388	79.8	91	3	US-09-955-502-5
13	387	79.6	87	3	US-09-955-502-7
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15	373	76.7	87	3	US-09-955-502-8
16	332	68.3	88	3	US-09-955-502-9
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19	255	52.5	87	3	US-09-955-502-3
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21	231	47.5	87	3	US-09-955-502-25
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ALIGNMENTS

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US-09-955-502-11
; Sequence 11, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655

US-09-955-502-11

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Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-955-502-12

; Sequence 12, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 12

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Escherichia coli O157:H7EDL933

US-09-955-502-12

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RESULT 3

US-09-955-502-13

; Sequence 13, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

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; TYPE: PRT

; ORGANISM: Escherichia coli O157:H7

US-09-955-502-13

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RESULT 4

US-09-955-502-14

; Sequence 14, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

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; TYPE: PRT

; ORGANISM: Salmonella paratyphi

US-09-955-502-14

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US-09-955-502-16

; Sequence 16, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; CURRENT FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 16

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella dublin

US-09-955-502-16

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Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:35:27 ; Search time 4.82187 Seconds
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Title: US-09-955-502A-36

Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGGQDFQ.....NFLPEGKEVHIEGYTPEDKK 91

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_AA_New:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	43.8	88	6	US-10-467-657-968 Sequence 968, App
2	66	13.6	593	7	US-11-194-246-317 Sequence 317, App
3	65.5	13.5	395	7	US-11-009-658-46 Sequence 46, Appl
4	65	13.4	478	6	US-10-821-234-915 Sequence 915, App
5	62	12.8	1501	6	US-10-793-626-2850 Sequence 2850, Ap
6	61.5	12.7	179	6	US-10-467-657-6542 Sequence 6542, Ap
7	60.5	12.4	264	6	US-10-821-234-1555 Sequence 1555, Ap
8	60.5	12.4	404	7	US-11-009-658-48 Sequence 48, Appl
9	60.5	12.4	834	6	US-10-453-372-658 Sequence 658, App
10	60	12.3	448	6	US-10-618-320A-25 Sequence 25, Appl
11	60	12.3	480	6	US-10-510-386-12 Sequence 12, Appl
12	60	12.3	667	6	US-10-793-626-198 Sequence 198, Appl
13	59.5	12.2	177	6	US-10-467-657-1658 Sequence 1658, Ap
14	59	12.1	266	5	US-09-995-493-6 Sequence 6, Appl
15	59	12.1	604	6	US-10-942-072-4 Sequence 4, Appl
16	59	12.1	1142	7	US-11-109-156-22 Sequence 22, Appl
17	59	12.1	1167	6	US-10-942-072-6 Sequence 6, Appl
18	58.5	12.0	336	6	US-10-453-372-640 Sequence 640, App
19	58.5	12.0	349	6	US-10-821-234-1387 Sequence 1387, Ap
20	58.5	12.0	577	7	US-11-072-175-187 Sequence 187, App
21	58.5	12.0	695	6	US-10-453-372-648 Sequence 648, App
22	58.5	12.0	700	6	US-10-995-561-922 Sequence 922, App
23	58.5	12.0	700	6	US-10-995-561-924 Sequence 924, App
24	58.5	12.0	775	6	US-10-453-372-656 Sequence 656, App
25	58.5	12.0	793	6	US-10-995-561-925 Sequence 925, App

26	58.5	12.0	804	6	US-10-453-372-650 Sequence 650, App
27	58.5	12.0	847	6	US-10-453-372-654 Sequence 654, App
28	58.5	12.0	857	6	US-10-453-372-652 Sequence 652, App
29	58.5	12.0	905	6	US-10-453-372-638 Sequence 638, App
30	58.5	12.0	905	6	US-10-453-372-662 Sequence 662, App
31	58.5	12.0	905	6	US-10-453-372-664 Sequence 664, App
32	58.5	12.0	963	6	US-10-995-561-923 Sequence 923, App
33	58.5	12.0	963	6	US-10-453-372-660 Sequence 660, App
34	58.5	12.0	1012	6	US-10-453-372-646 Sequence 646, App
35	58.5	12.0	1299	6	US-10-821-234-1145 Sequence 1145, Ap
36	58.5	12.0	3803	6	US-10-995-561-773 Sequence 773, App
37	58.5	12.0	3960	6	US-10-995-561-771 Sequence 771, App
38	58.5	12.0	5335	6	US-10-995-561-777 Sequence 774, App
39	58.5	12.0	5406	6	US-10-995-561-774 Sequence 779, App
40	58.5	12.0	5415	6	US-10-995-561-779 Sequence 775, App
41	58.5	12.0	5464	6	US-10-995-561-775 Sequence 776, App
42	58.5	12.0	5935	6	US-10-995-561-776 Sequence 1496, Ap
43	58	11.9	251	7	US-11-054-515-1496 Sequence 60, Appl
44	58	11.9	1995	7	US-11-069-834-60 Sequence 3003, Ap
45	57.5	11.8	752	7	US-11-072-512-3003 Sequence 2906, Ap
46	57	11.7	194	7	US-11-072-512-2906 Sequence 10812, A
47	57	11.7	279	7	US-11-098-686-10812 Sequence 3467, Ap
48	57	11.7	504	7	US-11-072-512-3467 Sequence 10, Appl
49	56	11.5	296	7	US-11-087-227-10 Sequence 5, Appl
50	56	11.5	372	7	US-11-143-986-5 Sequence 6, Appl
51	56	11.5	372	7	US-11-143-986-6 Sequence 2, Appl
52	56	11.5	386	7	US-11-143-986-2 Sequence 3, Appl
53	56	11.5	386	7	US-11-143-986-3 Sequence 223, App
54	56	11.5	397	7	US-11-022-562-223 Sequence 10340, A
55	56	11.5	426	7	US-11-098-686-10340 Sequence 91, Appl
56	56	11.5	427	7	US-11-186-284-91 Sequence 28, Appl
57	56	11.5	581	6	US-10-793-626-28 Sequence 202, App
58	56	11.5	697	6	US-10-485-517-202 Sequence 1036, Ap
59	56	11.5	752	6	US-10-793-626-1036 Sequence 11, Appl
60	56	11.5	1168	7	US-10-942-072-11 Sequence 43, Appl
61	56	11.5	1188	7	US-11-115-639-42 Sequence 169, App
62	56	11.5	1188	7	US-11-115-639-43 Sequence 437, App
63	56	11.5	1404	6	US-10-878-556A-169 Sequence 436, App
64	55.5	11.4	207	7	US-11-124-367A-437 Sequence 3856, Ap
65	55.5	11.4	317	7	US-11-124-367A-437 Sequence 2547, Ap
66	55.5	11.4	328	7	US-11-124-367A-436 Sequence 23, Appl
67	55.5	11.4	440	7	US-11-072-512-3856 Sequence 61, Appl
68	55.5	11.4	623	7	US-11-072-512-2547 Sequence 1710, Ap
69	55.5	11.4	2101	6	US-10-857-780-23 Sequence 60, Appl
70	55	11.3	257	6	US-10-667-295-61 Sequence 59, Appl
71	55	11.3	257	7	US-11-054-515-1710 Sequence 8, Appl
72	55	11.3	286	6	US-10-667-295-60 Sequence 9, Appl
73	55	11.3	327	6	US-10-667-295-59 Sequence 6, Appl
74	55	11.3	359	7	US-11-087-227-8 Sequence 6, Appl
75	55	11.3	359	7	US-11-192-450-6

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

```

; SEQ ID NO 968
;
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

```

Query Match	43.8%	Score 213;	DB 6;	Length 88;
Best Local Similarity	44.3%	Pred. No. 7.3e-17;		
Matches 39;	Conservative 16;	Mismatches 33;	Indels 0;	Gaps 0;

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Qy      1 MSRTIFCTFLQREAEQGDPOLYEGELGKRIYNEISKEAWAQHQKOTMLINEKTLNNNA     600
          |::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      1 MARWVFCVKLNKEAEGMKFPPLNELGRIFENVSQEANAATTRHQTMLINNRSLADP    600
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Qy      61 EHRKLLQEEMVNFLEFGKEVHIEGYTPQ 88  
        | : | | : |          :: || | :  
Db      61 RAREYLAQQMEGYFFGGDADAVGIVPQ 88
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RESULT 2
US-11-19

; Sequence 317, Application US/11194246
 ; Publication No. US20050272089A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mott, John

```

; APPLICANT: Mott, John
; APPLICANT: Trepid, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (McR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

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Query Match	13.6%;	Score 66;	DB 7;	Length 593;
Best Local Similarity	44.4%;	Pred. No. 9.9;		
Matches 12;	Conservative 5;	Mismatches 10;	Indels 0;	Gaps 0;

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QY      35  SKEAWAQWQHQTMLINEKLNMMNAE  61
      ||:| |:| |:| ||| ::|
Db      296 SKQEWRYWEAKQDILKNTKLTALSKE  322
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RESULT 3

```

US-11-009-658-46
; Sequence 46, Application US/11009658
; Publication No. US20060003430A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours and Company
; TITLE OF INVENTION: Lysophosphatidic Acid Acetyltransferases
; FILE REFERENCE: BR1332
; CURRENT APPLICATION NUMBER: US/11/009,658
; CURRENT FILING DATE: 2004-12-10
; PRIOR APPLICATION NUMBER: US/09/914,098
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/121,119
; PRIOR FILING DATE: 1999-02-22
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 46
; LENGTH: 395
; TYPE: PRT
; ORGANISM: Zea mays

```

US-11-009-658-46

Query Match	13.5%	Score 65.5;	DB 7;	Length 395;
Best Local Similarity	21.9%	Pred. No. 6.9;		
Matches 28;	Conservative 19;	Mismatches 36;	Indels 45;	Gaps 4;

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Qy      1 MSRTIFCTFLÖREAEQÖDFÖLYPGEIGKRIYNEISKEAMAOÖHKÖTMLINE----- 52
        :::::|:::|:::|
Db      224 ISKLGCI FVÖRESKTPDFKVGSGAVSERIH-----RAHQÖKNAPMMLFPEGTTNGDY 278

```

```

Qy 53 -----KKLN-----MNAEHRKLLQEMVNPFLPGEKEVHIE 83
      | : | | | | | | | | | | | | | | | | | | | |
Db 279 LLPEKTGAFLAKAPVQPVILRYPRYKRFNAAMDMSGARHVFLLLCQFVNYL--EVRRLP 335

```

QY 84 GYTPEDKK 91
| | ::
Db 336 VYYPSEQE 343

RESULT 4
US-10-82

; Sequence 915, Application US/10821234
; Publication No. US2005025511A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan

```

; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 915
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-915

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Query Match	13.4%	Score 65;	DB 6;	Length 478;
Best Local Similarity	25.7%	Pred. No. 9.9;		
Matches 27; Conservative	18;	Mismatches 26;	Indels 34;	Gaps 5,

```

QY      8 TPLQREABGQDF--QLYP-----GELGKRIYNEISKEAWAQWQHKOQM 48
      ::|||::||::|
Db      380 SYLOREAYDRDFLARVYGAPOLOVEKVRTNDRKELGEVRVQYTGGRDSFKAF-----KALG 435

```

```
QY      49 LINEKLTNNMNAEHRKLLEQEMVNFLEFGKEVHI-----EGYTP   87
       . ::: | : | : | | | | : | : | : | | | |
Db     436 VMDDLKSGVPFRAGYRGI----VTFOFGRHVRHLAPPTWEGYDP   475
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RESULT 5

```

US-10-793-626-2850
: Sequence 2850, Application US/10793626
: Publication No. US20050255478A1
: GENERAL INFORMATION:
: APPLICANT: KIMBERLY, WILLIAM JOHN
: TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
: FILE REFERENCE: PU3480US
: CURRENT APPLICATION NUMBER: US/10/793,626
: CURRENT FILING DATE: 2004-03-04
: PRIOR APPLICATION NUMBER: 60/164,258
: PRIOR FILING DATE: 1999-11-09
: NUMBER OF SEQ ID NOS: 4472
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 2850
: LENGTH: 1501
: TYPE: PRT
: ORGANISM: Artificial Sequence

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 19:26:45 ; Search time 73.1567 Seconds
(without alignments)
540.539 Million cell updates/sec

Title: US-09-955-502A-37

Perfect score: 473
Sequence: 1 MSRTIFCTFLKDAERQDFQ.....VNFLPEGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	473	100.0	90	5	ABB78165
2	400	84.6	107	7	ABO65445
3	396	83.7	91	5	ABB78158
4	396	83.7	91	5	ABB78157
5	396	83.7	91	5	ABB78156
6	393	83.1	91	5	ABB78161
7	393	83.1	91	5	ABB78159
8	393	83.1	91	5	ABB78162
9	389	82.2	88	5	ABB78160
10	389	82.2	93	7	ADF05158
11	379	80.1	91	5	ABB78163
12	366	77.4	90	5	ABB78155
13	363	76.7	87	5	ABB78152
14	357	75.5	91	5	ABB78150
15	351	74.2	87	5	ABB78153
16	346	73.2	87	5	ABB78151
17	342	72.3	88	5	ABB78154
18	308	65.1	88	5	ABB78154
19	256	54.1	76	5	ABB78166
20	233	49.3	88	5	ABB78178
21	226	47.8	87	5	ABB78148
22	226	47.8	87	5	ABB78147
23	221	46.7	122	7	ABO74609
24	218.5	46.2	89	9	ABE41576

25	218.5	46.2	95	9	ABE38294	Aeb38294 L. pneumo
26	212	44.8	86	5	ABB78149	Abb78149 Amino aci
27	210	44.4	87	5	ABB78170	Abb78170 Amino aci
28	206	43.6	90	5	ABB78168	Abb78168 Amino aci
29	199	42.1	87	5	ABB78175	Abb78175 Amino aci
30	198	41.9	88	5	ABB78171	Abb78171 Amino aci
31	198	41.9	88	5	ABB78172	Abb78172 Amino aci
32	198	41.9	88	5	ABB78173	Abb78173 Amino aci
33	198	41.9	88	6	ABP77219	Abp77219 N. gonorr
34	194.5	41.1	90	5	ABB78167	Abb78167 Amino aci
35	193	40.8	87	5	ABB78174	Abb78174 Amino aci
36	188	39.7	87	5	ABB78169	Abb78169 Amino aci
37	186	39.3	87	5	ABB78177	Abb78177 Amino aci
38	186	39.3	87	5	ABB78176	Abb78176 Amino aci
39	176.5	37.3	92	6	ADA34169	Ada34169 Acinetoba
40	143	30.2	110	8	ADL05173	Adl05173 M. catarr
41	81	17.1	102	5	ABP31411	Abp31411 Human ORF
42	81	17.1	2000	6	ABR52622	AbR52622 Protein B
43	81	17.1	2000	7	ADK62602	Adk62602 Disease t
44	74	15.6	397	4	ABB11207	Abb11207 Human PI-
45	74	15.6	403	6	ABM71645	Abm71645 Staphyloc
46	74	15.6	506	5	AAU79180	Aau79180 Human par
47	74	15.6	576	4	ABG19914	Abg19914 Novel hum
48	74	15.6	589	5	AAB47871	Aab47871 ISIGP-1.
49	74	15.6	1116	4	AAU67293	Aau67293 Amino aci
50	74	15.6	1116	5	AAU79181	Aau79181 Human pho
51	74	15.6	1116	8	ADM87230	Adm87230 Human pro
52	73.5	15.5	641	6	ABM67978	Abm67978 Photorhab
53	73	15.4	397	8	ADM87687	Adm87687 Human EST
54	70.5	14.9	635	4	ABB69129	Abb69129 Drosophil
55	70	14.8	184	3	AAB16290	Aab16290 Pinus rad
56	70	14.8	869	8	ADW64441	Adw64441 Thermosta
57	69.5	14.7	867	6	ABU41082	Abu41082 Protein e
58	69.5	14.7	870	7	ADF04483	Adf04483 Bacterial
59	69.5	14.7	1589	4	ABG08898	Abg08898 Novel hum
60	69.5	14.7	1589	4	ABG22603	Abg22603 Novel hum
61	69.5	14.7	1589	4	ABG30099	Abg30099 Novel hum
62	69.5	14.7	1589	4	ABG28504	Abg28504 Novel hum
63	69.5	14.7	1589	7	ABO72159	AbO72159 Pseudomon
64	69	14.6	209	7	ABO72159	AbO72159 Pseudomon
65	68	14.4	256	6	ABU25179	Abu25179 Protein e
66	68	14.4	344	7	ABO23534	AbO23534 Borrelia
67	68	14.4	506	3	AAU74371	Aau74371 Neisseria
68	67.5	14.3	617	7	AAU49439	Aau49439 Pyrococcu
69	67.5	14.3	701	7	ABO74542	AbO74542 Pseudomon
70	67	14.2	415	2	AAW22982	Aaw22982 Canine he
71	67	14.2	415	2	AAW72649	Aaw72649 Canine he
72	67	14.2	415	4	AAB51306	Aab51306 Canine he
73	67	14.2	415	7	AAE39123	Aae39123 CHV PCGG
74	66.5	14.1	184	4	ABG04791	Abg04791 Novel hum
75	66.5	14.1	758	8	ADS21214	AdS21214 Bacterial

ALIGNMENTS

RESULT 1
ABB78165
ID ABB78165 standard; protein; 90 AA.
XX
AC ABB78165;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 473; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLKDAERODFOLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60
Db 1 MSRTIFCTFLKDAERQDFOLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60
QY 61 EDRKLLBQEMVNFLEGGQDVHIAGYTPPSK 90
Db 61 EDRKLLBQEMVNFLEGGQDVHIAGYTPPSK 90

RESULT 2
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
DB *Klebsiella pneumoniae* polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW *Klebsiella pneumoniae* protein; antibacterial; Vaccine.
XX
OS *Klebsiella pneumoniae*.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.

DR N-PSDB; ACH98996.
XX
PT New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
PT preparing a vaccine composition against *Klebsiella pneumoniae*.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a *Klebsiella*
CC *pneumoniae* polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against *Klebsiella pneumoniae*. This is the amino acid sequence of a
CC *Klebsiella pneumoniae* polypeptide of the invention
XX
SQ Sequence 107 AA;

Query Match 84.6%; Score 400; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.5e-39;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;
QY 1 MSRTIFCTFLKDAERQDFOLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60
Db 17 MSRTIFCTFLQREADQDFOLYPGELGKRIYNEISKEAWAQWQHKQTMLINEKLSMNNP 76
QY 61 EDRKLLBQEMVNFLEGGQDVHIAGYTPPSK 90
Db 77 EHRKLLBQEMVQFLFEGKDVHIEGYTPPEK 106

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX
AC ABB78158;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YgX homologue.
XX
KW Superoxide damage; cell; YgX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:22:21 ; Search time 9.7407 Seconds
(without alignments)
889.003 Million cell updates/sec

Title: US-09-955-502a-37
Perfect score: 473
Sequence: 1 MSRTIFCTFLKDAERQDFQ.....VNFLREGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	473	100.0	90	2	A10116	conserved hypothet
2	396	83.7	91	2	A85954	hypothetical prote
3	396	83.7	91	2	A65082	hypothetical prote
4	396	83.7	91	2	F91108	hypothetical prote
5	393	83.1	91	2	AH0879	conserved hypothet
6	374	79.1	90	2	C64013	hypothetical prote
7	366	77.4	90	2	C82320	conserved hypothet
8	256	54.1	93	2	E84994	hypothetical prote
9	221	46.7	90	2	H83003	conserved hypothet
10	203	42.9	105	2	C82624	conserved hypothet
11	198	41.9	88	2	H81014	conserved hypothet
12	81	17.1	2672	2	A48126	translation activa
13	76.5	16.2	511	2	A99574	ABC transporter at
14	74	15.6	403	2	B89808	hypothetical prote
15	71.5	15.1	1008	2	H72310	conserved hypothet
16	70	14.8	265	2	T46013	hypothetical prote
17	70	14.8	1119	2	T18491	hypothetical prote
18	69.5	14.7	996	2	A71080	hypothetical prote
19	69	14.6	1386	1	RNLVC2	DNA-directed RNA p
20	68.5	14.5	165	2	A81382	shikimate kinase (
21	68	14.4	344	2	D70126	hypothetical prote
22	68	14.4	583	2	T48365	hypothetical prote
23	68	14.4	820	2	G88996	protein C17B7.5 [i
24	67.5	14.3	160	2	E70416	hypothetical prote
25	67.5	14.3	336	2	C64468	hypothetical prote
26	67.5	14.3	617	2	B71071	probable prolyl en
27	67.5	14.3	629	2	B83107	chemotactic transd
28	67	14.2	394	2	B70206	hypothetical prote
29	66.5	14.1	139	2	E97709	hypothetical prote

30	66.5	14.1	420	2	A25876	vitellinogen III p
31	66.5	14.1	648	2	A71647	glycine-tRNA ligas
32	66	14.0	705	2	T47949	hypothetical prote
33	66	14.0	799	2	T02656	probable salt-indu
34	65.5	13.8	91	2	H90521	hypothetical prote
35	65.5	13.8	688	2	S57131	hypothetical prote
36	65	13.7	118	2	G64302	hypothetical prote
37	65	13.7	411	2	A48946	aspartate kinase (
38	65	13.7	738	2	B69863	two-component sens
39	65	13.7	2101	2	A42184	nuclear mitotic ap
40	64.5	13.6	245	2	AG2300	hypothetical prote
41	64	13.5	158	2	A59102	hypothetical prote
42	64	13.5	235	2	AD1735	hypothetical prote
43	64	13.5	346	2	F97871	uroporphyrinogen d
44	64	13.5	1611	1	WMTMPV	183K protein - pep
45	63.5	13.4	548	2	A54510	63K antigen - nema
46	63.5	13.4	548	2	A28209	60K filarial antig
47	63.5	13.4	715	2	D84480	Mutator-like trans
48	63.5	13.4	884	1	RNBPT3	DNA-directed RNA p
49	63.5	13.4	1010	2	F75134	hypothetical prote
50	63.5	13.4	1119	2	T15842	hypothetical prote
51	63	13.3	254	2	A64437	hypothetical prote
52	63	13.3	264	2	G89808	hypothetical prote
53	63	13.3	269	2	AE1286	hypothetical prote
54	63	13.3	507	2	C81063	hypothetical prote
55	63	13.3	546	2	A81807	fumarate hydratase
56	63	13.3	821	1	A39616	protein kinase RAD
57	63	13.3	974	2	A40580	Iodestar maternal-
58	63	13.3	1027	2	T27970	hypothetical prote
59	62.5	13.2	173	2	H86869	hypothetical prote
60	62.5	13.2	259	2	D69998	lysophospholipase
61	62.5	13.2	477	2	B61378	leukotoxin secreti
62	62.5	13.2	674	2	D97864	glycine-tRNA ligas
63	62.5	13.2	869	2	T22422	hypothetical prote
64	62.5	13.2	1939	2	T18372	repeat organellar
65	62	13.1	143	2	B83688	hypothetical prote
66	62	13.1	212	2	B71853	probable biotin ac
67	62	13.1	224	2	C64240	mobilization prote
68	62	13.1	353	1	FOMVGR	gag polyprotein -
69	62	13.1	375	2	A36898	maspin - human
70	62	13.1	498	2	C90413	dihydropterolate sy
71	62	13.1	593	2	C64097	probable soluble l
72	62	13.1	1030	2	T37868	probable helicase
73	61.5	13.0	222	2	S62001	MEIS protein - yea
74	61.5	13.0	287	2	F82265	conserved hypothet
75	61.5	13.0	339	2	A90395	conserved hypothet

ALIGNMENTS

RESULT 1
A10116
Conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10116
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: A10116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CA89796.1; PID:g15979022;
C/Genetics:
A/Gene: YPO0953
C/Superfamily: fe(II) trafficking protein YgsX
Query Match 100.0%; Score 473; DB 2; Length 90;

Best Local Similarity 100.0%; Pred. No. 1.2e-41;		Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
Db	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
RESULT 2			
Qy	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
Db	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
hypoetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL93			
C/Species: Escherichia coli			
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004			
C/Accession: A85954			
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew			
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,			
Nature 409, 529-533, 2001			
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.			
A/Reference number: A85480; MUID:21074935; PMID:11206551			
A/Accession: A85954			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-91 <STO>			
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F			
A/Experimental source: strain O157:H7, substrain EDL933			
C/Genetics:			
A/Gene: yggx			
C/Superfamily: fe(II) trafficking protein Yggx			
Query Match		83.7%;	Score 396; DB 2; Length 91;
Best Local Similarity		82.2%;	Pred. No. 9.4e-34;
Matches		74; Conservative	8; Mismatches 8; Indels 0; Gaps 0;
Qy	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
Db	1 MSRTIFCTFLQREAEQDFQLYPGEIGKRIYNEISKEAWAQWQHKTMLINEKLSMNA 60		
Qy	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
Db	61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPEDK 90		
RESULT 3			
A65082			
hypoetical protein b2962 - Escherichia coli (strain K-12)			
C/Species: Escherichia coli			
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004			
C/Accession: A65082			
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co			
.A.; Rose, D.J.; Mau, B.; Shao, Y.			
Science 277, 1453-1462, 1997			
A/Title: The complete genome sequence of Escherichia coli K-12.			
A/Reference number: A64720; MUID:97426617; PMID:9278503			
A/Accession: A65082			
A/Status: preliminary; nucleic acid sequence not shown; translation not shown			
A/Molecule type: DNA			
A/Residues: 1-91 <BLAT>			
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g			
A/Experimental source: strain K-12, substrain MG1655			
C/Superfamily: fe(II) trafficking protein Yggx			
Query Match		83.7%;	Score 396; DB 2; Length 91;
Best Local Similarity		82.2%;	Pred. No. 9.4e-34;
Matches		74; Conservative	8; Mismatches 8; Indels 0; Gaps 0;
Qy	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
Db	1 MSRTIFCTFLQREAEQDFQLYPGEIGKRIYNEISKEAWAQWQHKTMLINEKLSMNA 60		

Qy	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
Db	61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPEDK 90		
RESULT 4			
F91108			
hypoetical protein EC6388 [imported] - Escherichia coli (strain O157:H7, substrain R1			
C/Species: Escherichia coli			
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004			
C/Accession: F91108			
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.			
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.			
DNA Res. 8, 11-22, 2001			
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno			
A/Reference number: A99629; MUID:21156231; PMID:11258796			
A/Accession: F91108			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-91 <HAY>			
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;			
A/Experimental source: strain O157:H7, substrain R1MD 0509952			
C/Genetics:			
A/Gene: EC6388			
C/Superfamily: fe(II) trafficking protein Yggx			
Query Match		83.7%;	Score 396; DB 2; Length 91;
Best Local Similarity		82.2%;	Pred. No. 9.4e-34;
Matches		74; Conservative	8; Mismatches 8; Indels 0; Gaps 0;
Qy	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
Db	1 MSRTIFCTFLQREAEQDFQLYPGEIGKRIYNEISKEAWAQWQHKTMLINEKLSMNA 60		
Qy	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
Db	61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPEDK 90		
RESULT 5			
AH0879			
conserved hypoetical protein STY3266 [imported] - Salmonella enterica subsp. enterica			
C/Species: Salmonella enterica subsp. enterica serovar Typhi			
A/Note: this species has also been called Salmonella typhi			
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004			
C/Accession: AH0879			
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,			
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,			
, S.; Moule, S.; O'Gaora, P.			
Nature 413, 848-852, 2001			
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;			
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov			
A/Reference number: AB0502; MUID:21534947; PMID:11677608			
A/Accession: AH0879			
A/Status: preliminary			
A/Molecule type: DNA			
A/Residues: 1-91 <PAR>			
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;			
C/Genetics:			
A/Gene: STY3266			
C/Superfamily: fe(II) trafficking protein Yggx			
Query Match		83.1%;	Score 393; DB 2; length 91;
Best Local Similarity		81.1%;	Pred. No. 1.9e-33;
Matches		73; Conservative	9; Mismatches 8; Indels 0; Gaps 0;
Qy	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60		
Db	1 MSRTIFCTYLLQREAEQDFQLYPGEIGKRIYNEISKDAWAQWQHKTMLINEKLSMNA 60		
Qy	61 EDRKLLLEQEMVNFLEFGQDVHIAGYTPPSK 90		
Db	61 EHRKLLLEQEMVNFLEFGKDVHIIEGYTPEDK 90		

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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:37:29 : Search time 65.4453 Seconds
(without alignments)
970.238 Million cell updates/sec

Title: US-09-955-502A-37

Perfect score: 473

Sequence: 1 MSRTIFCTFLKDAERQDFQ.....VNFLFEGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	473	100.0	90	1	FETP_YERPE	Q8zhe7 Yersinia pe
2	466	98.5	90	1	FETP_YERPS	Q66m3 Yersinia ps
3	412	87.1	90	1	FETP_ERWCT	Q6d8j9 Yersinia car
4	391	82.7	90	1	FETP_ECO57	P0a8p4 escherichia
5	391	82.7	90	1	FETP_ECOLI	P0a8p3 escherichia
6	391	82.7	90	1	FETP_SHIFL	P0a8p5 shigella fl
7	388	82.0	90	1	FETP_SALCH	Q57k04 salmonella
8	388	82.0	90	1	FETP_SALPA	Q5pmu1 salmonella
9	388	82.0	90	1	FETP_SALTI	P67618 salmonella
10	388	82.0	90	1	FETP_SALTY	P67617 salmonella
11	387	81.8	90	1	FETP_ECOL6	Q8fe19 escherichia
12	379	80.1	90	1	FETP_PHOLL	Q7n711 photorhabdu
13	377	79.7	90	1	FETP_PHOPR	Q6lmk7 photobacter
14	374	79.1	90	1	FETP_HABIN	P44048 haemophilus
15	374	79.1	90	2	Q4QMD9_HAB18	Q4qmd9 haemophilus
16	366	77.4	90	1	FETP_VIBCH	Q9kur4 vibrio chol
17	362	76.5	90	1	FETP_VIBPA	Q87115 vibrio para
18	357	75.5	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
19	357	75.5	90	1	FETP_VIBVY	Q7mh14 vibrio vuln
20	355	75.1	90	1	FETP_PASMU	Q9c1b9 pascuarella
21	354	74.8	91	1	FETP_MASNM	Q65vt7 mannheimia
22	351	74.2	94	1	FETP_HAEDU	Q7vxb6 haemophilus
23	330	69.8	90	1	FETP_VIBF1	Q5e7c0 vibrio fisc
24	308	65.1	92	1	FETP_SHRON	Q8bxb6 shewanella
25	305	64.5	90	1	FETP_IDILO	Q5qy58 idiomarina
26	256	54.1	77	1	FETP_BUCAI	P57618 buchnera ap
27	240	50.7	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
28	237	50.1	90	1	FETP_BORBR	Q7wh06 bordetella
29	237	50.1	90	1	FETP_BORPA	Q7w9q2 bordetella
30	237	50.1	90	1	FETP_BORPE	Q7w9q2 bordetella
31	234	49.5	78	1	FETP_BUCAP	Q8k925 buchnera ap

32	233	49.3	90	1	FETP_COXBU	Q83d06 coxiella bu
33	228	48.2	90	1	FETP_NITEU	Q82xf2 nictrosomona
34	222.5	47.0	89	1	FETP_LEGFL	Q5wvc4 legionella
35	221	46.7	90	1	FETP_PSEAB	Q9h336 pseudomonas
36	220	46.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
37	218.5	46.2	89	1	FETP_LEGPA	Q5x3x9 legionella
38	218.5	46.2	89	1	FETP_LEGPH	Q5zu80 legionella
39	216	45.7	87	1	FETP_BUCBP	Q89a44 buchnera ap
40	216	45.7	92	1	FETP_XANOR	Q5gy22 xanthomonas
41	213	45.0	90	1	FETP_CHRVO	Q7n8r4 chromobacte
42	210	44.4	92	1	FETP_XANCP	Q8p829 xanthomonas
43	210	44.4	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
44	208	44.0	90	2	Q4J228_AZOVI	Q4j228 azotobacter
45	208	44.0	91	1	FETP_BURMA	Q621u9 burkholderi
46	208	44.0	91	1	FETP_BURPS	Q63ej4 burkholderi
47	207	43.8	90	1	FETP_XYLF1	Q87d06 xylella fas
48	206	43.6	90	1	FETP_PSESM	Q87uf5 pseudomonas
49	206	43.6	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
50	206	43.6	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
51	206	43.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
52	203	42.9	90	1	FETP_XYLF2	Q9pc73 xylella fas
53	203	42.9	91	1	FETP_RALSO	Q8y010 ralstonia s
54	199	42.1	79	1	FETP_CANBF	Q7vrg9 candidatus
55	198	41.9	88	1	FETP_NEIG1	Q5f553 neisseria g
56	198	41.9	88	1	FETP_NEIMA	P67615 neisseria m
57	198	41.9	88	1	FETP_NEIMB	P67616 neisseria m
58	197	41.6	90	1	FETP_PSEBP	Q60aj7 pseudomonas
59	193	40.8	90	1	FETP_METCA	Q60aj7 methylococc
60	188	39.7	90	2	Q4KJT2_PSEBF5	Q4kjt2 pseudomonas
61	184	38.9	87	1	FETP_FRATT	Q5nhj8 francisella
62	167.5	35.4	90	1	FETP_AC1AD	Q6fbf3 acinetobact
63	148	31.3	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	138	29.2	92	2	Q4NMQ4_9DELT	Q4nmq4 anaeromyxob
65	82	17.3	1555	2	Q9U0N0_PLAF7	Q9u0n0 plasmodium
66	81	17.1	2672	1	GCN1_YEAST	P33892 saccharomyc
67	78.5	16.6	502	2	Q4T616_TETNG	Q4t616 tetraodon n
68	77.5	16.4	452	2	Q8F6U1_LEPIN	Q8f6u1 leptospira
69	77.5	16.4	464	2	Q72P14_LEPIC	Q72p14 leptospira
70	77	16.3	2248	2	Q4UB40_THEAN	Q4ub40 theileria a
71	76.5	16.2	511	2	Q98Q71_MYCPU	Q98q71 mycoplasma
72	76	16.1	2249	2	Q4MYU4_THERPA	Q4myu4 theileria p
73	75	15.9	1032	2	Q4XVW2_PLACH	Q4xvw2 plasmodium
74	74	15.6	330	2	Q8XKS4_CLOPR	Q8xks4 clostridium
75	74	15.6	403	2	Q5HIP0_STAAC	Q5hip0 staphylococ

ALIGNMENTS

RESULT 1
FETP_YERPE
ID FETP_YERPE STANDARD; PRT; 90 AA.
AC Q8ZHE7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=YPO0953, Y3340, YP3488;
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Titchball R.W., Holden M.T.G.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltham S., Hamlin N., Holtroyd S., Jagels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.,


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RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC -----
CC EMBL; AJ14145; CAC89796.1; -; Genomic DNA.
DR EMBL; AE013935; AAM86890.1; -; Genomic DNA.
DR EMBL; AE017140; AAS63643.1; -; Genomic DNA.
DR SMR; Q8ZHE7; 1-90.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
KW CONFLICT 16 16 R -> G (in Ref. 3).
SQ SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;

Query Match 100.0%; Score 473; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMMNI 60
DB 1 MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMMNI 60
QY 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
DB 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90

RESULT 2
FETP_YERPS STANDARD; PRT; 90 AA.
AC Q666M3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=YPTB3225;
OS Yersinia pseudotuberculosis.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
ON NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinnebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; BX936398; CAH22463.1; -; Genomic DNA.
DR SMR; Q666M3; 1-90.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10608 MW; C7375B7954752E64 CRC64;

Query Match 98.5%; Score 466; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 3.4e-40;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1 MSRTIFCTFLKDAEQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMMNI 60
QY 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
DB 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90

RESULT 3
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ID FETP_ERWCT
AC Q6D8U9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=ECA0975;
OS Erwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
ON NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:25:19 ; Search time 18.0609 Seconds
(without alignments)
411.985 Million cell updates/sec

Title: US-09-955-502A-37

Perfect score: 473
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued_Patents_AA:*
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2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	400	84.6	107	2	US-09-489-039A-11962
2	389	82.2	93	2	US-09-543-681A-5443
3	221	46.7	122	2	US-09-252-991A-23355
4	176.5	37.3	92	2	US-09-328-352-5456
5	143	30.2	110	2	US-09-540-236-2859
6	69.5	14.7	870	2	US-09-543-681A-4768
7	69	14.6	209	2	US-09-252-991A-20905
8	67.5	14.3	701	2	US-09-252-991A-23288
9	67	14.2	415	1	US-08-602-010A-10
10	67	14.2	415	1	US-08-680-726A-10
11	67	14.2	415	2	US-09-092-409-10
12	65	13.7	411	1	US-07-684-135A-2
13	65	13.7	1559	2	US-09-949-016-10190
14	65	13.7	2101	1	US-08-466-390-4
15	65	13.7	2101	1	US-08-470-950-4
16	65	13.7	2101	1	US-08-467-781-4
17	65	13.7	2101	1	US-08-195-487-4
18	65	13.7	2101	1	US-08-483-924-4
19	65	13.7	2101	2	US-09-452-294-1
20	65	13.7	2101	2	US-09-452-294-1
21	65	13.7	2101	4	PCT-US93-06160-4
22	65	13.7	2107	2	US-09-949-016-7646
23	65	13.7	2107	2	US-09-949-016-7647
24	65	13.7	2107	2	US-09-949-016-7647
25	64.5	13.6	242	2	US-09-296-662-33
26	64	13.5	184	2	US-08-908-332-1
27	64	13.5	534	2	US-09-325-932A-66

28	64	13.5	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
29	63.5	13.4	548	2	US-09-167-299-3	Sequence 3, Appli
30	63	13.3	240	2	US-08-908-332-9	Sequence 9, Appli
31	63	13.3	242	2	US-08-908-332-2	Sequence 2, Appli
32	63	13.3	776	1	US-08-198-446B-17	Sequence 17, Appli
33	63	13.3	776	1	US-08-870-693-17	Sequence 6, Appli
34	63	13.3	821	1	US-08-198-446B-6	Sequence 17, Appli
35	63	13.3	821	1	US-08-870-693-6	Sequence 6, Appli
36	62.5	13.2	217	2	US-09-746-359A-38	Sequence 38, Appli
37	62.5	13.2	259	2	US-09-355-166-21	Sequence 21, Appli
38	62.5	13.2	514	2	US-09-746-359A-39	Sequence 39, Appli
39	62.5	13.2	546	2	US-09-746-359A-37	Sequence 37, Appli
40	62	13.1	375	1	US-08-121-714-2	Sequence 2, Appli
41	62	13.1	375	1	US-08-477-108A-2	Sequence 2, Appli
42	62	13.1	375	1	US-08-477-112-2	Sequence 2, Appli
43	62	13.1	375	2	US-09-886-319A-4	Sequence 4, Appli
44	62	13.1	375	4	PCT-US93-08322-2	Sequence 2, Appli
45	61.5	13.0	329	2	US-09-602-787A-306	Sequence 306, App
46	61.5	13.0	459	2	US-09-602-787A-302	Sequence 302, App
47	61	12.9	550	2	US-09-107-532A-7201	Sequence 7201, Ap
48	61	12.9	920	2	US-09-934-868-52	Sequence 52, Appli
49	61	12.9	920	2	US-10-701-200-52	Sequence 52, Appli
50	61	12.9	922	2	US-10-104-047-2694	Sequence 2694, Ap
51	61	12.9	1575	2	US-09-917-254-83	Sequence 83, Appli
52	61	12.9	1575	2	US-09-949-016-6743	Sequence 6743, Ap
53	60.5	12.8	302	2	US-09-830-433A-34	Sequence 34, Appli
54	60	12.7	192	2	US-08-545-573A-9	Sequence 9, Appli
55	60	12.7	306	2	US-09-538-092-262	Sequence 262, App
56	60	12.7	556	2	US-10-012-896-1005	Sequence 1005, Ap
57	60	12.7	571	2	US-10-104-047-3814	Sequence 3814, Ap
58	60	12.7	837	2	US-10-012-231A-253	Sequence 253, App
59	60	12.7	837	2	US-10-015-389A-253	Sequence 253, App
60	60	12.7	837	2	US-10-006-768A-253	Sequence 253, App
61	60	12.7	837	2	US-10-015-671A-253	Sequence 253, App
62	60	12.7	837	2	US-10-011-833A-253	Sequence 253, App
63	60	12.7	837	2	US-10-012-064A-253	Sequence 253, App
64	60	12.7	837	2	US-10-012-064A-253	Sequence 253, App
65	60	12.7	837	2	US-10-012-064A-253	Sequence 253, App
66	59.5	12.6	308	2	US-09-248-796A-14928	Sequence 14928, A
67	59.5	12.6	310	2	US-09-489-039A-13674	Sequence 13674, A
68	59.5	12.6	532	1	US-08-657-192-9	Sequence 9, Appli
69	59.5	12.6	532	2	US-08-523-373-7	Sequence 7, Appli
70	59.5	12.6	604	2	US-09-248-796A-14489	Sequence 14489, A
71	59.5	12.6	796	2	US-08-868-699A-2	Sequence 2, Appli
72	59.5	12.6	796	2	US-09-757-014-2	Sequence 2, Appli
73	59	12.5	217	2	US-09-543-681A-7862	Sequence 7862, Ap
74	59	12.5	228	2	US-09-328-352-5001	Sequence 5001, Ap
75	59	12.5	281	2	US-09-949-016-8397	Sequence 8397, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 84.6%; Score 400; DB 2; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.4e-44;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMMNI 60
17 MSRTIFCTFLQREADGQDFQLYPGEIGKRIYNEISKEAWAQWQHQTMLINEKLSMMNP 76

DB 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
77 EHRKLEQEMVOFLFEGKDVHIEGYTPPEK 106

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128, 706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 82.2%; Score 389; DB 2; Length 93;
Best Local Similarity 80.0%; Pred. No. 3.3e-43;
Matches 72; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

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4 MSRTIFCTFLNKEADGLDFQLYPGEIGKRIYNEISKEAWGQWMAKQTMLINEKLSMMNP 63

DB 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
64 DDRKLEQEMVRFLEGGHVDHIDGYTPPEK 93

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 46.7%; Score 221; DB 2; Length 122;
Best Local Similarity 51.1%; Pred. No. 4.8e-21;
Matches 46; Conservative 13; Mismatches 29; Indels 2; Gaps 2;

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DB 33 MSRTVMCKRYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQHQTMLINERLNMMNA 92

QY 61 EDRKLEQEMVNFLEGGQDVHIA-GYTPPS 89
93 EDRKFLQEMDKFL-SGEDYAKADGYVPPS 121

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328, 352
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 37.3%; Score 176.5; DB 2; Length 92;
Best Local Similarity 38.6%; Pred. No. 2.2e-15;
Matches 34; Conservative 18; Mismatches 35; Indels 1; Gaps 1;

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4 MSROVFCRKYQKEMEGLDPAFPGAKGQEFENVSQAWQEWLQHQTMLINEKRLNVFEP 63

DB 61 EDRKLEQEMVNFLEGGQDVHIA-GYTP 87
64 EAKKFLBQREKFFNNDSEVEKAEGWKP 91

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540, 236
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M. catarrhalis
US-09-540-236-2859

Query Match 30.2%; Score 143; DB 2; Length 110;
Best Local Similarity 36.1%; Pred. No. 6.9e-11;
Matches 30; Conservative 17; Mismatches 36; Indels 0; Gaps 0;

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DB 65 LLEQEMVNFLEGGQDVHIAGYTP 87
85 YLNEQREKFLDNGDYEKPAGYKP 107

RESULT 6
US-09-543-681A-4768
; Sequence 4768, Application US/09543681A

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502A-37

Perfect score: 473
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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

Published Applications_AA_Main: *
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep: *
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep: *
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep: *
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep: *
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep: *
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	473	100.0	90	3	US-09-955-502-20
2	396	83.7	91	3	US-09-955-502-11
3	396	83.7	91	3	US-09-955-502-12
4	396	83.7	91	3	US-09-955-502-13
5	393	83.1	91	3	US-09-955-502-14
6	393	83.1	91	3	US-09-955-502-16
7	393	83.1	91	3	US-09-955-502-17
8	389	82.2	88	3	US-09-955-502-15
9	379	80.1	91	3	US-09-955-502-18
10	366	77.4	90	3	US-09-955-502-10
11	363	76.7	87	3	US-09-955-502-7
12	357	75.5	91	3	US-09-955-502-5
13	351	74.2	87	3	US-09-955-502-8
14	346	73.2	87	3	US-09-955-502-6
15	342	72.3	78	3	US-09-955-502-19
16	308	65.1	88	3	US-09-955-502-9
17	256	54.1	76	3	US-09-955-502-21
18	233	49.3	88	3	US-09-955-502-33
19	226	47.8	87	3	US-09-955-502-2
20	226	47.8	87	3	US-09-955-502-2
21	212	44.8	86	3	US-09-955-502-4
22	210	44.4	87	3	US-09-955-502-25
23	206	43.6	90	3	US-09-955-502-23
24	203	42.9	89	3	US-09-955-502-22
25	199	42.1	87	3	US-09-955-502-29
26	199	42.1	87	3	US-09-955-502-30
27	198	41.9	88	3	US-09-955-502-26

28	198	41.9	88	3	US-09-955-502-27	Sequence 27, Appl
29	198	41.9	88	3	US-09-955-502-28	Sequence 28, Appl
30	188	39.7	87	3	US-09-955-502-24	Sequence 24, Appl
31	186	39.3	87	3	US-09-955-502-31	Sequence 31, Appl
32	186	39.3	87	3	US-09-955-502-32	Sequence 32, Appl
33	81	17.1	102	3	US-09-864-408A-768	Sequence 768, App
34	74	15.6	397	4	US-10-276-774-1577	Sequence 1577, Ap
35	74	15.6	506	4	US-10-343-663A-26	Sequence 26, Appl
36	74	15.6	576	5	US-10-450-763-50273	Sequence 50273, A
37	74	15.6	589	4	US-10-297-880-1	Sequence 1, Appli
38	74	15.6	770	4	US-10-343-663A-68	Sequence 68, Appl
39	74	15.6	1116	3	US-09-790-318-2	Sequence 2, Appli
40	74	15.6	1116	4	US-10-112-944-323	Sequence 27, Appl
41	74	15.6	1116	4	US-10-343-663A-27	Sequence 780, App
42	73	15.4	397	4	US-10-112-944-780	Sequence 34179, A
43	70.5	14.9	635	6	US-11-097-143-34179	Sequence 52, Appl
44	70	14.8	184	4	US-10-393-840-52	Sequence 104086,
45	69.5	14.7	600	4	US-10-437-963-104086	Sequence 69006, A
46	69.5	14.7	867	4	US-10-282-122A-69006	Sequence 34556, A
47	69.5	14.7	1589	5	US-10-450-763-34556	Sequence 39257, A
48	69.5	14.7	1589	5	US-10-450-763-39257	Sequence 52962, A
49	69.5	14.7	1589	5	US-10-450-763-52962	Sequence 58863, A
50	69.5	14.7	1589	5	US-10-450-763-58863	Sequence 60458, A
51	69.5	14.7	1589	5	US-10-450-763-60458	Sequence 53103, A
52	68	14.4	256	4	US-10-282-122A-53103	Sequence 35, Appl
53	68	14.4	344	3	US-09-820-843A-35	Sequence 10, Appl
54	67	14.2	415	4	US-10-156-275-10	Sequence 189166,
55	67	14.2	1261	4	US-10-437-963-189166	Sequence 35150, A
56	66.5	14.1	184	5	US-10-450-763-35150	Sequence 10247, A
57	66.5	14.1	758	4	US-10-369-493-10247	Sequence 12814, A
58	66.5	14.1	1317	5	US-10-732-923-12814	Sequence 239277,
59	66	14.0	268	4	US-10-424-599-239277	Sequence 30849, A
60	66	14.0	582	5	US-10-450-763-30849	Sequence 147933,
61	66	14.0	1006	4	US-10-437-963-147933	Sequence 7224, Ap
62	65	13.7	842	4	US-10-032-585-7224	Sequence 1548, Ap
63	65	13.7	1575	5	US-10-741-600-1548	Sequence 1549, Ap
64	65	13.7	1575	5	US-10-741-600-1549	Sequence 1550, Ap
65	65	13.7	1640	5	US-10-741-600-1550	Sequence 32, Appl
66	65	13.7	2101	5	US-10-977-955-32	Sequence 18, Appl
67	65	13.7	2101	5	US-10-723-681-18	Sequence 33, Appl
68	65	13.7	2115	5	US-10-977-955-33	Sequence 5050, Ap
69	64.5	13.6	242	5	US-10-756-149-5050	Sequence 189628,
70	64.5	13.6	553	4	US-10-437-963-189628	Sequence 66, Appl
71	64	13.5	184	4	US-10-219-220-66	Sequence 118, App
72	64	13.5	184	4	US-10-393-840-118	Sequence 5, Appli
73	64	13.5	534	3	US-09-312-762A-5	Sequence 43781, A
74	64	13.5	681	4	US-10-767-701-43781	Sequence 22170, A
75	63	13.3	470	6	US-11-097-143-22170	

ALIGNMENTS

RESULT 1
US-09-955-502-20
; Sequence 20, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 20
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Yersinia pestis

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 73.8041 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-23
Perfect score: 485
Sequence: 1 MTRRTVMCRKYKEELPGLERA.....DKFLSGBEYVAQEGYVPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	100.0	90	5	ABB78168
2	432	89.1	87	5	ABB78169
3	415	85.6	122	7	ABO74609
4	408	84.1	87	5	ABB78170
5	253.5	52.3	92	6	ADA34169
6	239	49.3	91	5	ABB78150
7	234	48.2	89	9	AEB41576
8	234	48.2	95	9	AEB38294
9	230	47.4	87	5	ABB78152
10	228	47.0	88	5	ABB78154
11	228	47.0	90	5	ABB78155
12	228	47.0	93	7	ADF05158
13	228	47.0	107	7	ABO65445
14	227	46.8	91	5	ABB78158
15	227	46.8	91	5	ABB78157
16	227	46.8	91	5	ABB78156
17	226	46.6	87	5	ABB78177
18	224	46.2	87	5	ABB78151
19	222	45.8	91	5	ABB78161
20	222	45.8	91	5	ABB78159
21	222	45.8	91	5	ABB78162
22	221	45.6	87	5	ABB78153
23	219	45.2	87	5	ABB78176
24	218	44.9	87	5	ABB78148

25	218	44.9	87	5	ABB78147	Abb78147 Amino aci
26	216	44.5	88	5	ABB78160	Abb78160 Amino aci
27	215	44.3	88	5	ABB78178	Abb78178 Amino aci
28	212	43.7	91	5	ABB78163	Abb78163 Amino aci
29	208	42.9	87	5	ABB78175	Abb78175 Amino aci
30	207	42.7	110	8	ADL05173	Adl05173 M. catarr
31	206	42.5	90	5	ABB78165	Abb78165 Amino aci
32	202	41.6	87	5	ABB78174	Abb78174 Amino aci
33	200.5	41.3	86	5	ABB78149	Abb78149 Amino aci
34	198	40.8	88	5	ABB78171	Abb78171 Amino aci
35	198	40.8	88	5	ABB78172	Abb78172 Amino aci
36	198	40.8	88	5	ABB78173	Abb78173 Amino aci
37	198	40.8	88	5	ABB77219	Abp77219 N. gonorr
38	195	40.2	78	5	ABB78164	Abb78164 Amino aci
39	190.5	39.3	90	5	ABB78167	Abb78167 Amino aci
40	165	34.0	76	5	ABB78166	Abb78166 Amino aci
41	72	14.8	97	5	ABG70345	Abg70345 Novel hum
42	70.5	14.5	1091	5	ABB48258	Abb48258 Listeria
43	69	14.2	468	2	AAV41734	Aay41734 Human PRO
44	69	14.2	468	3	AAB33436	Aab33436 Human PRO
45	69	14.2	468	3	AAV87339	Aay87339 Human sig
46	69	14.2	468	3	AAAB44290	Aab44290 Human PRO
47	69	14.2	468	3	AAAB24418	Aab24418 Human PRO
48	69	14.2	468	3	AAAB23628	Aab23628 Human sec
49	69	14.2	468	4	AAAB80398	Aab80398 Secreted
50	69	14.2	468	4	AAAB64998	Aab64998 Human sec
51	69	14.2	468	5	ABBB4866	Abb4866 Human PRO
52	69	14.2	468	5	ABG65287	Abg65287 Human alb
53	69	14.2	468	5	ABP65092	Abp65092 Hypoxia-i
54	69	14.2	468	5	ABB95472	Abb95472 Human ang
55	69	14.2	468	6	ABO25236	Abu25236 Novel hum
56	69	14.2	468	6	ABU72242	Abu72242 Novel hum
57	69	14.2	468	6	ABU84922	Abu84922 Human sec
58	69	14.2	468	6	ABU61120	Abu61120 Human PRO
59	69	14.2	468	6	ABU80389	Abu80389 Human sec
60	69	14.2	468	6	ADA24876	Ada24876 Novel hum
61	69	14.2	468	6	ABO19691	Abol19691 Novel hum
62	69	14.2	468	6	ADA12537	Ada12537 Human sec
63	69	14.2	468	6	ABO19582	Abol19582 Novel hum
64	69	14.2	468	7	ADB73843	Adb73843 Human PRO
65	69	14.2	468	7	ADB76559	Adb76559 Human PRO
66	69	14.2	468	7	ADC43985	Adc43985 Human sec
67	69	14.2	468	7	ADC61745	Adc61745 Human sec
68	69	14.2	468	7	ADC63709	Adc63709 Human sec
69	69	14.2	468	7	ADC66809	Adc66809 Human sec
70	69	14.2	468	7	ADC68933	Adc68933 Human sec
71	69	14.2	468	7	ADC62993	Adc62993 Human sec
72	69	14.2	468	7	ADC68058	Adc68058 Human sec
73	69	14.2	468	7	ADC41378	Adc41378 Human sec
74	69	14.2	468	7	ADC67433	Adc67433 Human sec
75	69	14.2	468	7	ADC62369	Adc62369 Human sec

ALIGNMENTS

RESULT 1
ABB78168 standard; protein; 90 AA.
XX ABB78168;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YgX homologue.
XX
KW Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YgX homologue.
OS Pseudomonas syringae.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
XX 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 485; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.2e-53;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTRVTWCRKYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTLLINERRLNMMNA 60
|||
1 MTRVTWCRKYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTLLINERRLNMMNA 60

Db 61 EDRKFLQTEMDFKLSGEEYVAQAEGYVPEK 90
|||
61 EDRKFLQTEMDFKLSGEEYVAQAEGYVPEK 90

RESULT 2
ABB78169
ID ABB78169 standard; protein; 87 AA.
XX
XX ABB78169;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE
XX
KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS *Pseudomonas putida*.
XX
XX US2002072118-A1.
PN
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX
PS Example; Fig 1A; 16pp; English.
XX
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 89.1%; Score 432; DB 5; Length 87;
Best Local Similarity 88.5%; Pred. No. 6.8e-47;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

QY 1 MTRVTWCRKYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTLLINERRLNMMNA 60
|||
1 MTRVTWCRKYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTLLINERRLNMMNA 60

Db 61 EDRKFLQTEMDFKLSGEEYVAQAEGYVP 87
|||
61 EDRKFLQAEEMDKFPAGEEYVAQAEGYVP 87

RESULT 3
ABO74609
ID ABO74609 standard; protein; 122 AA.
XX
XX ABO74609;
AC
XX
DT 29-JUL-2004 (first entry)
XX
XX *Pseudomonas aeruginosa* polypeptide #6784.
DE
XX
KW Bacterial infection; *Pseudomonas aeruginosa* infection; antibacterial.
XX
XX *Pseudomonas aeruginosa*.
OS
XX
XX US6551795-B1.
PN
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
XX 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
XX WPI; 2003-615309/58.
DR N-PSDB; ABD08180.
XX
XX
PT Novel isolated nucleic acid encoding *Pseudomonas aeruginosa* polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 23355; 455pp; English.
XX
XX The invention relates to *Pseudomonas aeruginosa* polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.84055 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-23
Perfect score: 485
Sequence: 1 MTRITVMCRKYKEELPGLERA.....DKFLSGERYAQAEGVPPK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	415	85.6	90	2	H83003	conserved hypotnet
2	237	48.9	90	2	C64013	hypothetical prote
3	228	47.0	90	2	C82320	conserved hypotnet
4	227	46.8	91	2	A85954	hypothetical prote
5	227	46.8	91	2	A65082	hypothetical prote
6	227	46.8	91	2	F91108	hypothetical prote
7	222	45.8	91	2	AH0879	conserved hypotnet
8	206	42.5	90	2	AI0116	conserved hypotnet
9	200	41.2	105	2	C82624	conserved hypotnet
10	198	40.8	88	2	H81014	conserved hypotnet
11	165	34.0	93	2	E84994	hypothetical prote
12	70.5	14.5	1091	2	AF1380	glycosidase homolo
13	69.5	14.3	1090	2	AG1749	glycosidase homolo
14	67.5	13.9	297	2	T47857	myb protein-like -
15	67.5	13.9	421	2	A83039	conserved hypotnet
16	67.5	13.9	508	2	S74848	neopululanase - S
17	67	13.8	670	2	T29898	kinasin protein OS
18	66.5	13.7	1083	1	S53048	alpha-mannosidase
19	66.5	13.7	1121	2	I38127	phosphoprotein pho
20	65.5	13.5	767	2	T31558	hypothetical prote
21	65.5	13.5	879	2	PC1225	protein-tyrosine k
22	65.5	13.5	1308	2	T05178	hypothetical prote
23	65	13.4	165	2	C75419	hypothetical prote
24	64.5	13.3	181	2	E97341	rubrerythrin [limpo
25	64.5	13.3	181	2	F97341	rubrerythrin [limpo
26	64.5	13.3	2131	2	S01446	hypothetical prote
27	64	13.2	205	2	D71440	GTP-binding protei
28	64	13.2	559	2	AB2202	hypothetical prote
29	64	13.2	909	2	AC2365	hypothetical prote

30	64	13.2	3430	1	GNWVWV	genome polypeptide
31	64	13.2	4717	2	T41581	hypothetical coile
32	63.5	13.1	284	2	D82486	probable lipase ac
33	63.5	13.1	388	1	QOYV	transforming prote
34	63.5	13.1	419	2	AB1340	maltose/maltodextr
35	63.5	13.1	419	2	ACT1711	hypothetical prote
36	63.5	13.1	959	2	H69344	hypothetical prote
37	63	13.0	435	2	D82905	hypothetical prote
38	63	13.0	643	2	S55610	polyprotein - equi
39	63	13.0	995	2	A84014	SNF2 helicase BH29
40	62.5	12.9	458	2	F84275	hypothetical prote
41	62.5	12.9	559	2	H82532	conserved hypotnet
42	62.5	12.9	585	1	F64159	hypothetical prote
43	62.5	12.9	887	2	B96598	hypothetical prote
44	62.5	12.9	985	2	S15965	hypothetical prote
45	62	12.8	1104	2	T01811	hypothetical prote
46	61.5	12.7	382	2	JC5531	c-Jun amino-termi
47	61.5	12.7	465	2	T41830	LEF-4 orf90 - Bomb
48	61.5	12.7	470	2	D84614	hypothetical prote
49	61.5	12.7	505	2	I37206	protein-tyrosine k
50	61.5	12.7	773	2	G86856	hypothetical prote
51	61	12.6	150	2	F90212	hypothetical prote
52	61	12.6	211	2	S71559	GTP-binding protei
53	61	12.6	297	2	AE0400	probable membrane
54	61	12.6	298	2	B98066	primosome componen
55	61	12.6	774	2	T14555	DNA polymerase hom
56	61	12.6	796	1	JV0107	glucose dehydrogen
57	61	12.6	796	2	H85495	glucose dehydrogen
58	61	12.6	796	2	H90644	glucose dehydrogen
59	61	12.6	1486	2	E85618	hypothetical prote
60	61	12.6	1486	2	G90754	hypothetical prote
61	61	12.6	1486	2	C64832	kinasin-like cell
62	61	12.6	4540	2	T30838	cell division prot
63	60.5	12.5	288	2	T45715	cytoplasmic dynein
64	60.5	12.5	339	2	AG2041	hypothetical prote
65	60.5	12.5	713	2	B84583	queuine tRNA-ribos
66	60.5	12.5	985	2	T10339	hypothetical prote
67	60.5	12.5	1047	2	T16203	DNA-directed DNA p
68	60.5	12.5	1128	1	QOBB47	hypothetical prote
69	60	12.4	133	2	A72229	DNA-binding protei
70	60	12.4	177	2	D70862	hypothetical prote
71	60	12.4	245	2	S49045	luxp protein - Vib
72	60	12.4	276	2	H81931	probable bis(5'-nu
73	60	12.4	295	2	G64407	heterodisulfide re
74	60	12.4	437	2	C96840	hypothetical prote
75	60	12.4	651	2	AI3294	cell division prot

ALIGNMENTS

RESULT 1
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C/Accession: H83003
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; Llm,
.i. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathc
A/Reference number: A82950; MUID:20437337; PMID:10984043
A/Accession: H83003
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: UNIPARC:UPI00000C5F26; GB:AB004927; GB:AB004091; NID:g9951437; PIDN:
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5148
C/Superfamily: fe(II) trafficking protein YggX

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 66.4237 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-23
Perfect score: 485
Sequence: 1 MTRVTMCRKYKEELPGLERA.....DKFLSGEERYAQAEQYVPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	485	100.0	90	1 FETP_PSESM	Q87uf5 pseudomonas
2	485	100.0	90	2 Q4ZLF3_PSESY	Q4zlp3 pseudomonas
3	439	90.5	90	1 FETP_PSEPK	Q88r49 pseudomonas
4	425	87.6	90	2 Q4KJt2_PSEF5	Q4kjt2 pseudomonas
5	419	86.4	90	2 Q6T7F6_PSEFL	Q6t7f6 pseudomonas
6	415	85.6	90	1 FETP_PSEAB	Q9hu36 pseudomonas
7	410	84.5	90	2 Q4J2Z8_AZOV1	Q4j2z8 azotobacter
8	264	54.4	90	1 FETP_IDILO	Q5qy58 idiomarina
9	253.5	52.3	90	1 FETP_ACTAD	Q6fjb3 acinetobact
10	244	50.3	90	1 FETP_PHOPR	Q6lmk7 photobacter
11	237	48.9	90	1 FETP_HABIN	P44048 haemophilus
12	237	48.9	90	1 FETP_VIBPA	Q87ll5 vibrio para
13	237	48.9	90	2 Q4QMD9_HAB18	Q4qmd9 haemophilus
14	236	48.7	90	1 FETP_VIBVU	Q8dcs5 vibrio vuln
15	236	48.7	90	1 FETP_VIBVY	Q7mh14 vibrio vuln
16	235	48.5	90	1 FETP_PHOHL	Q5x3x9 legionella
17	234	48.2	89	1 FETP_LEGPA	Q5zu80 legionella
18	234	48.2	89	1 FETP_LEGPH	Q5wvc4 legionella
19	233	48.0	89	1 FETP_LEGPL	Q60aj7 methylococc
20	233	48.0	90	1 FETP_METCA	Q65vt7 manheimia
21	233	48.0	90	1 FETP_PASMS	Q9clb9 pasteurella
22	231	47.6	90	1 FETP_PASMU	Q82xf2 nitrosomona
23	229	47.2	90	1 FETP_NITEU	Q9kura2 vibrio chol
24	228	47.0	90	1 FETP_VIBCH	Q5e7t0 vibrio fisc
25	228	47.0	92	1 FETP_SHRON	Q8ebx6 shewanella
26	228	47.0	96	2 Q4FVJ7_9GAMM	Q4fvj7 psychrobact
27	228	47.0	90	1 FETP_SHOBR	Q7wh06 bordetella
28	225	46.4	90	1 FETP_BORBP	Q7w9q2 bordetella
29	225	46.4	90	1 FETP_BORPE	Q7wvc4 bordetella
30	225	46.4	90	1 FETP_BORPE	Q6d8j9 erwina car
31	224	46.2	90	1 FETP_ERWCT	

32	222	45.8	90	1 FETP_ECOS7	P0a8p4 escherichia
33	222	45.8	90	1 FETP_ECOLI	P0a8p3 escherichia
34	222	45.8	90	1 FETP_SHIFL	P0a8p5 shigella fl
35	222	45.8	91	1 FETP_RALSO	Q8y010 ralstonia s
36	221	45.6	94	1 FETP_HABDU	Q7vkb6 haemophilus
37	218	44.9	90	1 FETP_ECOL6	Q8fel9 escherichia
38	217	44.7	90	1 FETP_SALCH	Q57k04 salmonella
39	217	44.7	90	1 FETP_SALPA	Q5pmmi salmonella
40	217	44.7	90	1 FETP_SALTI	P67617 salmonella
41	217	44.7	90	1 FETP_SALTY	P67617 salmonella
42	215	44.3	90	1 FETP_COXBU	Q83d06 coxiella bu
43	215	44.3	91	1 FETP_BURMA	Q62iu9 burkholderi
44	215	44.3	91	1 FETP_BURPS	Q63sj4 burkholderi
45	214	44.1	90	1 FETP_YERPS	Q66m3 yersinia ps
46	211	43.5	92	1 FETP_XANOR	Q59y22 xanthomonas
47	209	43.1	91	2 Q4LSI9_9BURK	Q4ls19 burkholderi
48	206	42.5	90	1 FETP_YERPE	Q8zhe7 yersinia pe
49	204	42.1	90	1 FETP_XYLFY	Q87d06 xylella fas
50	202	41.6	91	1 FETP_XANAC	Q8pjh7 xanthomonas
51	200	41.2	90	1 FETP_XYLPY	Q9pc73 xylella fas
52	198	40.8	88	1 FETP_NEIGI	Q5f553 neisseria g
53	198	40.8	88	1 FETP_NEIMA	P67615 neisseria m
54	198	40.8	88	1 FETP_NEIMB	P67616 neisseria m
55	198	40.8	92	1 FETP_XANCP	Q8p829 xanthomonas
56	198	40.8	92	2 Q4UW14_XANCP	Q4uw14 xanthomonas
57	195	40.2	90	1 FETP_CHRVO	Q7nsr4 chromobacte
58	189	39.0	78	1 FETP_WIGBR	Q8d3c5 wigleswort
59	189	39.0	87	1 FETP_FRATT	Q5nhj8 francisella
60	179	36.9	79	1 FETP_CANBF	Q7vrg9 candidatus
61	175	36.1	78	1 FETP_BUCAP	Q8k925 buchnera ap
62	170	35.1	87	1 FETP_BUCBP	Q89a44 buchnera ap
63	165	34.0	77	1 FETP_BUCAT	P57618 buchnera ap
64	165	34.0	92	2 Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	74.5	15.4	406	2 Q5B5X5_EMENT	Q5b5x5 aspergillus
66	74.5	15.4	603	2 Q6BPW5_ORYSA	Q6epw5 oryza sativ
67	73.5	15.2	456	2 Q93D60_ECOLI	Q93d60 escherichia
68	73.5	15.2	614	2 Q4I5C8_GIBZE	Q4isc8 gibberella
69	73	15.1	703	2 Q4WPT2_ASPPU	Q4wpt2 aspergillus
70	73	15.1	1328	2 Q8IDY9_PLAF7	Q8idy9 plasmodium
71	71.5	14.7	326	2 Q55GT4_DICDI	Q55gt4 dictyosteli
72	71.5	14.7	950	2 Q6BU74_DEBHA	Q6bu74 debaryomyce
73	70.5	14.5	303	2 Q8KL27_RHIFT	Q8kl27 rhizobium e
74	70.5	14.5	327	2 Q54X22_DICDI	Q54x22 dictyosteli
75	70.5	14.5	502	2 Q5AUL5_EMENT	Q5aul5 aspergillus

ALIGNMENTS

RESULT 1
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ID FETP_PSESM STANDARD; PRT; 90 AA.
AC Q87UF5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocuNames=PSPT05343;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouiri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Uterback T.R., Van Aken S.B., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Carlinhour S., Chatterjee A.K.,

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 18.246 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-23

Perfect score: 485
Sequence: 1 MTRVTMCRKYKEELPGERRA.....DKPLSGEEVYAQAGYVPPEK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	415	85.6	122	2	US-09-252-991A-23355 Sequence 23355, A
2	253.5	52.3	92	2	US-09-328-352-5456 Sequence 5456, Ap
3	228	47.0	93	2	US-09-543-681A-5443 Sequence 5443, Ap
4	228	47.0	107	2	US-09-489-039A-11962 Sequence 11962, A
5	207	42.7	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	69	14.2	468	2	US-09-976-594-462 Sequence 462, App
7	69	14.2	468	2	US-09-999-833A-337 Sequence 337, App
8	69	14.2	468	2	US-10-020-445A-337 Sequence 337, App
9	69	14.2	588	2	US-09-902-540-13586 Sequence 13586, A
10	67.5	13.9	502	2	US-09-252-991A-26986 Sequence 26986, A
11	66.5	13.7	1122	2	US-10-146-704-2 Sequence 2, Appli
12	66	13.6	148	2	US-09-673-395A-389 Sequence 389, App
13	66	13.6	381	2	US-10-104-047-3313 Sequence 3313, Ap
14	66	13.6	401	2	US-09-489-847-202 Sequence 202, App
15	66	13.6	401	2	US-10-012-231A-100 Sequence 100, App
16	66	13.6	401	2	US-10-015-389A-100 Sequence 100, App
17	66	13.6	401	2	US-10-006-768A-100 Sequence 100, App
18	66	13.6	401	2	US-10-015-671A-100 Sequence 100, App
19	66	13.6	401	2	US-10-015-393A-100 Sequence 100, App
20	66	13.6	401	2	US-10-011-833A-100 Sequence 100, App
21	66	13.6	401	2	US-10-006-041A-100 Sequence 100, App
22	66	13.6	401	2	US-10-012-064A-100 Sequence 100, App
23	66	13.6	401	2	US-10-030-269A-8 Sequence 8, Appli
24	66	13.6	422	2	US-09-489-847-357 Sequence 357, App
25	65	13.4	451	2	US-09-543-681A-7401 Sequence 7401, Ap
26	65	13.4	582	2	US-09-902-540-11161 Sequence 11161, A
27	64.5	13.3	600	2	US-10-104-047-3845 Sequence 3845, Ap

28	64	13.2	314	2	US-09-716-865-4	Sequence 4, Appli
29	64	13.2	443	2	US-09-248-796A-16816	Sequence 16816, A
30	63.5	13.1	305	2	US-09-902-540-12811	Sequence 12811, A
31	63	13.0	551	2	US-09-138-172-2	Sequence 2, Appli
32	62.5	12.9	284	2	US-09-934-899-14	Sequence 14, Appli
33	62.5	12.9	284	2	US-09-934-868-34	Sequence 34, Appli
34	62.5	12.9	284	2	US-10-701-200-34	Sequence 34, Appli
35	62.5	12.9	375	2	US-09-583-110-4950	Sequence 4950, Ap
36	62.5	12.9	382	2	US-09-107-433-3837	Sequence 3837, Ap
37	62	12.8	420	2	US-09-248-796A-15323	Sequence 15323, A
38	62	12.8	1042	2	US-09-792-024-106	Sequence 106, App
39	61.5	12.7	271	1	US-08-664-596B-11	Sequence 11, Appli
40	61.5	12.7	454	2	US-09-771-161A-95	Sequence 95, Appli
41	61.5	12.7	469	2	US-09-131-750-29	Sequence 29, Appli
42	61.5	12.7	477	2	US-09-949-016-10716	Sequence 10716, A
43	61.5	12.7	504	2	US-09-538-092-1170	Sequence 1170, Ap
44	61.5	12.7	505	2	US-09-949-016-6117	Sequence 6117, Ap
45	61.5	12.7	505	2	US-09-771-161A-186	Sequence 186, App
46	61.5	12.7	506	1	US-08-849-480A-5	Sequence 5, Appli
47	61.5	12.7	513	2	US-09-949-016-11517	Sequence 11517, A
48	61	12.6	263	2	US-09-248-796A-17596	Sequence 17596, A
49	61	12.6	298	2	US-09-583-110-3140	Sequence 3140, Ap
50	61	12.6	298	2	US-09-107-433-4965	Sequence 4965, Ap
51	61	12.6	553	2	US-09-134-000C-4071	Sequence 4071, Ap
52	61	12.6	671	2	US-09-248-796A-17595	Sequence 17595, A
53	60.5	12.5	464	2	US-09-724-864-40	Sequence 40, Appli
54	60.5	12.5	464	2	US-09-823-038A-47	Sequence 47, Appli
55	60.5	12.5	536	2	US-09-594-506-32	Sequence 32, Appli
56	60	12.4	163	2	US-09-270-767-33714	Sequence 33714, A
57	60	12.4	217	2	US-09-543-681A-7862	Sequence 7862, Ap
58	60	12.4	342	2	US-10-227-327-1	Sequence 1, Appli
59	60	12.4	499	2	US-09-561-763-2	Sequence 2, Appli
60	60	12.4	499	2	US-09-431-367B-2	Sequence 2, Appli
61	60	12.4	1244	2	US-09-543-681A-6274	Sequence 6274, Ap
62	59.5	12.3	247	2	US-09-489-039A-13121	Sequence 13121, A
63	59	12.2	212	1	US-08-531-525-18	Sequence 18, Appli
64	59	12.2	212	1	US-08-718-270A-18	Sequence 18, Appli
65	59	12.2	212	2	US-09-399-913-67	Sequence 67, Appli
66	59	12.2	212	2	US-09-350-614-67	Sequence 67, Appli
67	59	12.2	216	2	US-09-949-016-10750	Sequence 10750, A
68	59	12.2	317	2	US-09-107-532A-4653	Sequence 4653, Ap
69	59	12.2	1487	2	US-09-489-039A-12113	Sequence 12113, A
70	58.5	12.1	257	2	US-09-949-002-491	Sequence 491, App
71	58.5	12.1	282	2	US-10-000-489-28	Sequence 28, Appli
72	58.5	12.1	312	1	US-08-525-505A-4	Sequence 4, Appli
73	58.5	12.1	312	2	US-09-976-594-1009	Sequence 1009, Ap
74	58.5	12.1	312	2	US-09-949-002-367	Sequence 367, App
75	58.5	12.1	382	2	US-09-025-580-29	Sequence 29, Appli

ALIGNMENTS

RESULT 1

US-09-252-991A-23355

Sequence 23355, Application US/09252991A

Patent No. 6551795

GENERAL INFORMATION:

APPLICANT: Marc J. Rubenfield et al.

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,788

PRIOR FILING DATE: 1998-02-18

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

SEQ ID NO 23355

LENGTH: 122

TYPE: PRT

ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 56.7882 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-23

Perfect score: 485

Sequence: 1 MTRVTVMCRKYKEELPGLERA.....DKFLGSEHYAQAEGYVPEK 90

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : Published Applications AA Main:*

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3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	100.0	90	3	US-09-955-502-23
2	432	89.1	87	3	US-09-955-502-24
3	408	84.1	87	3	US-09-955-502-25
4	239	49.3	91	3	US-09-955-502-5
5	230	47.4	87	3	US-09-955-502-7
6	228	47.0	88	3	US-09-955-502-9
7	228	47.0	90	3	US-09-955-502-10
8	227	46.8	91	3	US-09-955-502-11
9	227	46.8	91	3	US-09-955-502-12
10	227	46.8	91	3	US-09-955-502-13
11	226	46.6	87	3	US-09-955-502-32
12	224	46.2	87	3	US-09-955-502-6
13	222	45.8	91	3	US-09-955-502-14
14	222	45.8	91	3	US-09-955-502-16
15	222	45.8	91	3	US-09-955-502-17
16	221	45.6	87	3	US-09-955-502-8
17	219	45.2	87	3	US-09-955-502-31
18	218	44.9	87	3	US-09-955-502-2
19	218	44.9	87	3	US-09-955-502-3
20	216	44.5	88	3	US-09-955-502-15
21	215	44.3	88	3	US-09-955-502-33
22	212	43.7	91	3	US-09-955-502-18
23	208	42.9	87	3	US-09-955-502-29
24	208	42.9	87	3	US-09-955-502-30
25	206	42.5	90	3	US-09-955-502-20
26	200.5	41.3	86	3	US-09-955-502-4
27	200	41.2	89	3	US-09-955-502-22

28	198	40.8	88	3	US-09-955-502-26	Sequence 26, Appl
29	198	40.8	88	3	US-09-955-502-27	Sequence 27, Appl
30	198	40.8	88	3	US-09-955-502-28	Sequence 28, Appl
31	195	40.2	78	3	US-09-955-502-19	Sequence 19, Appl
32	165	34.0	76	3	US-09-955-502-21	Sequence 21, Appl
33	74.5	15.4	596	4	US-10-437-963-130475	Sequence 130475,
34	72	14.8	97	3	US-09-778-927A-45	Sequence 45, Appl
35	69.5	14.3	902	4	US-10-437-963-156143	Sequence 156143,
36	69	14.2	468	3	US-09-726-643-51	Sequence 51, Appl
37	69	14.2	468	3	US-09-978-295A-337	Sequence 337, App
38	69	14.2	468	3	US-09-978-697-337	Sequence 337, App
39	69	14.2	468	3	US-09-978-192A-337	Sequence 337, App
40	69	14.2	468	3	US-09-999-832A-337	Sequence 337, App
41	69	14.2	468	3	US-09-978-189-337	Sequence 337, App
42	69	14.2	468	3	US-09-978-608A-337	Sequence 337, App
43	69	14.2	468	3	US-09-978-585A-337	Sequence 337, App
44	69	14.2	468	3	US-09-978-191A-337	Sequence 337, App
45	69	14.2	468	3	US-09-978-403A-337	Sequence 337, App
46	69	14.2	468	3	US-09-978-564A-337	Sequence 337, App
47	69	14.2	468	3	US-09-999-833A-337	Sequence 337, App
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ALIGNMENTS

RESULT 1

US-09-955-502-23

; Sequence 23, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 23

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Pseudomonas syringae

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.92027 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-23

Perfect score: 485

Sequence: 1 MTRVTMCRKYKELPGLERA.....DKFLSGEYVAQAEGYVPEK 90

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	198	40.8	88	6	US-10-467-657-968
2	66	13.6	381	7	US-11-072-512-3313
3	66	13.6	401	6	US-10-131-826A-486
4	66	13.6	1560	7	US-11-059-982-1
5	65.5	13.5	879	6	US-10-770-726-78
6	64.5	13.3	600	7	US-11-072-512-3845
7	63.5	13.1	746	7	US-11-072-175-169
8	63	13.0	844	6	US-10-453-372-852
9	63	13.0	844	6	US-10-453-372-856
10	61	12.6	3433	6	US-10-714-781A-67
11	58.5	12.1	313	7	US-11-156-084-335
12	58.5	12.1	1308	6	US-10-912-971-12
13	58.5	12.1	1308	7	US-11-113-202-16
14	58	12.0	415	6	US-10-763-712A-25
15	58	12.0	436	6	US-10-763-712A-5
16	57.5	11.9	689	7	US-11-121-438-2
17	57.5	11.9	844	7	US-11-097-463-4
18	57.5	11.9	1386	7	US-11-091-643-6
19	57	11.8	166	7	US-11-176-830-954
20	56	11.5	307	6	US-10-454-437-268
21	56	11.5	370	6	US-10-873-528-160
22	56	11.5	805	6	US-10-485-517-198
23	56	11.5	928	7	US-11-130-594-8
24	55.5	11.4	691	7	US-11-098-686-1189
25	55	11.3	426	6	US-10-858-730-81

26	54.5	11.2	312	6	US-10-986-501-124	Sequence 124, App
27	54.5	11.2	320	6	US-10-467-657-3254	Sequence 3254, Ap
28	54.5	11.2	423	7	US-11-070-080-16	Sequence 16, Appl
29	54.5	11.2	2335	6	US-10-821-234-1610	Sequence 1610, Ap
30	54	11.1	504	7	US-11-055-822-136	Sequence 136, App
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32	54	11.1	1102	7	US-11-098-686-10951	Sequence 10951, A
33	53.5	11.0	293	7	US-11-072-512-2088	Sequence 2088, Ap
34	53.5	11.0	408	7	US-11-135-855-39	Sequence 39, Appl
35	53.5	11.0	434	7	US-11-135-855-40	Sequence 40, Appl
36	53.5	11.0	441	7	US-11-174-150-48	Sequence 48, Appl
37	53.5	11.0	526	7	US-11-055-822-124	Sequence 124, App
38	53.5	11.0	856	6	US-10-510-947-8	Sequence 8, Appli
39	53.5	11.0	856	7	US-11-042-988-13	Sequence 13, Appl
40	53.5	11.0	856	7	US-11-135-235-1	Sequence 1, Appli
41	53.5	11.0	1122	6	US-10-995-561-705	Sequence 705, App
42	53.5	11.0	1129	6	US-10-995-561-706	Sequence 706, App
43	53.5	11.0	1432	6	US-10-510-386-218	Sequence 218, App
44	53.5	11.0	1704	7	US-11-075-046-40	Sequence 40, Appl
45	53	10.9	289	7	US-11-093-118-39	Sequence 39, Appl
46	53	10.9	327	7	US-11-093-118-37	Sequence 37, Appl
47	53	10.9	479	7	US-11-024-251-33	Sequence 33, Appl
48	53	10.9	502	7	US-11-182-016-30	Sequence 30, Appl
49	53	10.9	627	6	US-10-493-909-47	Sequence 47, Appl
50	53	10.9	677	6	US-10-982-545-12	Sequence 12, Appl
51	53	10.9	833	6	US-10-667-295-102	Sequence 102, App
52	53	10.9	839	6	US-10-667-295-101	Sequence 101, App
53	53	10.9	856	6	US-10-467-657-8534	Sequence 8534, Ap
54	53	10.9	876	7	US-11-242-730-5	Sequence 5, Appli
55	53	10.9	1196	6	US-10-667-295-100	Sequence 100, App
56	52.5	10.8	139	7	US-10-793-626-1310	Sequence 1310, Ap
57	52.5	10.8	180	7	US-11-103-957-87	Sequence 87, Appl
58	52.5	10.8	181	6	US-10-467-657-1918	Sequence 1918, Ap
59	52.5	10.8	362	6	US-10-517-939-88	Sequence 88, Appl
60	52	10.7	106	7	US-11-072-512-2218	Sequence 2218, Ap
61	52	10.7	362	7	US-11-098-686-11138	Sequence 11138, A
62	52	10.7	418	7	US-11-072-512-3417	Sequence 3417, Ap
63	52	10.7	426	6	US-10-858-730-80	Sequence 80, Appl
64	52	10.7	488	7	US-11-055-822-850	Sequence 850, App
65	52	10.7	645	6	US-10-510-386-32	Sequence 32, Appl
66	52	10.7	913	7	US-11-018-868-164	Sequence 164, App
67	52	10.7	1450	6	US-10-485-517-152	Sequence 152, App
68	51.5	10.6	279	6	US-10-055-877-197	Sequence 197, App
69	51.5	10.6	377	7	US-11-072-512-3433	Sequence 3433, Ap
70	51.5	10.6	520	7	US-11-072-512-2424	Sequence 2424, Ap
71	51.5	10.6	520	7	US-11-072-512-2730	Sequence 2730, Ap
72	51.5	10.6	552	6	US-10-131-826A-196	Sequence 196, App
73	51.5	10.6	552	7	US-11-072-512-2405	Sequence 2405, Ap
74	51.5	10.6	690	6	US-10-467-657-4758	Sequence 4758, Ap
75	51.5	10.6	1449	7	US-11-052-554A-237	Sequence 237, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OR INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-24

Perfect score: 472
Sequence: 1 MTRVTWCRKYQBELPGLERP.....AEMDKFPAGEEYAQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	472	100.0	87	5	ABB78169 Amino aci
2	432	91.5	90	5	ABB78168 Amino aci
3	400	84.7	87	5	ABB78170 Amino aci
4	400	84.7	122	7	ABO74609 Pseudomon
5	265.5	56.2	92	6	ADA34169 Acinetoba
6	239	50.6	87	5	ABB78177 Amino aci
7	237	50.2	87	5	ABB78176 Amino aci
8	237	50.2	88	5	ABB78154 Amino aci
9	232	49.2	89	9	AEBA1576 L. pneumo
10	232	49.2	95	9	ABB38294 L. pneumo
11	229	48.5	87	5	ABB78175 Amino aci
12	229	48.5	87	5	ABB78152 Amino aci
13	228	48.3	90	5	ABB78155 Amino aci
14	228	48.3	91	5	ABB78150 Amino aci
15	225	47.7	87	5	ABB78151 Amino aci
16	225	47.7	91	5	ABB78158 Amino aci
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18	225	47.7	91	5	ABB78156 Amino aci
19	224	47.5	110	8	ADL05173 M. catarr
20	223	47.2	87	5	ABB78174 Amino aci
21	222	47.0	87	5	ABB78148 Amino aci
22	222	47.0	87	5	ABB78147 Amino aci
23	219	46.4	87	5	ABB78153 Amino aci
24	219	46.4	88	5	ABB78171 Amino aci

25	219	46.4	88	5	ABB78172 Amino aci
26	219	46.4	88	5	ABB78173 Amino aci
27	219	46.4	88	6	ABP77219 N. gonorr
28	218	46.2	88	5	ABB78160 Amino aci
29	218	46.2	91	5	ABB78161 Amino aci
30	218	46.2	91	5	ABB78159 Amino aci
31	218	46.2	91	5	ABB78162 Amino aci
32	213	45.1	107	7	ABO65445 Klebsiell
33	211	44.7	91	5	ABB78163 Amino aci
34	209	44.3	93	7	ADF05158 Bacterial
35	204.5	43.3	86	5	ABB78149 Amino aci
36	204	43.2	88	5	ABB78178 Amino aci
37	197.5	41.8	78	5	ABB78164 Amino aci
38	188.5	39.9	90	5	ABB78167 Amino aci
39	188	39.8	90	5	ABB78165 Amino aci
40	159	33.7	76	5	ABB78166 Amino aci
41	73	15.5	451	7	ADF07116 Bacterial
42	72	15.3	259	3	AAG43535 Arabidops
43	72	15.3	307	3	AAG43534 Arabidops
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48	72	15.3	901	8	ADT49817 Murine LO
49	70	14.8	670	8	ADN23314 Bacterial
50	69.5	14.7	1091	5	ABB48258 Bacteria
51	69	14.6	247	6	ABU33468 Protein e
52	69	14.6	251	4	AAM93928 Human pol
53	69	14.6	251	8	ADI32064 Human pro
54	67.5	14.3	689	5	ABB49714 Listeria
55	67.5	14.3	689	6	ABU33095 Protein e
56	67	14.2	559	8	ADN21954 Bacterial
57	67	14.2	567	8	ADN24711 Bacterial
58	66	14.0	140	5	ABB47391 Listeria
59	66	14.0	250	8	ADN47605 Thermococ
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63	66	14.0	2142	6	ABP98818 Human str
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74	64	13.6	317	7	ADC95026 E. faeciu
75	64	13.6	1042	4	AAU15096 Protein e

ALIGNMENTS

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AC	ABB78169;	
XX		
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Pseudomonas putida.	
XX		
PN	US2002072118-A1.	
XX		

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR MPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match	100.0%;	Score 472;	DB 5;	Length 87;
Best Local Similarity	100.0%;	Pred. No. 1.8e-51;		
Matches 87;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 MTRIVMCRKYOEBELPGLERPPYPGAKGODIFEHISQKAWDWQKHQMTL INEKKLNMMNA 600
|||||
Db 1 MTRIVMCRKYOEBELPGLERPPYPGAKGODIFEHISQKAWDWQKHQMTL INEKKLNMMNA 600

Qy	61	EDRKFLQAE	MDKFFAG	EETAAQAE	GYVP	87
Db	61	EDRKFLQAE	MDKFFAG	EETAAQAE	GYVP	87

RESULT 2	
ABB78168	
ID	ABB78168 standard; protein; 90 AA.
XX	
AC	ABB78168;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW	hydroxyl radical; DNA damage; YggX homologue.
XX	
OS	Pseudomonas syringae.
XX	
PN	US2002072118-A1.
XX	
PD	13-JUN-2002.
XX	
PF	18-SEP-2001; 2001US-00955502.
XX	
PR	22-SEP-2000; 2000US-0234588P.
XX	
PA	(DOWN/) DOWNS D.
PA	(GRAL/) GRALNICK J A.
XX	
PI	Downs D, Gralnick JA;
XX	

DR WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more YggX protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX
SQ Sequence 90 AA;

Query Match	91.5%;	Score 432;	DB 5;	Length 90;
Best Local Similarity	88.5%;	Pred. No. 2.2e-46;		
Matches 77; Conservative	6;	Mismatches 4;	Indels 0;	Gaps 0;

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QY 61 EDRKFLQAE~~MDKFF~~AGGEYAQAEGYVP 87
||||| : |||||
Db 61 EDRKFLQTE~~MDKFL~~SGGEYAQAEGYVP 87

RESULT 3
ABB78170
ID ABB78170 standard; protein; 87 AA.

AC ABB78170;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium, hydroxyl radical; DNA damage; YggX homologue.

OS unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

PI Downs D, Graintck JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-24

Perfect score: 472

Sequence: 1 MTRITVCRKRYQELPLGLERP.....AEMDKFFAGBEYVAQAEQYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	400	84.7	90	2	H83003	conserved hypothet
2	229	48.5	90	2	C64013	hypothetical prote
3	228	48.3	90	2	C82320	conserved hypothet
4	225	47.7	91	2	A85954	hypothetical prote
5	225	47.7	91	2	A65082	hypothetical prote
6	225	47.7	91	2	F91108	hypothetical prote
7	219	46.4	88	2	H81014	conserved hypothet
8	218	46.2	91	2	AH0879	conserved hypothet
9	198	41.9	105	2	C82624	conserved hypothet
10	188	39.8	90	2	AI0116	conserved hypothet
11	159	33.7	93	2	B84994	hypothetical prote
12	70	14.8	670	2	T29898	kinesin protein OS
13	69.5	14.7	1091	2	AF1380	glycosidase homolo
14	69	14.6	165	2	C75419	hypothetical prote
15	68.5	14.5	1090	2	AG1749	glycosidase homolo
16	68	14.4	388	1	QOYV	transferring prote
17	67.5	14.3	689	2	AC1408	transcription anti
18	66.5	14.1	1124	2	T30340	dsRNA adenosine de
19	66	14.0	140	2	AB1428	transcription regu
20	66	14.0	1553	2	S67483	adenosinetriphosph
21	65.5	13.9	926	2	T24923	hypothetical prote
22	65.5	13.9	959	2	H69344	hypothetical prote
23	65	13.8	528	2	T24730	hypothetical prote
24	64.5	13.7	767	2	T31558	hypothetical prote
25	64	13.6	140	2	AI1801	transcription regu
26	64	13.6	732	2	S23001	tral protein - Bsc
27	63.5	13.5	288	2	T45715	hypothetical prote
28	63.5	13.5	397	2	C87470	hypothetical prote
29	63.5	13.5	689	2	AC1784	transcription anti

30	63	13.3	150	2	F90212	hypothetical prote
31	63	13.3	555	2	C87515	ABC transporter, A
32	63	13.3	559	2	T12680	peroxisomal target
33	63	13.3	561	2	T06628	hypothetical prote
34	63	13.3	568	2	G84455	hypothetical prote
35	62.5	13.2	352	2	F84799	hypothetical prote
36	62.5	13.2	677	2	G69895	formate dehydrogen
37	62.5	13.2	985	2	S15965	hypothetical prote
38	62	13.1	242	2	S67270	CCAAT-binding fact
39	62	13.1	1175	2	D35815	myosin heavy chain
40	62	13.1	1175	2	C35815	myosin heavy chain
41	62	13.1	1201	2	A35815	myosin heavy chain
42	62	13.1	1201	2	B35815	myosin heavy chain
43	62	13.1	2385	2	A32491	myosin heavy chain
44	62	13.1	2411	2	B32491	myosin heavy chain
45	61.5	13.0	284	2	D82486	probable lipase ac
46	61.5	13.0	339	2	AG2041	queuine tRNA-ribos
47	61.5	13.0	430	2	I48755	mSAP1a - mouse
48	61.5	13.0	470	2	D84614	hypothetical prote
49	61.5	13.0	709	2	D86907	elongation factor
50	61.5	13.0	863	2	JC7537	beta-N-acetylgluco
51	61	12.9	213	2	B27898	luxP protein - Vib
52	61	12.9	245	2	S49045	arabinose operon r
53	61	12.9	310	2	A25027	hypothetical prote
54	61	12.9	389	2	T14751	hypothetical prote
55	61	12.9	410	1	O4BS6M	cytochrome P450 10
56	61	12.9	474	2	S16250	phytoene dehydroge
57	61	12.9	604	2	S36493	E1 protein - human
58	61	12.9	1212	2	B82809	exodeoxyribonuclea
59	60.5	12.8	88	2	AI3122	IS3 family transpo
60	60.5	12.8	88	2	F98164	insertion element
61	60.5	12.8	142	2	F81296	hypothetical prote
62	60.5	12.8	323	2	B83215	conserved hypothet
63	60.5	12.8	335	2	T33483	hypothetical prote
64	60.5	12.8	458	2	F84275	hypothetical prote
65	60.5	12.8	508	2	S74848	neopullulanase - S
66	60.5	12.8	843	2	A47132	major vault protei
67	60.5	12.8	1083	1	S53048	alpha-mannosidase
68	60	12.7	177	2	D70862	hypothetical prote
69	60	12.7	282	2	D97138	DNA replicational pr
70	60	12.7	290	2	JN0904	H+/K+-exchanging A
71	60	12.7	310	2	AB0275	arabinose operon r
72	60	12.7	326	2	G96812	protein F3F9.6 (lm
73	60	12.7	352	2	F89884	phe-tRNA synthetas
74	60	12.7	373	2	A96927	probable N6-adenin
75	60	12.7	426	2	D87153	serine hydroxymeth

ALIGNMENTS

RESULT 1

H83003 Conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)

C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004

C;Accession: H83003
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brj

adhan, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

.; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: H83003

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-90 <STO>

A;Cross-references: UNIPARC:UPI00000C5F26; GB:AE004927; GB:AE004091; NID:9951437; PIDN:f

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA5148

C;Superfamily: fe(IT) trafficking protein YggX

Query Match 84.7%; Score 400; DB 2; Length 90;
Best Local Similarity 79.3%; Pred. No. 3.4e-35;
Matches 69; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

QY 1 MTRTYMCRKYQEBLPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINERLNNMNA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSRTVMCRKYHBEPLGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERLNNMNA 60

QY 61 EDRKFLQAEEMDKF-PAGEBYAQAEGYVP 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EDRKFLQAEEMDKFLSGEDYAKADGYVP 87

RESULT 2
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C:Accession: C64013

R:Flaischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodex, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.; Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A:Reference number: A64000; MUID:95350630; PMID:7542800
A:Accession: C64013
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-90 <ITIGR>
A:Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:I42023; NID:g15
C:Superfamily: fe(II) trafficking protein YgX

Query Match 48.5%; Score 229; DB 2; Length 90;
Best Local Similarity 52.3%; Pred. No. 3.4e-17;
Matches 46; Conservative 14; Mismatches 26; Indels 2; Gaps 2;

QY 1 MTRTYMCRKYQEBLPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINERLNNMNA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MARTVFCEYLKKEAEGLDFOLYPSELGKRIFDSVSKQAWGEWIKKQTMVLNKKLNNMNA 60

QY 61 EDRKFLQAEEMDKF-PAGEBYAQAEGYVP 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVNFLEFGKD-VHIEGYVP 87

RESULT 3
C82320
hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogroup C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C:Accession: C82320
R:Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82320
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-90 <HEI>
A:Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:A; Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC0451
A:Map position: 1
C:Superfamily: fe(II) trafficking protein YgX

Query Match 48.3%; Score 228; DB 2; Length 90;
Best Local Similarity 53.4%; Pred. No. 4.3e-17;
Matches 47; Conservative 12; Mismatches 27; Indels 2; Gaps 2;

QY 1 MTRTYMCRKYQEBLPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINERLNNMNA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MARTVFCTRLQKEADGLDFOLYPSELGKRIFDNIKKEAWAQWTKQTMLINEKLLNNMNDP 60

QY 61 EDRKFLQAEEMDKF-PAGEBYAQAEGYVP 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVNFLEFGKE-VHIEGYTP 87

RESULT 4
A85954
hypothetical protein ygX [imported] - Escherichia coli (strain O157:H7, substrain EDL933:
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, Hler, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954

A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P1
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: YgX
C:Superfamily: fe(II) trafficking protein YgX

Query Match 47.7%; Score 225; DB 2; Length 91;
Best Local Similarity 53.4%; Pred. No. 9.1e-17;
Matches 47; Conservative 10; Mismatches 29; Indels 2; Gaps 2;

QY 1 MTRTYMCRKYQEBLPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINERLNNMNA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSRTIFCTFLQREAGQDFOLYPSELGKRIYNEISKEAWAQWTKQTMLINEKLLNNMNA 60

QY 61 EDRKFLQAEEMDKF-PAGEBYAQAEGYVP 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVNFLEFGKE-VHIEGYTP 87

RESULT 5
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C:Species: Escherichia coli
C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C:Accession: A65082
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col .A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A:Title: The complete genome sequence of Escherichia coli K-12.
A:Reference number: A64720; MUID:97426617; PMID:9278503
A:Accession: A65082
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-91 <BLAT>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g1
A:Experimental source: strain K-12, substrain MG1655
C:Superfamily: fe(II) trafficking protein YgX

Query Match 47.7%; Score 225; DB 2; Length 91;
Best Local Similarity 53.4%; Pred. No. 9.1e-17;
Matches 47; Conservative 10; Mismatches 29; Indels 2; Gaps 2;

QY 1 MTRTYMCRKYQEBLPGLERPPYPGAKGODIFEHISQKAWADWQKHQTMLINERLNNMNA 60
|:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 MSRTIFCTFLQREAGQDFOLYPSELGKRIYNEISKEAWAQWTKQTMLINEKLLNNMNA 60

QY 61 EDRKFLQAEEMDKF-PAGEBYAQAEGYVP 87
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 EHRKLEQEMVNFLEFGKE-VHIEGYTP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-24
Perfect score: 472
Sequence: 1 MTRIVMCRKQGEELPGLERP.....AEMDKFPAGEEYQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	472	100.0	90	1 FETP_PSEBK	Q88R49 pseudomonas
2	439	93.0	90	2 Q4KJT2_PSEF5	Q4KJT2 pseudomonas
3	432	91.5	90	1 FETP_PSEBM	Q87UFS pseudomonas
4	432	91.5	90	2 Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
5	411	87.1	90	2 Q6T7F6_PSEFL	Q6T7F6 pseudomonas
6	400	84.7	90	1 FETP_PSEAB	Q9HU36 pseudomonas
7	393	83.3	90	2 Q4J228_AZOVI	Q4J228 azotobacter
8	261.5	55.4	90	1 FETP_ACIAA	Q6FEB3 acinetobacter
9	250	53.0	90	1 FETP_IDILO	Q5GY58 idiomarina
10	244	51.7	96	2 Q4FVU7_9GAMM	Q4FVJ7 psychrobact
11	239	50.6	90	1 FETP_METCA	Q60AJ7 methylococc
12	237	50.2	92	1 FETP_SHEON	Q8EBX6 shewanella
13	234	49.6	91	1 FETP_MANSN	Q65VT7 manheimia
14	233	49.4	91	1 FETP_RALSO	Q8YU10 ralstonia s
15	232	49.2	89	1 FETP_LEGPA	Q5X3X9 legionella
16	232	49.2	89	1 FETP_LEGPH	Q5ZU80 legionella
17	232	49.2	90	1 FETP_NITEU	Q82XF2 nitrosomona
18	231	48.9	89	1 FETP_NITEU	Q5WVC4 legionella
19	229	48.5	90	1 FETP_HAEIN	P44048 haemophilus
20	229	48.5	90	1 FETP_PHOPR	Q6LHK7 photobacter
21	229	48.5	90	2 Q4QMD9_HAEIB	Q4QMD9 haemophilus
22	229	48.5	91	1 FETP_BURMA	Q63J44 burkholderi
23	229	48.5	91	1 FETP_BURPS	Q9KUR4 vibrio chol
24	228	48.3	90	1 FETP_VIBCH	Q8DCS5 vibrio vuln
25	226	47.9	90	1 FETP_VIBVU	Q7MH14 vibrio vuln
26	226	47.9	90	1 FETP_VIBVY	Q9CLB9 pasteurella
27	225	47.7	90	1 FETP_PASMU	Q87L15 vibrio para
28	225	47.7	90	1 FETP_VIBPA	Q4LS19 burkholderi
29	223	47.2	91	2 Q4LS19_9BURK	Q7WH06 bordetella
30	222	47.0	90	1 FETP_BORBR	Q7W9G2 bordetella
31	222	47.0	90	1 FETP_BORPA	

32	222	47.0	90	1 FETP_BORPE	Q7WVC4 bordetella
33	220	46.6	90	1 FETP_ECO57	P0A8P4 escherichia
34	220	46.6	90	1 FETP_ECOLI	P0A8P3 escherichia
35	220	46.6	90	1 FETP_PHOLL	Q7N711 photorhabdu
36	220	46.6	90	1 FETP_SHIFL	P0A8P5 shigella fl
37	219	46.4	88	1 FETP_NEIG1	Q5F553 neisseria g
38	219	46.4	88	1 FETP_NEIMA	P67615 neisseria m
39	219	46.4	88	1 FETP_NEIMB	P67616 neisseria m
40	219	46.4	90	1 FETP_ERMCT	Q6D8J9 erwinia car
41	219	46.4	90	1 FETP_VIBF1	Q5E7C0 vibrio fisc
42	219	46.4	94	1 FETP_HAEDU	Q7VKB6 haemophilus
43	216	45.8	90	1 FETP_ECOL6	Q8FE19 escherichia
44	213	45.1	90	1 FETP_SALCH	Q57K04 salmonella
45	213	45.1	90	1 FETP_SALPA	Q5PMU1 salmonella
46	213	45.1	90	1 FETP_SALTI	P67618 salmonella
47	213	45.1	90	1 FETP_SALTY	P67617 salmonella
48	207	43.9	90	1 FETP_CHRVO	Q7NSR4 chromobacte
49	206	43.6	91	1 FETP_XANAC	Q8PJH7 xanthomonas
50	206	43.6	92	1 FETP_XANOR	Q5GY22 xanthomonas
51	204	43.2	90	1 FETP_COXBU	Q83D06 coxiella bu
52	199	42.2	92	1 FETP_XANCP	Q8P829 xanthomonas
53	199	42.2	92	2 Q4UW14_XANCP	Q4UW14 xanthomonas
54	198	41.9	90	1 FETP_XYFLA	Q9PC73 xylella fas
55	196	41.5	90	1 FETP_YERPS	Q66M3 yersinia ps
56	194	41.1	90	1 FETP_XYFLT	Q87D06 xylella fas
57	193	40.9	78	1 FETP_WIGBR	Q8D3C5 wiggleswort
58	188	39.8	90	1 FETP_YERPE	Q8ZHE7 yersinia pe
59	185	39.2	87	1 FETP_FRAYT	Q5NHJ8 francisella
60	180	38.1	79	1 FETP_CANBF	Q7VRG9 candidatus
61	177	37.5	78	1 FETP_BUCAP	Q8K925 buchnera ap
62	172	36.4	92	2 Q4NWQ4_9DELT	Q4NWQ4 anaeromyxob
63	159	33.7	77	1 FETP_BUCAL	P57618 buchnera ap
64	157	33.3	87	1 FETP_BUCBP	Q89A44 buchnera ap
65	84	17.8	703	2 Q4WPT2_ASPEFU	Q4WPT2 aspergillus
66	79.5	16.8	280	2 Q81BK9_BACCR	Q81BK9 bacillus ce
67	78.5	16.6	603	2 Q6BPW5_ORYSA	Q6BPW5 oryza sativ
68	74	15.7	220	2 Q5WAF4_BACSK	Q5WAF4 bacillus ci
69	74	15.7	1141	2 Q5B3I8_EMENI	Q5B3I8 aspergillus
70	72	15.3	307	2 Q9FJU6_ARATH	Q9FJF6 arabidopsis
71	72	15.3	844	1 PRIC2_HUMAN	Q7Z3G6 homo sapien
72	72	15.3	845	1 PRIC2_MOUSE	Q80Y24 mus musculu
73	71	15.0	437	2 Q60EH0_ORYSA	Q60EH0 oryza sativ
74	70.5	14.9	259	2 Q52J13_BRARE	Q52J13 brachydanio
75	70.5	14.9	353	2 Q6NN67_DROME	Q6NN67 drosophila

ALIGNMENTS

RESULT 1
FETP_PSEBK
ID FETP_PSEBK STANDARD; PRT; 90 AA.
AC Q88R49;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=PF0285;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP MEDLINE=22423060; PubMed=12534463;
RX DOI=10.1046/j.1462-2920.2002.00366.x;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzaple B.K., Scanlan D., Tran K.,
RA Moazzez A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-24
Perfect score: 472
Sequence: 1 MTRTVMCRKYQBELPGLERP.....AEMDKFPAGEEYQAQEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	400	84.7	122	2	US-09-252-991A-23355
2	265.5	56.2	92	2	US-09-328-352-5456
3	224	47.5	110	2	US-09-540-236-2859
4	213	45.1	107	2	US-09-489-039A-11962
5	209	44.3	93	2	US-09-543-681A-5443
6	73	15.5	451	2	US-09-543-681A-7401
7	69	14.6	443	2	US-09-248-796A-16816
8	64.5	13.7	163	2	US-09-270-767-33714
9	64	13.6	317	2	US-09-107-532A-4653
10	64	13.6	420	2	US-09-248-796A-15323
11	64	13.6	1042	2	US-09-792-024-106
12	63	13.3	314	2	US-09-716-865-4
13	62.5	13.2	284	2	US-09-934-899-14
14	62.5	13.2	284	2	US-09-934-868-34
15	62.5	13.2	284	2	US-10-701-200-34
16	62	13.1	242	2	US-09-538-092-763
17	62	13.1	448	2	US-09-107-532A-4482
18	62	13.1	1156	2	US-08-996-083-1
19	62	13.1	1156	2	US-09-429-516-1
20	62	13.1	1156	2	US-09-429-516-3
21	61.5	13.0	689	2	US-10-200-012-2
22	61	12.9	342	2	US-10-227-327-1
23	61	12.9	381	2	US-09-949-016-9788
24	61	12.9	381	2	US-09-964-899-13
25	60.5	12.8	205	2	US-09-919-039-258
26	60	12.7	352	1	US-08-785-052-2
27	60	12.7	352	1	US-08-913-581-2

28	60	12.7	569	2	US-09-252-991A-32290	Sequence 32290, A
29	60	12.7	689	2	US-09-489-039A-7677	Sequence 7677, Ap
30	59.5	12.6	468	2	US-09-976-594-462	Sequence 462, App
31	59.5	12.6	468	2	US-09-999-833A-337	Sequence 337, App
32	59.5	12.6	468	2	US-10-020-445A-337	Sequence 337, App
33	59	12.5	184	2	US-09-040-229B-9	Sequence 9, Appli
34	59	12.5	212	1	US-08-531-525-18	Sequence 18, Appl
35	59	12.5	212	1	US-08-718-270A-18	Sequence 18, Appl
36	59	12.5	212	2	US-09-399-913-67	Sequence 67, Appl
37	59	12.5	212	2	US-09-350-614-67	Sequence 67, Appl
38	59	12.5	216	2	US-09-949-016-10750	Sequence 10750, A
39	59	12.5	278	2	US-09-328-352-7544	Sequence 7544, Ap
40	59	12.5	298	2	US-09-543-681A-8107	Sequence 8107, Ap
41	59	12.5	454	2	US-09-771-161A-95	Sequence 95, Appl
42	59	12.5	477	2	US-09-949-016-10716	Sequence 10716, A
43	59	12.5	504	2	US-09-538-092-1170	Sequence 1170, Ap
44	59	12.5	505	2	US-09-949-016-6117	Sequence 6117, Ap
45	59	12.5	505	2	US-09-771-161A-186	Sequence 186, App
46	59	12.5	513	2	US-09-949-016-11517	Sequence 11517, A
47	59	12.5	1242	2	US-09-583-110-5051	Sequence 5051, Ap
48	59	12.5	1243	2	US-09-107-433-3942	Sequence 3942, Ap
49	58.5	12.4	205	2	US-09-216-393B-124	Sequence 124, App
50	58.5	12.4	361	2	US-09-270-767-37733	Sequence 37733, A
51	58.5	12.4	783	2	US-09-902-540-11823	Sequence 11823, A
52	58.5	12.4	913	2	US-09-623-624-2	Sequence 2, Appli
53	58.5	12.4	913	2	US-10-270-595-2	Sequence 2, Appli
54	58.5	12.4	1122	2	US-10-146-704-2	Sequence 2, Appli
55	58	12.3	129	2	US-09-489-039A-11601	Sequence 11601, A
56	58	12.3	140	2	US-09-248-796A-15755	Sequence 15755, A
57	58	12.3	292	2	US-09-328-352-5836	Sequence 5836, Ap
58	58	12.3	444	2	US-09-861-451A-16	Sequence 16, Appl
59	58	12.3	582	2	US-09-902-540-11161	Sequence 11161, A
60	58	12.3	861	2	US-09-826-312A-10	Sequence 10, Appl
61	58	12.3	861	2	US-09-542-497A-10	Sequence 10, Appl
62	58	12.3	861	2	US-10-108-767-10	Sequence 10, Appl
63	58	12.3	903	1	US-08-220-151-8	Sequence 8, Appli
64	58	12.3	903	1	US-08-413-118-8	Sequence 8, Appli
65	58	12.3	903	2	US-08-804-439A-22	Sequence 22, Appl
66	58	12.3	903	2	US-08-473-446-8	Sequence 8, Appli
67	58	12.3	903	2	US-08-720-229-22	Sequence 22, Appl
68	58	12.3	904	2	US-08-632-537-1	Sequence 1, Appli
69	58	12.3	904	4	PCT-US96-05316-1	Sequence 1, Appli
70	58	12.3	904	6	5244792-4	Patent No. 5244792
71	57.5	12.2	324	2	US-09-252-991A-26001	Sequence 26001, A
72	57.5	12.2	332	2	US-09-252-991A-24826	Sequence 24826, A
73	57.5	12.2	337	2	US-09-489-039A-14173	Sequence 14173, A
74	57.5	12.2	368	2	US-09-252-991A-19658	Sequence 19658, A
75	57.5	12.2	502	2	US-09-252-991A-26986	Sequence 26986, A

ALIGNMENTS

RESULT 1

US-09-252-991A-23355

; Sequence 23355, Application US/09252991A

; Patent No. 6551795

; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.

; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252, 991A

; PRIOR FILING DATE: 1999-02-18

; PRIOR APPLICATION NUMBER: US 60/074, 788

; PRIOR FILING DATE: 1998-02-18

; PRIOR APPLICATION NUMBER: US 60/094, 190

; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 23355

; LENGTH: 122

; TYPE: PRT

; ORGANISM: Pseudomonas aeruginosa



GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-24
Perfect score: 472
Sequence: 1 MTRVTWCRKYQEBLPGLERP.....AEMDKFPAGEBYAQAEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	432	91.5	90	3	US-09-955-502-23 Sequence 23, Appl
3	400	84.7	87	3	US-09-955-502-25 Sequence 25, Appl
4	239	50.6	87	3	US-09-955-502-32 Sequence 32, Appl
5	237	50.2	87	3	US-09-955-502-31 Sequence 31, Appl
6	237	50.2	88	3	US-09-955-502-9 Sequence 9, Appl
7	229	48.5	87	3	US-09-955-502-7 Sequence 7, Appl
8	229	48.5	87	3	US-09-955-502-29 Sequence 29, Appl
9	229	48.5	87	3	US-09-955-502-30 Sequence 30, Appl
10	228	48.3	90	3	US-09-955-502-10 Sequence 10, Appl
11	228	48.3	91	3	US-09-955-502-5 Sequence 5, Appl
12	225	47.7	87	3	US-09-955-502-6 Sequence 6, Appl
13	225	47.7	91	3	US-09-955-502-11 Sequence 11, Appl
14	225	47.7	91	3	US-09-955-502-12 Sequence 12, Appl
15	225	47.7	91	3	US-09-955-502-13 Sequence 13, Appl
16	222	47.0	87	3	US-09-955-502-2 Sequence 2, Appl
17	222	47.0	87	3	US-09-955-502-3 Sequence 3, Appl
18	219	46.4	87	3	US-09-955-502-8 Sequence 8, Appl
19	219	46.4	88	3	US-09-955-502-26 Sequence 26, Appl
20	219	46.4	88	3	US-09-955-502-27 Sequence 27, Appl
21	219	46.4	88	3	US-09-955-502-28 Sequence 28, Appl
22	218	46.2	88	3	US-09-955-502-15 Sequence 15, Appl
23	218	46.2	91	3	US-09-955-502-14 Sequence 14, Appl
24	218	46.2	91	3	US-09-955-502-16 Sequence 16, Appl
25	218	46.2	91	3	US-09-955-502-17 Sequence 17, Appl
26	211	44.7	91	3	US-09-955-502-18 Sequence 18, Appl
27	204.5	43.3	86	3	US-09-955-502-4 Sequence 4, Appl

28	204	43.2	88	3	US-09-955-502-33	Sequence 33, Appl
29	198	41.9	89	3	US-09-955-502-22	Sequence 22, Appl
30	197.5	41.8	78	3	US-09-955-502-19	Sequence 19, Appl
31	188	39.8	90	3	US-09-955-502-20	Sequence 20, Appl
32	159	33.7	76	3	US-09-955-502-21	Sequence 21, Appl
33	78.5	16.6	596	4	US-10-437-963-130475	Sequence 130475,
34	73	15.5	766	4	US-10-437-963-146099	Sequence 146099,
35	72	15.3	795	5	US-10-450-763-37384	Sequence 37384, A
36	71	15.0	313	4	US-10-437-963-173240	Sequence 173240,
37	70	14.8	451	4	US-10-437-963-137284	Sequence 137284,
38	70	14.8	670	4	US-10-369-493-5967	Sequence 5967, Ap
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40	69.5	14.7	902	4	US-10-437-963-156143	Sequence 156143,
41	69	14.6	247	4	US-10-282-122A-61392	Sequence 61392, A
42	69	14.6	897	4	US-10-437-963-165505	Sequence 165505,
43	69	14.6	981	4	US-10-437-963-165498	Sequence 165498,
44	68.5	14.5	526	4	US-10-437-963-156176	Sequence 156176,
45	68	14.4	794	4	US-10-437-963-173233	Sequence 173233,
46	68	14.4	900	4	US-10-437-963-126879	Sequence 126879,
47	67.5	14.3	689	4	US-10-282-122A-61019	Sequence 61019, A
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49	67.5	14.3	890	4	US-10-437-963-156221	Sequence 156221,
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53	67	14.2	561	5	US-10-732-923-13915	Sequence 13915, A
54	67	14.2	567	4	US-10-369-493-7364	Sequence 7364, Ap
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61	66	14.0	1152	4	US-10-437-963-173239	Sequence 173239,
62	66	14.0	1501	5	US-10-732-923-22706	Sequence 22706, A
63	66	14.0	1553	5	US-10-732-923-22705	Sequence 22705, A
64	66	14.0	1555	5	US-10-732-923-22584	Sequence 22584, A
65	66	14.0	1651	5	US-10-450-763-45007	Sequence 45007, A
66	66	14.0	2202	4	US-10-094-466-12	Sequence 12, Appl
67	65.5	13.9	202	4	US-10-767-701-34267	Sequence 34267, A
68	65.5	13.9	284	4	US-10-437-963-156187	Sequence 156187,
69	65.5	13.9	534	5	US-10-732-923-13918	Sequence 13918, A
70	65.5	13.9	571	5	US-10-732-923-13917	Sequence 13917, A
71	65.5	13.9	639	4	US-10-437-963-177051	Sequence 177051,
72	65.5	13.9	682	4	US-10-437-963-177042	Sequence 177042,
73	65.5	13.9	926	4	US-10-369-493-6955	Sequence 6955, Ap
74	65	13.8	391	5	US-10-732-923-13919	Sequence 13919, A
75	65	13.8	1011	4	US-10-437-963-173228	Sequence 173228,

ALIGNMENTS

RESULT 1
US-09-955-502-24
Sequence 24, Application US/099555502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 87
TYPE: PRT
ORGANISM: Pseudomonas putida

US-09-955-502-24

Query Match 100.0%; Score 472; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 6.4e-49;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 61 EDRKFLQAEMDKFPAGEBYAQAEGYVP 87

RESULT 2

US-09-955-502-23
; Sequence 23, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 23
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Pseudomonas syringae
US-09-955-502-23

Query Match 91.5%; Score 432; DB 3; Length 90;
Best Local Similarity 88.5%; Pred. No. 4.4e-44;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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Db 1 MTRTWCKRYKEELPGLERAPYPGAKGEDIFNHVSQKAWADWQKHQTMLINERLNMNNA 60
Oy 61 EDRKFLQAEMDKFPAGEBYAQAEGYVP 87
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Db 61 EDRKFLQTEMDFLGSGBEYQAQAEGYVP 87

RESULT 3

US-09-955-502-25
; Sequence 25, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 25
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-955-502-25

Query Match 84.7%; Score 400; DB 3; Length 87;

Best Local Similarity 79.3%; Pred. No. 3.1e-40;
Matches 69; Conservative 13; Mismatches 5; Indels 0; Gaps 0;

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Db 1 MSRTWCKRYKEELPGLDRPYPYGAKGEDYNNVSRKAWDEWQKHQTMLINERLNMNNA 60
Oy 61 EDRKFLQAEMDKFPAGEBYAQAEGYVP 87
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Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 4

US-09-955-502-32
; Sequence 32, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 32
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Methylococcus capsulatus
US-09-955-502-32

Query Match 50.6%; Score 239; DB 3; Length 87;
Best Local Similarity 51.7%; Pred. No. 8.2e-21;
Matches 45; Conservative 12; Mismatches 30; Indels 0; Gaps 0;

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Db 1 MARRIICAKLGIEADGLDAPFPFGQRIFEHVSKEAWQDWLKLQTMLINEHRLTPPEA 60
Oy 61 EDRKFLQAEMDKFPAGEBYAQAEGYVP 87
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RESULT 5

US-09-955-502-31
; Sequence 31, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 31
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Thiobacillus ferrooxidans
US-09-955-502-31

Query Match 50.2%; Score 237; DB 3; Length 87;
Best Local Similarity 49.4%; Pred. No. 1.4e-20;
Matches 43; Conservative 16; Mismatches 28; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-24

Perfect score: 472

Sequence: 1 MTRIVMCRKRYQELPLGLERP.....AEMDKFFAGEEYQAEGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications AA New: *
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep: *
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep: *
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep: *
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	219	46.4	88	US-10-467-657-968	Sequence 968, App
2	72	15.3	844	US-10-453-372-852	Sequence 852, App
3	72	15.3	844	US-10-453-372-856	Sequence 856, App
4	64.5	13.7	1560	US-11-059-982-1	Sequence 1, Appli
5	61.5	13.0	689	US-11-121-438-2	Sequence 2, Appli
6	61	12.9	3433	US-10-714-781A-67	Sequence 67, Appl
7	60.5	12.8	645	US-10-510-386-32	Sequence 32, Appl
8	60	12.7	426	US-10-858-730-81	Sequence 81, Appl
9	59.5	12.6	690	US-10-467-657-4758	Sequence 4758, Ap
10	58	12.3	697	US-11-074-176-62	Sequence 62, Appl
11	57	12.1	426	US-10-858-730-80	Sequence 80, Appl
12	57	12.1	1386	US-11-091-643-6	Sequence 6, Appli
13	57	12.1	1618	US-10-984-645-2	Sequence 2, Appli
14	56	11.9	211	US-11-124-368A-175	Sequence 175, App
15	56	11.9	211	US-11-124-368A-176	Sequence 176, App
16	55.5	11.8	341	US-11-055-822-1054	Sequence 1054, Ap
17	55.5	11.8	1432	US-10-510-386-218	Sequence 218, App
18	55	11.7	106	US-11-072-512-2218	Sequence 2218, Ap
19	55	11.7	806	US-11-098-686-10278	Sequence 10278, A
20	55	11.7	1102	US-11-098-686-10951	Sequence 10951, A
21	54.5	11.5	310	US-11-198-746-88	Sequence 88, Appl
22	54.5	11.5	310	US-11-198-794-88	Sequence 88, Appl
23	54.5	11.5	315	US-11-198-746-91	Sequence 91, Appl
24	54.5	11.5	315	US-11-198-794-91	Sequence 91, Appl
25	54.5	11.5	320	US-10-467-657-3254	Sequence 3254, Ap

26	54.5	11.5	322	7	US-11-198-746-89	Sequence 89, Appl
27	54.5	11.5	322	7	US-11-198-794-89	Sequence 89, Appl
28	54.5	11.5	528	7	US-11-198-746-90	Sequence 90, Appl
29	54.5	11.5	528	7	US-11-198-794-90	Sequence 90, Appl
30	54.5	11.5	548	7	US-11-198-746-86	Sequence 86, Appl
31	54.5	11.5	548	7	US-11-198-794-86	Sequence 86, Appl
32	54.5	11.5	577	7	US-11-072-175-187	Sequence 187, App
33	54.5	11.5	648	6	US-10-467-657-2802	Sequence 2802, Ap
34	54.5	11.5	665	7	US-11-113-837-19	Sequence 19, Appl
35	54.5	11.5	695	7	US-11-198-746-87	Sequence 87, Appl
36	54.5	11.5	695	7	US-11-198-794-87	Sequence 87, Appl
37	54.5	11.5	832	7	US-11-065-943-100	Sequence 100, App
38	54.5	11.5	832	7	US-11-007-797A-11	Sequence 11, Appl
39	54.5	11.5	832	7	US-11-007-642B-11	Sequence 11, Appl
40	54.5	11.5	832	7	US-11-198-746-4	Sequence 4, Appli
41	54.5	11.5	832	7	US-11-198-794-4	Sequence 4, Appli
42	54.5	11.5	832	7	US-11-242-730-1	Sequence 1, Appli
43	54.5	11.5	833	7	US-11-198-746-85	Sequence 85, Appl
44	54.5	11.5	833	7	US-11-198-794-85	Sequence 85, Appl
45	54	11.4	312	6	US-10-986-501-124	Sequence 124, App
46	54	11.4	313	7	US-11-156-084-335	Sequence 335, App
47	54	11.4	362	6	US-10-517-939-88	Sequence 88, Appl
48	53.5	11.3	203	6	US-10-454-437-326	Sequence 326, App
49	53.5	11.3	293	7	US-11-072-512-2088	Sequence 2088, Ap
50	53.5	11.3	432	6	US-10-454-437-140	Sequence 140, App
51	53.5	11.3	432	7	US-11-055-822-184	Sequence 184, App
52	53.5	11.3	453	7	US-11-072-512-3394	Sequence 3394, Ap
53	53.5	11.3	691	7	US-11-098-686-11189	Sequence 11189, A
54	53.5	11.3	746	7	US-11-072-175-169	Sequence 169, App
55	53.5	11.3	919	6	US-10-821-234-1144	Sequence 1144, Ap
56	53.5	11.3	2335	6	US-10-821-234-1610	Sequence 1610, Ap
57	53	11.2	289	7	US-11-093-118-39	Sequence 39, Appl
58	53	11.2	327	7	US-11-093-118-37	Sequence 37, Appl
59	53	11.2	876	7	US-11-242-730-5	Sequence 5, Appli
60	53	11.2	1596	7	US-11-060-005-4	Sequence 4, Appli
61	52.5	11.1	215	6	US-10-131-826A-488	Sequence 488, App
62	52.5	11.1	215	7	US-11-080-991-112	Sequence 112, App
63	52.5	11.1	736	6	US-10-467-657-4780	Sequence 4780, Ap
64	52.5	11.1	926	7	US-11-232-405A-34	Sequence 34, Appl
65	52	11.0	236	6	US-10-927-641-72	Sequence 72, Appl
66	52	11.0	370	6	US-10-873-528-160	Sequence 160, App
67	52	11.0	381	7	US-11-072-512-3313	Sequence 3313, Ap
68	52	11.0	401	6	US-10-131-826A-486	Sequence 486, App
69	52	11.0	505	6	US-10-514-878A-3	Sequence 3, Appli
70	52	11.0	505	6	US-10-514-878A-5	Sequence 5, Appli
71	52	11.0	505	6	US-10-514-878A-7	Sequence 7, Appli
72	52	11.0	505	6	US-10-514-878A-13	Sequence 13, Appl
73	52	11.0	505	7	US-11-179-478-2	Sequence 2, Appli
74	52	11.0	593	7	US-11-194-246-317	Sequence 317, App
75	52	11.0	924	6	US-10-467-657-4290	Sequence 4290, Ap

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 71.344 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477

Sequence: 1 MSRTVMCRKHYHEELPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	477	100.0	87	5	ABB78170 Amino aci
2	477	100.0	122	7	ABO74609 Pseudomon
3	408	85.5	90	5	ABB78168 Amino aci
4	400	83.9	87	5	ABB78169 Amino aci
5	262.5	55.0	92	6	ADA34169 Acinetoba
6	242	50.7	87	5	ABB78176 Amino aci
7	241	50.5	89	9	AEB41576 L. pneumo
8	241	50.5	95	9	AEB38294 L. pneumo
9	240	50.3	87	5	ABB78148 Amino aci
10	240	50.3	87	5	ABB78147 Amino aci
11	236	49.5	87	5	ABB78152 Amino aci
12	235	49.3	87	5	ABB78177 Amino aci
13	235	49.3	88	5	ABB78154 Amino aci
14	235	49.3	110	8	ADL05173 M. catarr
15	233	48.8	91	5	ABB78150 Amino aci
16	231	48.4	91	5	ABB78158 Amino aci
17	231	48.4	91	5	ABB78157 Amino aci
18	230	48.2	91	5	ABB78156 Amino aci
19	230	48.2	87	5	ABB78151 Amino aci
20	230	48.2	93	7	ADP05158 Bacterial
21	228	47.8	88	5	ABB78160 Amino aci
22	228	47.8	91	5	ABB78161 Amino aci
23	228	47.8	91	5	ABB78159 Amino aci
24	228	47.8	91	5	ABB78162 Amino aci

25	227	47.6	87	5	ABB78175 Amino aci	Abb78175 Amino aci
26	223	46.8	90	5	ABB78155 Amino aci	Abb78155 Amino aci
27	223	46.8	107	7	ABO65445 Klebsiell	AbO65445 Klebsiell
28	222.5	46.6	86	5	ABB78149 Amino aci	Abb78149 Amino aci
29	222	46.5	87	5	ABB78153 Amino aci	Abb78153 Amino aci
30	221	46.3	87	5	ABB78174 Amino aci	Abb78174 Amino aci
31	221	46.3	91	5	ABB78163 Amino aci	Abb78163 Amino aci
32	220	46.1	88	5	ABB78178 Amino aci	Abb78178 Amino aci
33	211	44.2	78	5	ABB78164 Amino aci	Abb78164 Amino aci
34	210	44.0	90	5	ABB78165 Amino aci	Abb78165 Amino aci
35	207	43.4	88	5	ABB78171 Amino aci	Abb78171 Amino aci
36	207	43.4	88	5	ABB78172 Amino aci	Abb78172 Amino aci
37	207	43.4	88	5	ABB78173 Amino aci	Abb78173 Amino aci
38	207	43.4	88	6	ABP77219 N. gonorr	Abp77219 N. gonorr
39	182.5	38.3	90	5	ABB78167 Amino aci	Abb78167 Amino aci
40	175	36.7	76	5	ABB78166 Amino aci	Abb78166 Amino aci
41	75	15.7	681	8	ADN73327 Thale cre	Adn73327 Thale cre
42	73	15.3	158	3	AAQ10836 Arabidops	Aaq10836 Arabidops
43	73	15.3	487	8	ADN74065 Thale cre	Adn74065 Thale cre
44	73	15.3	500	5	AAE27877 Arabidops	Aae27877 Arabidops
45	72.5	15.2	333	4	AAO23396 Pseudomon	Aao23396 Pseudomon
46	72	15.1	314	7	AAO23396 Plant ful	Aao23396 Plant ful
47	72	15.1	732	8	ADX92564 Polypepti	Adm48031 Polypepti
48	72	15.1	1043	8	ADM48031 Polypepti	Aar97281 Helicobac
49	71.5	15.0	506	2	AAR97281 Helicobac	Abt52698 Protein s
50	71.5	15.0	2000	6	ABR52698 Protein s	Adk61900 Disease t
51	71.5	15.0	2000	7	ADK61900 Disease t	Abu24966 Protein e
52	70.5	14.8	401	6	ABU24966 Protein e	Aay60188 Human end
53	70	14.7	148	2	AAV60188 Human end	Adp64626 Human onc
54	70	14.7	171	8	ADP64626 Human onc	Adp64627 Human onc
55	70	14.7	185	8	ADP64627 Human onc	Adb65159 Human pro
56	70	14.7	381	7	ADB65159 Human pro	Aab24352 Human pro
57	70	14.7	400	3	AAAB24352 Human pro	Abt47475 Breast ca
58	70	14.7	400	6	ABR47475 Breast ca	Abd75332 Prostate
59	70	14.7	400	7	ADB75332 Prostate	Ady72549 Human GP7
60	70	14.7	400	9	ADY72549 Human GP7	Aay91526 Human sec
61	70	14.7	401	3	AAV91526 Human sec	Aay99368 Human PRO
62	70	14.7	401	3	AAV99368 Human PRO	Aab66117 Protein o
63	70	14.7	401	4	AAAB66117 Protein o	Aau12414 Human PRO
64	70	14.7	401	4	AAU12414 Human PRO	Aab49770 Amyloid-b
65	70	14.7	401	4	AAAB93295 Human pro	Aab93295 Human pro
66	70	14.7	401	4	AAAB93295 Human pro	Aab88480 Human mem
67	70	14.7	401	4	AAAB88480 Human mem	Abp65020 Human pro
68	70	14.7	401	5	ABP65020 Human pro	Abp65020 Human pro
69	70	14.7	401	6	ABO17858 Human PRO	Abu81112 Human PRO
70	70	14.7	401	6	ABU81112 Human PRO	Abu66812 Human PRO
71	70	14.7	401	6	ABU66812 Human PRO	Abu59893 Novel sec
72	70	14.7	401	6	ABU59893 Novel sec	AbO25083 Human sec
73	70	14.7	401	6	ABO25083 Human sec	Abu67088 Human sec
74	70	14.7	401	6	ABU67088 Human sec	Ada46005 Novel hum
75	70	14.7	401	6	ADA46005 Novel hum	

ALIGNMENTS

RESULT 1
ID ABB78170 standard; protein; 87 AA.
XX ABB78170;
AC
XX 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of a YggX homologue.
DE
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnck JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 477; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.9e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60
Db 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 2
ABO74609
ID ABO74609 standard; protein; 122 AA.
XX
AC ABO74609;
XX
DT 29-JUL-2004 (first entry)
XX
DE Pseudomonas aeruginosa polypeptide #6784.
XX
KW Bacterial infection; Pseudomonas aeruginosa infection; antibacterial.
XX
OS Pseudomonas aeruginosa.
XX
PN US6551795-B1.
XX
PD 22-APR-2003.
XX
PF 18-FEB-1999; 99US-00252991.
XX
PR 18-FEB-1998; 98US-0074788P.
PR 27-JUL-1998; 98US-0094190P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Rubenfield MJ, Nolling J, Deloughery C, Bush D;
XX
DR WPI; 2003-615309/58.

DR N-PSDB; ABD08180.
XX
PT Novel isolated nucleic acid encoding Pseudomonas aeruginosa polypeptide,
PT useful as molecular targets for diagnostics, prophylaxis and treatment of
PT pathological conditions resulting from bacterial infection.
XX
PS Disclosure; SEQ ID NO 23355; 455pp; English.
XX

XX The invention relates to Pseudomonas aeruginosa polypeptides and the
CC polynucleotides encoding them. The sequences are useful in diagnosis and
CC therapy of pathological conditions, as molecular targets for diagnostics,
CC prophylaxis and treatment of pathological conditions resulting from a
CC bacterial infection, for evaluating a compound, such as a polypeptide,
CC for the ability to bind a P. aeruginosa nucleic acid, as components of
CC effective antibacterial targets, as targets for antibacterial drugs,
CC including anti-P. aeruginosa drugs, as templates for recombinant
CC production of P. aeruginosa-derived peptides or polypeptides, as target
CC components for diagnosis and/or treatment of P. aeruginosa-caused
CC infection, and in detection of P. aeruginosa sequences or other sequences
CC of Pseudomonas species using biochip technology. Sequences ABO67826-
CC ABO84396 represent P. aeruginosa polypeptides of the invention. Note: The
CC sequence data for this patent did not form part of the printed
CC specification but was obtained in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX

Query Match 100.0%; Score 477; DB 7; Length 122;
Best Local Similarity 100.0%; Pred. No. 3e-52;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 60
Db 33 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 92

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
Db 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 3
ABB78168
ID ABB78168 standard; protein; 90 AA.
XX
AC ABB78168;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Pseudomonas syringae.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnck JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.51253 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477
Sequence: 1 MSRTVMCRKHYHEELPGILDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	477	100.0	90	2 H83003	conserved hypothet
2	236	49.5	90	2 C64013	hypothetical prote
3	231	48.4	91	2 A85954	hypothetical prote
4	231	48.4	91	2 A65082	hypothetical prote
5	231	48.4	91	2 F91108	hypothetical prote
6	228	47.8	91	2 AH0879	conserved hypothet
7	223	46.8	90	2 C82320	conserved hypothet
8	210	44.0	90	2 A10116	conserved hypothet
9	207	43.4	88	2 H81014	conserved hypothet
10	192	40.3	105	2 C82624	conserved hypothet
11	175	36.7	93	2 B84994	hypothetical prote
12	80.5	16.9	314	2 JC5534	catechol 2,3-dioxy
13	73	15.3	500	2 B96739	hypothetical prote
14	72	15.1	435	2 D82905	hypothetical prote
15	71.5	15.0	314	2 S31402	catechol 2,3-dioxy
16	71.5	15.0	2748	2 S57976	nuclear migration
17	69	14.5	926	2 T24923	hypothetical prote
18	68.5	14.4	506	2 H64618	sigma-54 interacti
19	68	14.3	1083	1 S53048	alpha-mannosidase
20	68	14.3	1148	2 D85360	hypothetical prote
21	67	14.0	282	2 D97138	DNA replication pr
22	66.5	13.9	532	2 H72730	probable acyl-CoA
23	66	13.8	1638	2 D87749	protein unc-73b [i
24	66	13.8	2488	2 T42739	guanine nucleotide
25	65.5	13.7	314	2 JE0127	catechol 2,3-dioxy
26	65.5	13.7	342	2 T19021	probable inositol
27	65.5	13.7	2485	1 H71621	serine/threonine-s
28	65	13.6	468	1 T33857	hypothetical prote
29	64.5	13.5	523	2 S23384	protein kinase (EC

30	64.5	13.5	766	2 T48463	hypothetical prote
31	64	13.4	283	2 H86839	hypothetical prote
32	64	13.4	642	2 D96777	hypothetical prote
33	64	13.4	670	2 T29898	kinesin protein OS
34	64	13.4	1553	2 S67483	adenosinetriphosph
35	63.5	13.3	613	2 AH2398	hypothetical prote
36	63	13.2	331	2 G84646	hypothetical prote
37	63	13.2	506	2 F71895	hypothetical prote
38	63	13.2	900	2 T33734	hypothetical prote
39	63	13.2	1645	2 A37792	spectrin beta-H ch
40	62.5	13.1	316	2 T50027	annexin-like prote
41	62.5	13.1	433	2 G70345	hypothetical prote
42	62.5	13.1	637	2 S66236	acetylcholinestera
43	62.5	13.1	985	2 T10339	DNA-directed DNA p
44	62	13.0	244	2 C90580	DNA processing pro
45	62	13.0	442	2 B81418	adenylosuccinate 1
46	62	13.0	830	2 S56940	factor arrest prot
47	62	13.0	921	2 A83968	isoleucyl-tRNA syn
48	62	13.0	1290	1 DVBY86	mating pheromone a
49	62	13.0	4063	2 T42993	probable spectrin
50	62	13.0	4101	2 T23630	hypothetical prote
51	61.5	12.9	218	2 C70536	hypothetical prote
52	61.5	12.9	455	2 D75043	sexyl-tRNA synthet
53	61.5	12.9	509	2 T21512	hypothetical prote
54	61.5	12.9	767	2 T31558	hypothetical prote
55	61.5	12.9	1090	2 AG1749	glycosidase homolo
56	61.5	12.9	1091	2 AF1380	glycosidase homolo
57	61.5	12.9	1111	2 A86922	probable arabinosy
58	61.5	12.9	1120	2 H88449	protein F54D8.1 [i
59	61	12.8	284	2 G72662	hypothetical prote
60	61	12.8	367	2 E81379	probable membrane
61	61	12.8	378	2 H95045	mannitol-1-phospha
62	61	12.8	389	2 T14751	hypothetical prote
63	61	12.8	552	2 C83965	transposase (12) B
64	61	12.8	583	2 A70380	arginine-tRNA liga
65	61	12.8	964	2 T01860	reverse transcript
66	61	12.8	1203	2 A39607	DNA-directed RNA p
67	61	12.8	1232	2 D64413	cobalamin biosynth
68	61	12.8	1822	2 S44849	K12H4.8 protein -
69	60.5	12.7	71	2 H97137	hypothetical prote
70	60.5	12.7	299	2 T29546	protein SPE-11 - C
71	60.5	12.7	303	2 A64423	modification methy
72	60.5	12.7	460	2 G71117	serine-tRNA ligase
73	60.5	12.7	1067	2 D96545	probable DNA polym
74	60.5	12.7	1142	2 B96519	hypothetical prote
75	60	12.6	150	2 F90212	hypothetical prote

ALIGNMENTS

RESULT 1
H83003
conserved hypothetical protein PA5148 [imported] - Pseudomonas aeruginosa (strain PA01)
C/Species: Pseudomonas aeruginosa
C/Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 05-Oct-2004
C/Accession: H83003
R/Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A/Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A/Reference number: AB2950; MUID:20437337; PMID:10984043
A/Accession: H83003
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <STO>
A/Cross-references: UNIPARC:UPI000000C5F26; GB:AE004927; GB:AE004091; NID:g9951437; PIDN:7
A/Experimental source: strain PA01
C/Genetics:
A/Gene: PA5148
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 100.0%; Score 477; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60
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Db 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
|||||
Db 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87

RESULT 2
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R./Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A./Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd. A./Reference number: A64000; MUID:95350630; PMID:7542800
A./Accession: C64013
A./Status: nucleic acid sequence not shown; translation not shown
A./Molecule type: DNA
A./Residues: 1-90 <TIGR>
A./Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C./Superfamily: fe(ii) trafficking protein YgX

Query Match 49.5%; Score 236; DB 2; Length 90;
Best Local Similarity 54.5%; Pred. No. 1.3e-17;
Matches 48; Conservative 14; Mismatches 24; Indels 2; Gaps 2;

QY 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60
|||||
Db 1 MARTVFCYLLKKEAEGLDFOLYPSELGKRIFDSVSKQAWGEWIKQOTMLVNEKLLNMNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
|||||
Db 61 EHRKLLQOEMVNFLEFGKD-VHIEGYVP 87

RESULT 3
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R./Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A./Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A./Reference number: A85480; MUID:21074935; PMID:11206551
A./Accession: A85954
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-91 <STO>
A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A./Experimental source: strain O157:H7, substrain EDL933
C./Genetics:
A./Gene: yggX
C./Superfamily: fe(ii) trafficking protein YgX

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60
|||||
Db 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60

Db 1 MSRTICTFLQREAGQDFQLYPSELGKRIYNEISKEAWAQWQKHQTMLINEKLLNMNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
|||||
Db 61 EHRKLLQOEMVNFLEFGKEVHIEGYTP 87

RESULT 4
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R./Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Coi
.A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997
A./Title: The complete genome sequence of Escherichia coli K-12.
A./Reference number: A64720; MUID:97426617; PMID:9278503
A./Accession: A65082
A./Status: preliminary; nucleic acid sequence not shown; translation not shown
A./Molecule type: DNA
A./Residues: 1-91 <BLAT>
A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g1
A./Experimental source: strain K-12, substrain MG1655
C./Superfamily: fe(ii) trafficking protein YgX

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60
|||||
Db 1 MSRTICTFLQREAGQDFQLYPSELGKRIYNEISKEAWAQWQKHQTMLINEKLLNMNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
|||||
Db 61 EHRKLLQOEMVNFLEFGKEVHIEGYTP 87

RESULT 5
F91108
hypothetical protein EC8383 [imported] - Escherichia coli (strain O157:H7, substrain R1
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R./Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.;
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001
A./Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A./Reference number: A99629; MUID:21156231; PMID:11258796
A./Accession: F91108
A./Status: preliminary
A./Molecule type: DNA
A./Residues: 1-91 <HAY>
A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A./Experimental source: strain O157:H7, substrain R1MD 0509952
C./Genetics:
A./Gene: EC8383
C./Superfamily: fe(ii) trafficking protein YgX

Query Match 48.4%; Score 231; DB 2; Length 91;
Best Local Similarity 51.7%; Pred. No. 4.2e-17;
Matches 45; Conservative 10; Mismatches 32; Indels 0; Gaps 0;

QY 1 MSRTVMCRKYHEELPGLDPRPPYGAKEGEDIYNNVSRKAWDEWQKHQTMLINERRLLNMNNA 60
|||||
Db 1 MSRTICTFLQREAGQDFQLYPSELGKRIYNEISKEAWAQWQKHQTMLINEKLLNMNNA 60

QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
|||||
Db 61 EHRKLLQOEMVNFLEFGKEVHIEGYTP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.2096 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477

Sequence: 1.MSRTVMCKRYHBLPLGLDRP.....QEMDKFLSGBDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database : UniProt_05.80:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	477	100.0	90	1	FETP_PSEAB
2	420	88.1	90	2	Q4J228 AZOVI
3	408	85.5	90	1	FETP_PSESM
4	408	85.5	90	2	Q4ZLP3_PSESY
5	401	84.1	90	2	Q4KJ22_PSEFS
6	400	83.9	90	1	FETP_PSEPK
7	383	80.3	90	2	Q6T7F6_PSEFL
8	258.5	54.2	90	1	FETP_ACTAD
9	250	52.4	96	2	Q4FVJ7_9GAMM
10	245	51.4	90	1	FETP_IDILIO
11	244	51.2	91	1	FETP_MANSN
12	241	50.5	89	1	FETP_LBGRP
13	241	50.5	89	1	FETP_LBGRH
14	240	50.3	89	1	FETP_LBGRU
15	240	50.3	90	1	FETP_BORBR
16	240	50.3	90	1	FETP_BORBR
17	240	50.3	90	1	FETP_BORBR
18	236	49.5	90	1	FETP_HABIN
19	236	49.5	90	2	Q4QMD9_HABIS
20	235	49.3	90	1	FETP_METCA
21	235	49.3	92	1	FETP_SHEON
22	233	48.8	90	1	FETP_VIBF1
23	230	48.2	90	1	FETP_PASNU
24	230	48.2	90	1	FETP_PASNU
25	229	48.0	90	1	FETP_ERMCT
26	228	47.8	90	1	FETP_PHOCR
27	228	47.8	91	1	FETP_RALSO
28	227	47.6	90	1	FETP_NITEU
29	227	47.6	90	1	FETP_VIBVU
30	227	47.6	90	1	FETP_VIBVU
31	227	47.6	91	1	FETP_BURMA

ALIGNMENTS

32	227	47.6	91	1	FETP_BURPS	Q63sj4 burkholderi
33	226	47.4	90	1	FETP_ECO57	P0a8p4 escherichia
34	226	47.4	90	1	FETP_ECOLI	P0a8p3 escherichia
35	226	47.4	90	1	FETP_SHIFL	P0a8p5 shigella fl
36	224	47.0	91	2	Q4L5T9_9BURK	Q41s19 burkholderi
37	223	46.8	90	1	FETP_SALCH	Q57k04 salmoneila
38	223	46.8	90	1	FETP_SALPA	Q5pmu1 salmoneila
39	223	46.8	90	1	FETP_SALTI	P67618 salmoneila
40	223	46.8	90	1	FETP_SALTY	P67617 salmoneila
41	223	46.8	90	1	FETP_VIBCH	Q9kur4 vibrio chol
42	222	46.5	90	1	FETP_ECOL6	Q8fe19 escherichia
43	222	46.5	90	1	FETP_VIBPA	Q871i5 vibrio para
44	222	46.5	94	1	FETP_HAEDU	Q7vkb6 haemophilus
45	220	46.1	90	1	FETP_COXBU	Q83d06 coxiella bu
46	218	45.7	90	1	FETP_YERPS	Q66m3 yersinia ps
47	215	45.1	78	1	FETP_WIGBR	Q8d3c5 wigglewort
48	210	44.0	90	1	FETP_CHRVO	Q7nsr4 chromobacte
49	210	44.0	90	1	FETP_YERPE	Q8zhe7 yersinia pe
50	208	43.6	92	1	FETP_XANOR	Q5gy22 xanthomonas
51	207	43.4	88	1	FETP_NEIG1	Q5f553 neisseria g
52	207	43.4	88	1	FETP_NEIMB	P67615 neisseria m
53	207	43.4	88	1	FETP_NEIMB	P67616 neisseria m
54	204	42.8	91	1	FETP_XANAC	Q8pjh7 xanthomonas
55	202	42.3	87	1	FETP_PRAIT	Q5nhj8 francisella
56	197	41.3	92	1	FETP_XANCP	Q8p829 xanthomonas
57	197	41.3	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
58	195	40.9	78	1	FETP_BUCAP	Q8K925 buchnera ap
59	193	40.5	90	1	FETP_XYLFT	Q87d06 xylella fas
60	192	40.3	90	1	FETP_XYLFA	Q9pc73 xylella fas
61	190	39.8	79	1	FETP_BUCAI	Q7vg19 candidatus
62	175	36.7	77	1	FETP_BUCAI	P57618 buchnera ap
63	174	36.5	87	1	FETP_BUCBP	Q89a44 buchnera ap
64	171	35.8	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	81.5	17.1	326	2	Q5SGT4_DICDI	Q55gt4 dictyosteli
66	80.5	16.9	314	2	Q7MOR6_BURCE	Q7m0r6 burkholderi
67	79	16.6	703	2	Q4WPT2_ASPFU	Q4wpt2 aspergillus
68	78.5	16.5	1097	1	KIFID_FAT	Q35787 rattus norv
69	78	16.4	410	2	Q8SRF4_ENCCU	Q8srf4 encephalito
70	76.5	16.0	314	2	Q9RB85_9BURK	Q9rb85 burkholderi
71	75.5	15.8	280	2	Q81BK9_BACCR	Q81bk9 bacillus ce
72	75	15.7	681	2	Q91V16_ARATH	Q91v16 arabidopsis
73	74	15.5	525	2	Q6BNV8_DEBHA	Q6bnv8 debaryomyce
74	73.5	15.4	307	2	Q6BFB3_PARTE	Q6bfb3 paramecium
75	73.5	15.4	549	2	Q6BKE2_DEBHA	Q6bke2 debaryomyce

RESULT 1

FETP_PSEAB
ID FETP_PSEAB STANDARD; PRT; 90 AA.
AC Q9HU36;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PA5148;
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Sailer M.H. Jr., Hancock R.E.W., Lory S., Olson M.V.,
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an

```
RT opportunistic pathogen.";
RL Nature 406:959-964(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE004927; AAG08533.1; -; Genomic_DNA.
DR PDB; 1T07; X-ray; A=1-90.
DR SMR; Q9HU36; 1-79.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
DR ProDom; PD029191; DUF495; 1.
DR 3D-structure; Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10625 MW; 02BB6CEBF7AEF39 CRC64;

Query Match 100.0%; Score 477; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.6e-42;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60
DB 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60

OY 61 EDRKFLQEMDKFLSGEDYAKADGYVP 87
DB 61 EDRKFLQEMDKFLSGEDYAKADGYVP 87

RESULT 2
Q4J228_AZOVI PRELIMINARY; PRT; 90 AA.
ID Q4J228;
AC Q4J228;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein.
GN ORFNames=AvindRAFT_6916;
OS Azotobacter vinelandii AVOP.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Azotobacter.
OX NCBI_TaxID=322710;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RT "Sequencing of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-ORNL);
RA Larimer F., Land M.;
RT "Annotation of the draft genome assembly of Azotobacter vinelandii
RT AVOP.";
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG DOE Joint Genome Institute;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
RN [4]
```

```
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=AVOP;
RG US DOE Joint Genome Institute (JGI-PGF);
RA Copeland A., Lucas S., Lapidus A., Barry K., Dettler C., Glavina T.,
RA Hammon N., Israni S., Pittluck S., Richardson P.;
RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC -----
DR EMBL; AAU03000001; EAM08363.1; -; Genomic_DNA.
DR KW Hypothetical protein.
SQ SEQUENCE 90 AA; 10777 MW; F6FE766143D3E5E1 CRC64;

Query Match 88.1%; Score 420; DB 2; Length 90;
Best Local Similarity 88.4%; Pred. No. 5.7e-36;
Matches 76; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 1 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMNNA 60
DB 1 MTRTVHCRKYKEELPGLDRPPYPGPKGEDIYNNVSRQAWDEWQKHQTMLINERRLNMNNA 60

OY 61 EDRKFLQEMDKFLSGEDYAKADGYVP 86
DB 61 EDRKFLQEMDKFLSGEDYAKADGYVP 86

RESULT 3
FETP_PSESM
ID FETP_PSESM STANDARD; PRT; 90 AA.
AC Q87UF5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=PSPT05343;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindberg M., Selengut J., Paulsen I.T.,
RA Gwin M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Daugherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidsen T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Utherback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collier A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000.";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE016853; AAO58769.1; -; Genomic_DNA.
DR SMR; Q87UF5; 1-79.
DR TIGR; PSPT05343; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YgX; 1.
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.6378 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477
Sequence: 1 MSRTVMCRKRYHEELPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents_AA:*

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- 5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	477	100.0	122	2	US-09-252-991A-23355 Sequence 23355, A
2	262.5	55.0	92	2	US-09-328-352-5456 Sequence 5456, Ap
3	235	49.3	110	2	US-09-540-236-2859 Sequence 2859, Ap
4	230	48.2	93	2	US-09-543-681A-5443 Sequence 5443, Ap
5	223	46.8	107	2	US-09-489-039A-11962 Sequence 11962, A
6	72	15.1	314	2	US-09-716-865-4 Sequence 4, Appli
7	71.5	15.0	506	1	US-08-849-480A-5 Sequence 5, Appli
8	70	14.7	148	2	US-09-673-395A-389 Sequence 389, App
9	70	14.7	381	2	US-10-104-047-3313 Sequence 3313, Ap
10	70	14.7	401	2	US-09-489-847-202 Sequence 202, App
11	70	14.7	401	2	US-10-012-231A-100 Sequence 100, App
12	70	14.7	401	2	US-10-015-389A-100 Sequence 100, App
13	70	14.7	401	2	US-10-006-768A-100 Sequence 100, App
14	70	14.7	401	2	US-10-015-671A-100 Sequence 100, App
15	70	14.7	401	2	US-10-015-393A-100 Sequence 100, App
16	70	14.7	401	2	US-10-011-833A-100 Sequence 100, App
17	70	14.7	401	2	US-10-006-041A-100 Sequence 100, App
18	70	14.7	401	2	US-10-012-064A-100 Sequence 100, App
19	70	14.7	401	2	US-10-030-269A-8 Sequence 8, Appli
20	70	14.7	422	2	US-09-489-847-357 Sequence 357, App
21	68	14.3	443	2	US-09-248-796A-16816 Sequence 16816, A
22	67.5	14.2	505	2	US-09-543-681A-7151 Sequence 7151, Ap
23	67	14.0	563	2	US-09-902-540-14552 Sequence 14552, A
24	66	13.8	361	2	US-09-134-001C-3862 Sequence 3862, Ap
25	65.5	13.7	375	2	US-09-583-110-4950 Sequence 4950, Ap
26	65.5	13.7	382	2	US-09-107-433-3837 Sequence 3837, Ap
27	65	13.6	163	2	US-09-270-767-33714 Sequence 33714, A

28	65	13.6	420	2	US-09-248-796A-15323	Sequence 15323, A
29	65	13.6	1042	2	US-09-792-024-106	Sequence 106, App
30	64.5	13.5	327	2	US-09-902-540-10864	Sequence 10864, A
31	64.5	13.5	343	2	US-09-270-767-41701	Sequence 41701, A
32	64.5	13.5	839	2	US-09-758-282B-232	Sequence 232, App
33	64.5	13.5	839	2	US-09-577-304A-232	Sequence 232, App
34	64	13.4	1103	2	US-09-162-373-1	Sequence 1, Appli
35	64	13.4	1103	2	US-09-467-946-1	Sequence 1, Appli
36	64	13.4	1123	2	US-09-949-016-9935	Sequence 9935, Ap
37	63.5	13.3	403	2	US-09-543-681A-6083	Sequence 6083, Ap
38	63.5	13.3	1967	2	US-09-849-602-16	Sequence 16, Appli
39	63	13.2	254	2	US-09-586-106D-111	Sequence 111, App
40	63	13.2	254	2	US-10-799-870-111	Sequence 111, App
41	62.5	13.1	3542	2	US-10-087-013-2	Sequence 2, Appli
42	62	13.0	595	2	US-09-902-540-16334	Sequence 16334, A
43	61	12.8	193	2	US-09-252-991A-17828	Sequence 17828, A
44	61	12.8	378	2	US-09-583-110-3941	Sequence 3941, Ap
45	61	12.8	378	2	US-09-107-433-5197	Sequence 5197, Ap
46	61	12.8	381	2	US-09-949-016-9788	Sequence 9788, Ap
47	61	12.8	381	2	US-09-964-899-13	Sequence 13, Appli
48	60.5	12.7	302	2	US-09-902-540-13084	Sequence 13084, A
49	60.5	12.7	315	2	US-10-164-595-12	Sequence 12, Appli
50	60	12.6	243	2	US-09-248-796A-20306	Sequence 20306, A
51	60	12.6	286	2	US-09-248-796A-20057	Sequence 20057, A
52	60	12.6	331	2	US-08-961-083-212	Sequence 212, App
53	60	12.6	331	2	US-09-536-784-212	Sequence 212, App
54	60	12.6	331	2	US-09-765-271-212	Sequence 212, App
55	60	12.6	331	2	US-09-765-272A-212	Sequence 212, App
56	60	12.6	338	2	US-09-328-352-7427	Sequence 7427, Ap
57	60	12.6	341	2	US-09-252-991A-32797	Sequence 32797, A
58	60	12.6	344	2	US-08-961-083-192	Sequence 192, App
59	60	12.6	344	2	US-09-536-784-192	Sequence 192, App
60	60	12.6	344	2	US-09-765-271-192	Sequence 192, App
61	60	12.6	344	2	US-09-765-272A-192	Sequence 192, App
62	60	12.6	370	2	US-09-583-110-5251	Sequence 5251, App
63	60	12.6	370	2	US-09-769-787-160	Sequence 160, App
64	60	12.6	375	2	US-09-107-433-4121	Sequence 4121, App
65	60	12.6	454	2	US-09-771-161A-95	Sequence 95, Appli
66	60	12.6	504	2	US-09-538-092-1170	Sequence 1170, Ap
67	60	12.6	505	2	US-09-949-016-6117	Sequence 6117, Ap
68	60	12.6	505	2	US-09-771-161A-186	Sequence 186, App
69	60	12.6	513	2	US-09-949-016-11517	Sequence 11517, A
70	60	12.6	531	2	US-09-540-236-2072	Sequence 2072, Ap
71	60	12.6	1122	2	US-10-146-704-2	Sequence 2, Appli
72	59.5	12.5	488	2	US-08-911-824-95	Sequence 95, Appli
73	59.5	12.5	491	1	US-08-912-129A-56	Sequence 56, Appli
74	59.5	12.5	491	2	US-08-911-824-56	Sequence 56, Appli
75	59.5	12.5	599	2	US-08-911-824-108	Sequence 108, App

ALIGNMENTS

RESULT 1
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252, 991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074, 788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094, 190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-23355

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Best Local Similarity 100.0%; Pred. No. 3.6e-55;
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QY 61 EDRKFLQOEMDKFLSGEDYAKADGYVP 87
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DB 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 2

US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Best Local Similarity 52.3%; Pred. No. 5.9e-27;
Matches 46; Conservative 19; Mismatches 22; Indels 1; Gaps 1;

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DB 4 MSRQVFCRKYQKMEGLDFAPFPGAKGQFFENVSKQAWQEWLQHTTLINERKLNVEEP 63

QY 61 EDRKFLQOEMDKFLSG-EDYAKADGYVP 87
|:||||:|:|:
DB 64 BAKKFLQOERKEFFNDESVEKAEGWKP 91

RESULT 3

US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:

; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

Query Match 49.3%; Score 235; DB 2; Length 110;
Best Local Similarity 48.2%; Pred. No. 3.3e-23;
Matches 40; Conservative 18; Mismatches 25; Indels 0; Gaps 0;

QY 5 VMCRTYHEELPGLDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNABDRK 64
|:||||:|:|:
DB 25 VFCRKYQQLPRLPNPFPNAKGQEIQDTISAKAWNAWLELQTMLINEKHLSPIDPAKK 84

QY 65 FLQOEMDKFLSGEDYAKADGYVP 87

DB 85 YLNEQREKFLDNGDYEKPAGYKP 107

RESULT 4
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:

; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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DB 4 MSRTIFCTFLNKADGLDFQLYPGELGKRIFNEISKEAWQMAKQTMLINEKLTWNP 63

QY 61 EDRKFLQOEMDKFL-SGEDYAKADGYVP 87
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DB 64 DDRKLEQEMVRFLEBGHD-VHIDGYTP 90

RESULT 5
US-09-489-039A-11962

; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 46.8%; Score 223; DB 2; Length 107;
Best Local Similarity 51.1%; Pred. No. 1.2e-21;
Matches 45; Conservative 13; Mismatches 28; Indels 2; Gaps 2;

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DB 17 MSRTIFCTFLQREADGDFQLYPGELGKRITNEYISKEAWQKHQTMLINEKLSMNP 76

QY 61 EDRKFLQOEMDKFL-SGEDYAKADGYVP 87
|:||||:|:|:
DB 77 EHRKLEQEMVQFLFEGKD-VHIEGYTP 103

RESULT 6
US-09-716-865-4
; Sequence 4, Application US/09716865

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 54.8952 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477

Sequence: 1 MSRTVMCRKYHEELPGIDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	408	85.5	90	3	US-09-955-502-23
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4	242	50.7	87	3	US-09-955-502-31
5	240	50.3	87	3	US-09-955-502-2
6	240	50.3	87	3	US-09-955-502-3
7	236	49.5	87	3	US-09-955-502-7
8	235	49.3	87	3	US-09-955-502-32
9	235	49.3	88	3	US-09-955-502-9
10	233	48.8	91	3	US-09-955-502-5
11	231	48.4	91	3	US-09-955-502-11
12	231	48.4	91	3	US-09-955-502-12
13	231	48.4	91	3	US-09-955-502-13
14	230	48.2	87	3	US-09-955-502-6
15	228	47.8	88	3	US-09-955-502-15
16	228	47.8	91	3	US-09-955-502-14
17	228	47.8	91	3	US-09-955-502-16
18	228	47.8	91	3	US-09-955-502-17
19	227	47.6	87	3	US-09-955-502-29
20	227	47.6	87	3	US-09-955-502-30
21	223	46.8	90	3	US-09-955-502-10
22	222.5	46.6	86	3	US-09-955-502-4
23	222	46.5	87	3	US-09-955-502-8
24	221	46.3	91	3	US-09-955-502-18
25	220	46.1	88	3	US-09-955-502-33
26	211	44.2	78	3	US-09-955-502-19
27	210	44.0	90	3	US-09-955-502-20

28	207	43.4	88	3	US-09-955-502-26	Sequence 26, Appl
29	207	43.4	88	3	US-09-955-502-27	Sequence 27, Appl
30	207	43.4	88	3	US-09-955-502-28	Sequence 28, Appl
31	192	40.3	89	3	US-09-955-502-22	Sequence 22, Appl
32	175	36.7	76	3	US-09-955-502-21	Sequence 21, Appl
33	72.5	15.2	333	6	US-11-097-143-16017	Sequence 16017, A
34	72	15.1	732	4	US-10-425-114-55228	Sequence 55228, A
35	72	15.1	1043	4	US-10-310-154-449	Sequence 449, App
36	72	15.1	1043	5	US-10-732-923-535	Sequence 535, App
37	71	14.9	372	4	US-10-424-599-239645	Sequence 239645, A
38	70.5	14.8	401	4	US-10-282-122A-52890	Sequence 52890, A
39	70	14.7	381	4	US-10-104-047-3313	Sequence 3313, Ap
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41	70	14.7	400	4	US-10-177-293-184	Sequence 184, App
42	70	14.7	400	5	US-10-759-803-2	Sequence 2, Appl1
43	70	14.7	400	5	US-10-934-520-2	Sequence 2, Appl1
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57	70	14.7	401	4	US-10-143-114-486	Sequence 486, App
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64	70	14.7	401	4	US-10-141-755-486	Sequence 486, App
65	70	14.7	401	4	US-10-143-032-486	Sequence 486, App
66	70	14.7	401	4	US-10-006-485A-100	Sequence 100, App
67	70	14.7	401	4	US-10-013-907A-100	Sequence 100, App
68	70	14.7	401	4	US-10-015-499A-100	Sequence 100, App
69	70	14.7	401	4	US-10-123-108-486	Sequence 486, App
70	70	14.7	401	4	US-10-123-236-486	Sequence 486, App
71	70	14.7	401	4	US-10-123-261-486	Sequence 486, App
72	70	14.7	401	4	US-10-140-921-486	Sequence 486, App
73	70	14.7	401	4	US-10-140-928-486	Sequence 486, App
74	70	14.7	401	4	US-10-015-393A-100	Sequence 100, App
75	70	14.7	401	4	US-10-015-869A-100	Sequence 100, App

ALIGNMENTS

RESULT 1
US-09-955-502-25
; Sequence 25, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:25:12 ; Search time 4.75626 Seconds
(without alignments)
272.313 Million cell updates/sec

Title: US-09-955-502A-25

Perfect score: 477
Sequence: 1 MSRTVMCRKYHEBLPGLDRP.....QEMDKFLSGEDYAKADGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA_New:*
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2: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	207	43.4	88	6	US-10-467-657-968	Sequence 968, App
2	70	14.7	381	7	US-11-072-512-3313	Sequence 3313, App
3	70	14.7	401	6	US-10-131-826A-486	Sequence 486, App
4	65	13.6	353	7	US-11-098-686-10774	Sequence 10774, A
5	64.5	13.5	1560	7	US-11-059-982-1	Sequence 1, Appli
6	60	12.6	370	6	US-10-873-528-160	Sequence 160, App
7	58.5	12.3	310	7	US-11-198-746-88	Sequence 88, Appl
8	58.5	12.3	310	7	US-11-198-794-88	Sequence 88, Appl
9	58.5	12.3	315	7	US-11-198-746-91	Sequence 91, Appl
10	58.5	12.3	315	7	US-11-198-794-91	Sequence 91, Appl
11	58.5	12.3	322	7	US-11-198-746-89	Sequence 89, Appl
12	58.5	12.3	322	7	US-11-198-794-89	Sequence 89, Appl
13	58.5	12.3	528	7	US-11-198-746-90	Sequence 90, Appl
14	58.5	12.3	528	7	US-11-198-794-90	Sequence 90, Appl
15	58.5	12.3	548	7	US-11-198-746-86	Sequence 86, Appl
16	58.5	12.3	548	7	US-11-198-794-86	Sequence 86, Appl
17	58.5	12.3	695	7	US-11-198-746-87	Sequence 87, Appl
18	58.5	12.3	695	7	US-11-198-794-87	Sequence 87, Appl
19	58.5	12.3	832	7	US-11-065-943-100	Sequence 100, App
20	58.5	12.3	832	7	US-11-007-797A-11	Sequence 11, Appl
21	58.5	12.3	832	7	US-11-007-642B-11	Sequence 11, Appl
22	58.5	12.3	832	7	US-11-198-746-4	Sequence 4, Appli
23	58.5	12.3	832	7	US-11-198-794-4	Sequence 4, Appli
24	58.5	12.3	832	7	US-11-242-730-1	Sequence 1, Appli
25	58.5	12.3	833	7	US-11-198-746-85	Sequence 85, Appl

26	58.5	12.3	833	7	US-11-198-794-85	Sequence 85, Appl
27	58	12.2	589	7	US-11-072-512-2914	Sequence 2914, Ap
28	58	12.2	1206	6	US-10-467-657-72	Sequence 72, Appl
29	58	12.2	1206	6	US-10-467-657-3892	Sequence 3892, Ap
30	57.5	12.1	383	6	US-10-793-626-2426	Sequence 2426, Ap
31	57.5	12.1	1077	7	US-11-054-281-110	Sequence 110, App
32	57	11.9	426	6	US-10-858-730-81	Sequence 81, Appl
33	57	11.9	456	7	US-11-069-642-8	Sequence 8, Appli
34	57	11.9	600	7	US-11-072-512-3845	Sequence 3845, Ap
35	57	11.9	645	6	US-10-510-386-32	Sequence 32, Appl
36	57	11.9	3748	7	US-11-132-686-8	Sequence 8, Appli
37	57	11.9	3749	7	US-11-132-686-6	Sequence 6, Appli
38	57	11.9	3749	7	US-11-132-686-12	Sequence 12, Appl
39	57	11.9	3912	7	US-11-132-686-7	Sequence 7, Appli
40	57	11.9	3913	7	US-11-132-686-5	Sequence 5, Appli
41	57	11.9	3913	7	US-11-132-686-9	Sequence 9, Appli
42	56.5	11.8	2871	7	US-11-124-367A-264	Sequence 264, App
43	56	11.7	315	6	US-10-878-556A-178	Sequence 178, App
44	56	11.7	333	6	US-10-821-234-1036	Sequence 1036, App
45	56	11.7	647	7	US-11-000-463-722	Sequence 722, App
46	56	11.7	1897	6	US-10-821-234-1635	Sequence 1635, Ap
47	56	11.7	1907	7	US-11-000-463-250	Sequence 250, App
48	55.5	11.6	357	7	US-11-053-100-33	Sequence 33, Appl
49	55.5	11.6	400	7	US-11-202-566-27	Sequence 27, Appl
50	55.5	11.6	526	7	US-11-055-822-124	Sequence 124, App
51	55.5	11.6	657	7	US-11-053-100-35	Sequence 35, Appl
52	55	11.5	211	7	US-11-124-368A-175	Sequence 175, App
53	55	11.5	211	7	US-11-124-368A-176	Sequence 176, App
54	55	11.5	395	6	US-10-793-626-656	Sequence 656, App
55	55	11.5	701	6	US-10-467-657-7872	Sequence 7872, Ap
56	55	11.5	805	6	US-10-485-517-198	Sequence 198, App
57	55	11.5	1386	7	US-11-091-643-6	Sequence 6, Appli
58	54.5	11.4	39	6	US-10-841-956A-3	Sequence 3, Appli
59	54.5	11.4	39	7	US-11-029-003-3	Sequence 3, Appli
60	54.5	11.4	40	7	US-11-112-277-34	Sequence 34, Appl
61	54.5	11.4	203	6	US-10-454-437-326	Sequence 326, App
62	54.5	11.4	415	6	US-10-763-712A-25	Sequence 25, Appl
63	54.5	11.4	436	6	US-10-763-712A-5	Sequence 5, Appli
64	54.5	11.4	746	7	US-11-072-175-169	Sequence 169, App
65	54	11.3	426	6	US-10-858-730-80	Sequence 80, Appl
66	54	11.3	3433	6	US-10-714-781A-67	Sequence 67, Appl
67	53.5	11.2	612	6	US-10-467-657-3988	Sequence 3988, Ap
68	53.5	11.2	1717	7	US-11-182-016-20	Sequence 20, Appl
69	53	11.1	120	6	US-10-793-626-958	Sequence 958, App
70	53	11.1	120	6	US-10-793-626-1444	Sequence 1444, Ap
71	53	11.1	383	7	US-11-072-512-3140	Sequence 3140, Ap
72	53	11.1	532	6	US-10-793-626-546	Sequence 546, App
73	53	11.1	618	7	US-11-110-082-25	Sequence 25, Appl
74	53	11.1	744	7	US-11-186-284-37	Sequence 37, Appl
75	53	11.1	744	7	US-11-186-284-39	Sequence 39, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWln9, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 72.164 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-26

Perfect score: 467

Sequence: 1 MARWVFCVTKLNKEABGMKP.....QMEQYFFGGADAVQGYVPQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database:

A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	88	5	ABB78171 Amino aci
2	467	100.0	88	5	ABB78172 Amino aci
3	467	100.0	88	5	ABB78173 Amino aci
4	467	100.0	88	6	ABP77219 N. gonorr
5	339	72.6	87	5	ABB78175 Amino aci
6	333	71.3	87	5	ABB78174 Amino aci
7	294	63.0	87	5	ABB78176 Amino aci
8	290	62.1	87	5	ABB78148 Amino aci
9	290	62.1	87	5	ABB78147 Amino aci
10	272.5	58.4	86	5	ABB78149 Amino aci
11	271	58.0	89	9	AEB41576 L. pneumo
12	271	58.0	95	9	AEB38294 L. pneumo
13	258	55.2	88	5	ABB78178 Amino aci
14	243	52.0	87	5	ABB78177 Amino aci
15	240	51.4	90	5	ABB78155 Amino aci
16	235	50.3	87	5	ABB78153 Amino aci
17	230	49.3	88	5	ABB78154 Amino aci
18	228	48.8	91	5	ABB78150 Amino aci
19	227	48.6	87	5	ABB78152 Amino aci
20	227	48.6	107	7	ABO65445 Klebsiell
21	225.5	48.3	92	6	ADA34169 Acinetoba
22	221	47.3	93	7	ADF05158 Bacteri
23	219	46.9	87	5	ABB78169 Amino aci
24	217	46.5	87	5	ABB78151 Amino aci

25	213	45.6	91	5	ABB78158 Amino aci
26	213	45.6	91	5	ABB78157 Amino aci
27	213	45.6	91	5	ABB78156 Amino aci
28	211	45.2	88	5	ABB78160 Amino aci
29	211	45.2	91	5	ABB78161 Amino aci
30	211	45.2	91	5	ABB78159 Amino aci
31	211	45.2	91	5	ABB78162 Amino aci
32	210	45.0	78	5	ABB78164 Amino aci
33	207	44.3	122	7	ABO74609 Pseudomon
34	207	44.3	87	5	ABB78170 Amino aci
35	202	43.3	91	5	ABB78163 Amino aci
36	198	42.4	90	5	ABB78165 Amino aci
37	198	42.4	90	5	ABB78168 Amino aci
38	193.5	41.4	90	5	ABB78167 Amino aci
39	182	39.0	110	8	ADL05173 M. catarr
40	158	33.8	76	5	ABB78166 Amino aci
41	74	15.8	1122	6	ABU22044 Protein e
42	70	15.0	202	7	ABM90380 Rice abio
43	70	15.0	1079	8	ADN19463 Bacterial
44	69	14.8	774	4	ABG29304 Novel hum
45	68.5	14.7	361	7	ABO76259 Pseudomon
46	68	14.6	189	9	ADW18357 Pinus rad.
47	67.5	14.5	466	7	ABO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221 Protein e
49	66	14.1	418	7	ABO66638 Klebsiell
50	65.5	14.0	649	7	ADC94671 E. faeciu
51	65.5	14.0	1443	7	ADJ68530 Human hea
52	65.5	14.0	1935	7	ADJ70260 Human hea
53	65.5	14.0	3830	5	ABB81168 TRRAP pro
54	65.5	14.0	3830	8	ADJ78499 PAF/TRRAP
55	65.5	14.0	3830	8	ADQ19749 Human sof
56	65.5	14.0	3830	8	ADQ89826 Antagonis
57	65.5	14.0	3859	7	ADJ68548 Human hea
58	65.5	14.0	3859	8	ADS88242 Human pro
59	65	13.9	255	7	ADM27073 Hyperther
60	65	13.9	296	4	AAU35611 Haemophil
61	65	13.9	296	6	ABU30521 Protein e
62	65	13.9	438	2	AAV11015 H. pylori
63	65	13.9	442	2	AAW20830 H. pylori
64	65	13.9	465	2	AAW20303 H. pylori
65	64.5	13.8	207	6	ABM73508 Staphyloc
66	64.5	13.8	207	9	ADV16859 Staphyloc
67	64.5	13.8	207	9	ADW94758 Prolifera
68	64.5	13.8	362	7	ADF89476 Human ery
69	64.5	13.8	362	8	ADK48858 Human tra
70	64.5	13.8	362	8	ADP12457 Protein e
71	64	13.7	260	4	AAAM38702 Human pol
72	64	13.7	378	4	AAAM40488 Human tes
73	64	13.7	656	4	ABU53239 Human tes
74	64	13.7	656	8	ADJ28417 Human nuc
75	64	13.7	2426	2	ADH11285 Vertebrat

ALIGNMENTS

RESULT 1	ABB78171	standard; protein; 88 AA.
ID	ABB78171	
XX		
AC	ABB78171;	
XX		
DT	29-AUG-2003	(revised)
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Neisseria gonorrhoeae.	
XX		
PN	US2002072118-A1.	

XX 13-JUN-2002.
PD
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARWFCVKLNKEAEGMKPPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
DB 1 MARWFCVKLNKEAEGMKPPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
OY 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88

RESULT 2
ABB78172

ID ABB78172 standard; protein; 88 AA.

AC ABB78172;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Neisseria meningitidis.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX

SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARWFCVKLNKEAEGMKPPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
DB 1 MARWFCVKLNKEAEGMKPPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRLSLADP 60
OY 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88
DB 61 RAREYLAQQMEQYFFGDGADAVQGYVPQ 88

RESULT 3
ABB78173

ID ABB78173 standard; protein; 88 AA.

AC ABB78173;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Neisseria meningitidis.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-26
Perfect score: 467
Sequence: 1 MARMVFCVKLNKBAEGMKFP.....QMEQYFPGDADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: PIR1:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	467	100.0	88	2	H81014	conserved hypothet
2	240	51.4	90	2	C82320	conserved hypothet
3	227	48.6	90	2	C64013	hypothetical prote
4	213	45.6	91	2	A85954	hypothetical prote
5	213	45.6	91	2	A65082	hypothetical prote
6	213	45.6	91	2	F91108	hypothetical prote
7	211	45.2	91	2	AH0879	conserved hypothet
8	207	44.3	90	2	H83003	conserved hypothet
9	201	43.0	105	2	C82624	conserved hypothet
10	198	42.4	90	2	A10116	conserved hypothet
11	158	33.8	93	2	E84994	hypothetical prote
12	72	15.4	1041	2	A81960	probable DNA helic
13	70	15.0	1079	2	T38913	translation initia
14	68.5	14.7	338	2	A83389	probable permease
15	68.5	14.7	549	2	A11457	ABC transporter ol
16	68	14.6	195	2	S74714	hypothetical prote
17	67.5	14.5	899	2	A83019	conserved hypothet
18	66.5	14.2	401	2	C70159	translation elonga
19	66	14.1	598	1	RGECONX	nitrate/nitrite se
20	66	14.1	598	2	F85702	nitrate/nitrite se
21	66	14.1	598	2	G90844	nitrate/nitrite se
22	65	13.9	296	2	A64110	cell division inh
23	65	13.9	465	2	C71870	hypothetical prote
24	65	13.9	590	2	E85057	probable transpos
25	64.5	13.8	207	2	E89952	conserved hypothet
26	64.5	13.8	362	2	T45072	erythroid Kruppel-
27	64.5	13.8	400	2	A39254	inositol-1,4-bisph
28	64.5	13.8	1553	2	S67483	adenosinetriphosph
29	64	13.7	676	2	A45984	sperm-binding glyc

30	64	13.7	677	2	S33664	flagella-associate
31	63.5	13.6	288	2	H95018	transcription regu
32	63.5	13.6	301	2	F82446	transcription regu
33	63	13.5	282	2	D97138	DNA replication pr
34	63	13.5	388	1	UC5461	cellulase (EC 3.2.
35	63	13.5	388	1	S43920	cellulase (EC 3.2.
36	62	13.3	120	2	G97833	cellulase (EC 3.2.
37	62	13.3	200	2	B82203	hypothetical prote
38	62	13.3	259	2	S55033	transcription init
39	62	13.3	570	2	D83177	probable phosphot
40	62	13.3	2314	2	T28698	hypothetical prote
41	61.5	13.2	211	2	T38645	transcription regu
42	61.5	13.2	288	2	B95122	hypothetical prote
43	61.5	13.2	374	2	A96502	transcription regu
44	61.5	13.2	412	2	G81581	probable acyl-acyl
45	61.5	13.2	422	2	G86535	tyrosyl-tRNA synth
46	61.5	13.2	422	2	D72088	tyrosyl tRNA synth
47	61.5	13.2	589	2	AE3530	tyrosine-tRNA liga
48	61	13.1	425	2	T50184	flagellar biosynth
49	61	13.1	563	2	F97028	mammalian swi/bnf
50	61	13.1	969	2	T33156	arginyl-tRNA synth
51	61	13.1	1639	2	T50119	hypothetical prote
52	60.5	13.0	186	1	WMR219	probable sensory t
53	60.5	13.0	186	2	JC4784	19k globulin precu
54	60.5	13.0	261	2	S14875	alpha-globulin pre
55	60.5	13.0	357	2	F82892	dnak-type molecula
56	60.5	13.0	448	2	T45145	heat-inducible tra
57	60.5	13.0	1888	2	T39009	glutamate-ammonia
58	60	12.8	292	2	A10422	hypothetical prote
59	60	12.8	306	2	A97249	conserved hypothet
60	60	12.8	309	2	D95843	zn-binding lipopro
61	60	12.8	323	2	T35734	probable transcrip
62	60	12.8	335	2	D83142	hypothetical prote
63	60	12.8	397	2	A75503	hypothetical prote
64	60	12.8	410	2	T39115	formamidase-like p
65	60	12.8	508	2	T02486	hypothetical prote
66	60	12.8	615	2	B81451	1-deoxyxylulose-5-
67	60	12.8	655	2	E75206	alpha-amylase (or
68	60	12.8	859	2	T29630	hypothetical prote
69	60	12.8	1006	2	A59384	oxycocinase/insuli
70	60	12.8	1021	2	AC2202	hypothetical prote
71	60	12.8	1025	2	A59383	oxycocinase/insuli
72	60	12.8	3788	2	T30851	lysosomal traffick
73	59.5	12.7	157	1	HHPM17	heat shock protein
74	59.5	12.7	237	2	A55218	sfp homolog gsp -
75	59.5	12.7	295	2	T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
Conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58 :
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
rt, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEXT>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AB002552; GB:AB002098; NID:G7227279; PIDN:J
A/Experimental source: serogroup B, strain MC58
R/Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jags, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds

(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-26

Perfect score: 467
Sequence: 1 MARWFEVYKLNKEAGMKP.....QMEQYFEGDADAVGVVPQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80:*

1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	DB ID	Description
1	467	100.0	88 1	FETP_NEIG1
2	467	100.0	88 1	FETP_NEIMA
3	467	100.0	88 1	FETP_NEIMB
4	354	75.8	91 1	FETP_RALSO
5	348	74.5	91 2	Q4LS19_9BURK
6	339	72.6	91 1	FETP_BURMA
7	339	72.6	91 1	FETP_BURPS
8	335	71.7	90 1	FETP_CHRYO
9	319	68.3	90 1	FETP_NITEU
10	290	62.1	90 1	FETP_BORBR
11	290	62.1	90 1	FETP_BORPA
12	290	62.1	90 1	FETP_BORPE
13	275	58.9	89 1	FETP_LEGPI
14	271	58.0	89 1	FETP_LEGPA
15	271	58.0	89 1	FETP_LEGPH
16	258	55.2	90 1	FETP_COXBU
17	254	54.4	90 1	FETP_VIBFI
18	252	54.0	92 2	Q4NWQ4_9DELT
19	243	52.0	90 1	FETP_MERTCA
20	242	51.8	90 1	FETP_IDILO
21	240	51.4	90 1	FETP_VIBCH
22	239	51.2	90 1	FETP_VIBPA
23	239	51.2	90 1	FETP_VIBVU
24	239	51.2	90 1	FETP_VIBVY
25	235	50.3	91 1	FETP_XANAC
26	235	50.3	94 1	FETP_HAEDU
27	233	49.9	92 1	FETP_XANOR
28	230	49.3	92 1	FETP_SHEON
29	227	48.6	90 1	FETP_HAEIN
30	227	48.6	90 2	Q4QMD9_HAEI8
31	225	48.2	92 1	FETP_XANCP

32	225	48.2	92 2	Q4UW14_XANCP	Q4UW14 xanthomonas
33	224	48.0	91 1	FETP_MANSM	Q65vt7 mannheimia
34	220.5	47.2	90 1	FETP_ACTAD	Q6ffB3 acinetobact
35	220	47.1	90 1	FETP_PHOPR	Q6lmk7 photobacter
36	219	46.9	90 1	FETP_PSEPK	Q88r49 pseudomonas
37	217	46.5	90 1	FETP_PASMU	Q9clb9 pasteurella
38	217	46.5	90 1	FETP_PHOLL	Q7n7i1 photorhabdu
39	211	45.2	90 2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
40	209	44.8	90 1	FETP_XYLFT	Q87d06 xylella faa
41	208	44.5	87 1	FETP_FRATT	Q5nhj8 francisella
42	208	44.5	90 1	FETP_ECO57	Q0a8p4 escherichia
43	208	44.5	90 1	FETP_ECOLI	Q0a8p3 escherichia
44	208	44.5	90 1	FETP_ERWCT	Q6d8j9 erwinia car
45	208	44.5	90 1	FETP_SHIFL	Q0a8p5 shigella fl
46	207	44.3	90 1	FETP_PSEAE	Q9hu36 pseudomonas
47	207	44.3	90 2	Q4KJ72_PSEFS	Q4Kjt2 pseudomonas
48	206	44.1	90 1	FETP_SALCH	Q57K04 salmoneilla
49	206	44.1	90 1	FETP_SALPA	Q5pmm1 salmoneilla
50	206	44.1	90 1	FETP_SALTI	Q67618 salmoneilla
51	206	44.1	90 1	FETP_SALTY	Q67617 salmoneilla
52	206	44.1	90 1	FETP_YERPS	Q66m3 yersinia ps
53	206	44.1	96 2	Q4PV07_9GAMM	Q4fvj7 psychrobact
54	204	43.7	90 1	FETP_ECOL6	Q8fei9 escherichia
55	201	43.0	90 1	FETP_XYLPA	Q9pc73 xylella faa
56	198	42.4	90 1	FETP_PSESM	Q87uf5 pseudomonas
57	198	42.4	90 1	FETP_YERPE	Q8zhe7 yersinia pe
58	198	42.4	90 2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
59	196	42.0	90 2	Q4J228_AZOVI	Q4j228 azotobacter
60	186	39.8	79 1	FETP_CANBF	Q7vrg9 candidatus
61	167	35.8	78 1	FETP_BUCAP	Q8d3c5 buchnera ap
62	167	35.8	78 1	FETP_WIGBR	Q8d3c5 wigglewort
63	158	33.8	77 1	FETP_BUCAI	P57618 buchnera ap
64	127	27.2	87 1	FETP_BUCBP	Q89a44 buchnera ap
65	75	16.1	359 2	Q7VKN4_HAEDU	Q7vkn4 haemophilus
66	74	15.8	453 2	Q4PBI1_USTMA	Q4pbi1 ustilago ma
67	74	15.8	1598 2	Q6ZCB0_BURMA	Q6zcb0 burkholderi
68	74	15.8	1599 2	Q63KSI_BURPS	Q63ksi burkholderi
69	73	15.6	820 2	Q521A7_MAGGR	Q521a7 magnaporthe
70	72.5	15.5	301 2	Q6LNI9_PHOPR	Q6lni9 photobacter
71	72	15.4	203 2	Q568W6_BRAPR	Q568w6 brachydanio
72	72	15.4	1041 2	Q9JWD5_NEIMA	Q9jwd5 neisseria m
73	71	15.2	346 2	Q8EF42_SHEON	Q8ef42 shewanella
74	70.5	15.1	320 2	Q6PKY5_XENLA	Q6pkys xenopus lae
75	70	15.0	1079 1	IF2P_SCHPO	Q10251 schizosacch

ALIGNMENTS

RESULT 1
FETP_NEIG1
ID FETP_NEIG1 STANDARD; PRT; 88 AA.
AC Q5F553;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocNames=NGO2083;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillaspay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT "The complete genome sequence of Neisseria gonorrhoeae."
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC

```

CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE004969; AAW90684.1; -; Genomic_DNA.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60
    |||
DB 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60

QY 61 RAREYLAQQOMEQYFFGDGADAVQGYVPQ 88
    |||
DB 61 RAREYLAQQOMEQYFFGDGADAVQGYVPQ 88

RESULT 2
FETP_NEIMA STANDARD; PRT; 88 AA.
ID FETP_NEIMA
AC P67615; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL162753; CAB83718.1; -; Genomic_DNA.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
CC DR ProDom; PD029191; DUF495; 1.

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KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60
    |||
DB 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60

QY 61 RAREYLAQQOMEQYFFGDGADAVQGYVPQ 88
    |||
DB 61 RAREYLAQQOMEQYFFGDGADAVQGYVPQ 88

RESULT 3
FETP_NEIMB STANDARD; PRT; 88 AA.
ID FETP_NEIMB
AC P67616; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Clifton H., Clark B.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzo M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon B.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58."
RL Science 287:1809-1815(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE002098; AAF42344.1; -; Genomic_DNA.
CC DR TIGR; NMB2021; -.
CC DR HAMAP; MF_00686; -; 1.
CC DR InterPro; IPR007457; YggX.
CC DR Pfam; PF04362; DUF495; 1.
CC DR ProDom; PD029191; DUF495; 1.
CC KW Complete proteome; Iron.
CC SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60
    |||
DB 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSOEAWAATRHQTMLINENRLSLADP 60

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-26

Perfect score: 467

Sequence: 1 MARMVFCVKLNKEAGMKFP.....QMEQYFFGDGADAVQGYVPQ 88

Scoring table: BLOSUM62

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*\n2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*\n3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*\n4: /cgn2_6/ptodata/1/1aa/PCRTUS_COMB.pep:*\n5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*\n6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	227	48.6	107	2	US-09-489-039A-11962
2	225.5	48.3	92	2	US-09-328-352-5456
3	221	47.3	93	2	US-09-543-681A-5443
4	207	44.3	122	2	US-09-252-991A-23355
5	182	39.0	110	2	US-09-540-236-2859
6	68.5	14.7	110	2	US-09-252-991A-25005
7	67.5	14.5	466	2	US-09-252-991A-32761
8	66	14.1	418	2	US-09-489-039A-13155
9	65.5	14.0	649	2	US-09-107-532A-4298
10	65.5	14.0	3838	2	US-09-949-016-10853
11	64.5	13.8	361	2	US-08-874-569B-21
12	64.5	13.8	361	2	US-09-955-518-21
13	63	13.5	351	2	US-09-248-796A-19129
14	63	13.5	461	1	US-08-672-571A-3
15	63	13.5	490	1	US-08-672-571A-1
16	62.5	13.4	263	2	US-09-252-991A-22230
17	62	13.3	360	2	US-09-543-681A-7067
18	62	13.3	671	2	US-09-252-991A-18020
19	61.5	13.2	422	2	US-09-198-452A-377
20	61.5	13.2	423	2	US-09-438-185A-363
21	60.5	13.0	478	2	US-09-489-039A-7300
22	60.5	13.0	596	2	US-09-902-540-10121
23	60	12.8	621	2	US-09-489-039A-10378
24	60	12.8	2186	1	US-08-822-445-2
25	60	12.8	2186	1	US-09-396-540-2
26	59.5	12.7	315	2	US-09-461-325-297
27	59.5	12.7	315	2	US-10-012-542-297

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
29	59.5	12.7	346	2	US-09-808-701A-32	Sequence 32, Appl
30	59.5	12.7	420	2	US-09-902-540-16463	Sequence 16463, A
31	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502A-26

Perfect score: 467
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	339	72.6	87	3	US-09-955-502-30
6	294	63.0	87	3	US-09-955-502-31
7	290	62.1	87	3	US-09-955-502-2
8	290	62.1	87	3	US-09-955-502-3
9	272.5	58.4	86	3	US-09-955-502-4
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11	243	52.0	87	3	US-09-955-502-32
12	240	51.4	90	3	US-09-955-502-10
13	235	50.3	87	3	US-09-955-502-8
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24	211	45.2	91	3	US-09-955-502-16
25	211	45.2	91	3	US-09-955-502-17
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46	65.5	14.0	3830	5	US-10-723-860-2568	Sequence 256, App
47	65.5	14.0	3830	5	US-10-745-237-256	Sequence 354, App
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52	65	13.9	448	4	US-10-335-977-9043	Sequence 8911, Ap
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61	64.5	13.8	1555	5	US-10-732-923-22584	Sequence 132, App
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65	62.5	13.4	126	4	US-10-437-963-172448	Sequence 4727, Ap
66	62	13.3	360	4	US-10-282-122A-68811	Sequence 7486, Ap
67	62	13.3	519	4	US-10-369-493-7486	Sequence 11951, A
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69	62	13.3	570	3	US-09-815-242-11951	Sequence 74, Appl
70	62	13.3	570	4	US-10-282-122A-66545	Sequence 149485, A
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ALIGNMENTS

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; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-09-955-502-26

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US-09-955-502-27

; Sequence 27, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 27
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US-09-955-502-27

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Best Local Similarity	100.0%;	Pred. No. 2.6e-50;		
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RESULT 3

US-09-955-502-28

; Sequence 28, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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; TYPE: PRT
; ORGANISM: Neisseria meningitidis A
US-09-955-502-28

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Dd

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RESULT 4

US-09-955-502-29

Sequence 29, Application US/09955502
; Patent No. US2002007218A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia mallei
US-09-955-502-29

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RESULT 5

US-09-955-502-30

; Sequence 30, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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; LENGTH: 87
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; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

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Best Local Similarity	67.8%;	Pred. No. 2.6e-34;		
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GenCore version 5.1.7
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OM protein - protein search, using sw model

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Title: US-09-955-502A-26

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	58	12.4	614	US-11-165-576-4	Sequence 4, Appli
6	57.5	12.3	200	US-10-793-626-1186	Sequence 1186, Ap
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8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, A
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, A
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39	53.5	11.5	432	7	US-11-056-354-4	Sequence 4, Appli
40	53.5	11.5	440	6	US-10-933-115-2	Sequence 2, Appli
41	53.5	11.5	473	6	US-10-131-826A-382	Sequence 382, App
42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, Ap
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
44	53	11.3	710	7	US-11-124-367A-354	Sequence 354, App
45	53	11.3	713	7	US-11-124-367A-355	Sequence 355, App
46	53	11.3	713	7	US-11-124-367A-356	Sequence 356, App
47	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
48	53	11.3	713	7	US-11-124-367A-358	Sequence 358, App
49	53	11.3	734	6	US-10-821-234-1056	Sequence 1056, Ap
50	53	11.3	3507	7	US-11-075-185-7	Sequence 7, Appli
51	52.5	11.2	197	6	US-10-986-501-296	Sequence 296, App
52	52.5	11.2	229	6	US-10-793-626-2818	Sequence 2818, Ap
53	52.5	11.2	335	7	US-11-072-175-245	Sequence 245, App
54	52.5	11.2	754	7	US-11-140-625-10	Sequence 10, Appl
55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appli
56	52.5	11.2	4128	6	US-10-770-726-77	Sequence 77, Appl
57	52	11.1	223	7	US-11-018-868-140	Sequence 140, Appl
58	52	11.1	381	7	US-11-024-959-418	Sequence 418, App
59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
60	52	11.1	390	7	US-11-219-282-12	Sequence 12, Appl
61	52	11.1	1022	7	US-11-156-084-118	Sequence 94, Appl
62	51.5	11.0	209	5	US-09-995-493-94	Sequence 2, Appli
63	51.5	11.0	396	7	US-11-202-731-2	Sequence 354, App
64	51.5	11.0	408	7	US-11-074-176-354	Sequence 186, App
65	51.5	11.0	408	7	US-11-074-176-186	Sequence 286, App
66	51.5	11.0	447	7	US-11-024-959-286	Sequence 871, App
67	51.5	11.0	479	6	US-10-821-234-871	Sequence 2343, Ap
68	51.5	11.0	1034	7	US-11-072-512-2343	Sequence 12, Appl
69	51.5	11.0	1159	6	US-10-613-744-12	Sequence 9, Appli
70	51.5	11.0	1159	6	US-10-957-116-9	Sequence 10173, A
71	51	10.9	326	7	US-11-098-686-10173	Sequence 20, Appl
72	51	10.9	387	7	US-11-219-282-20	Sequence 10, Appl
73	50.5	10.8	124	7	US-11-069-642-10	Sequence 45, Appl
74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 40, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04


```
; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
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Query Match      100.0%; Score 467; DB 6; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.7e-51;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 MARWVCYKLNKBAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60
          |||||
Db       1 MARWVCYKLNKBAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60
```

```
QY      61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
          |||||
Db       61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
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RESULT 2

```
US-10-821-234-999
; Sequence 999, Application US/10821234
; Publication No. US20050255114A1
; GENERAL INFORMATION:
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```
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 999
; LENGTH: 1092
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-999
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Query Match      12.8%; Score 60; DB 6; Length 1092;
Best Local Similarity 30.6%; Pred. No. 28;
Matches 15; Conservative 12; Mismatches 20; Indels 2; Gaps 2;
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```
QY      31 FENVSQEAWAAT-RHQTMLINENRLSLADP-AREYLAQOMEQYFFGD 77
          |||
Db       492 FEAGAMENWGILTFREETLLYDSNTSSMADRLVTKIHAHELHQWFGN 540
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RESULT 3

```
US-10-525-674-28
; Sequence 28, Application US/10525674
; Publication No. US20060003425A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Kroger, Burkhard
; APPLICANT: Zelder, Oskar
; APPLICANT: Kolprogge, Corina
; APPLICANT: Schroder, Hartwig
; APPLICANT: Hafner, Stefan
; TITLE OF INVENTION: Method for Zymotic Production of Fine Chemicals Containing
; FILE REFERENCE: 13111-00002-US
; CURRENT APPLICATION NUMBER: US/10/525,674
; CURRENT FILING DATE: 2005-02-24
; PRIOR APPLICATION NUMBER: PCT/EP 2003/009452
; PRIOR FILING DATE: 2003-08-26
; PRIOR APPLICATION NUMBER: DE 102 39 073.8
; PRIOR FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 28
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; LENGTH: 380
; TYPE: PRT
; ORGANISM: Thermus thermophilus
US-10-525-674-28
```

```
Query Match      12.4%; Score 58; DB 6; Length 380;
Best Local Similarity 26.3%; Pred. No. 13;
Matches 15; Conservative 14; Mismatches 22; Indels 6; Gaps 2;
```

```
QY      34 VSQEAWAATRHQTMLINENR--LSLADPRAREYLAQOMEQYFFGDGADAVQGYVPQ 88
          |||
Db       1 MSEIALEAWGEHEALLKPPRSPLSIPPPKPRTAULFPRREGFYTE---LGGYLPE 53
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RESULT 4

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US-11-165-576-2
; Sequence 2, Application US/11165576
; Publication No. US20060009388A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mi, Sha
; APPLICANT: Pepinsky, R. Blake
; APPLICANT: McCoy, John
; TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
; FILE REFERENCE: 2159.0460004
; CURRENT APPLICATION NUMBER: US/11/165,576
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/680,475
; PRIOR FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/628,435
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 60/617,297
; PRIOR FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: 60/582,966
; PRIOR FILING DATE: 2004-06-24
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 2
; LENGTH: 614
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-165-576-2
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```
Query Match      12.4%; Score 58; DB 7; Length 614;
Best Local Similarity 27.4%; Pred. No. 24;
Matches 17; Conservative 15; Mismatches 28; Indels 2; Gaps 1;
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QY      3 RMWVCYKLNKBA--EGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60
          |||
Db       47 RAVLCHRRKRVAVPEGIPETRLLDGKNRIKTLNODDEFASFPHLBELLENIVSAVER 106
```

```
QY      61 RA 62
          |
Db       107 GA 108
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RESULT 5

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US-11-165-576-4
; Sequence 4, Application US/11165576
; Publication No. US20060009388A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Mi, Sha
; APPLICANT: Pepinsky, R. Blake
; APPLICANT: McCoy, John
; TITLE OF INVENTION: Treatment of Conditions Involving Demyelination
; FILE REFERENCE: 2159.0460004
; CURRENT APPLICATION NUMBER: US/11/165,576
; CURRENT FILING DATE: 2005-06-24
; PRIOR APPLICATION NUMBER: 60/680,475
; PRIOR FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/628,435
; PRIOR FILING DATE: 2004-11-15
; PRIOR APPLICATION NUMBER: 60/617,297
; PRIOR FILING DATE: 2004-10-07
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:03:38 ; Search time 72.164 Seconds
(without alignments)
535.798 Million cell updates/sec

Title: US-09-955-502A-27

Perfect score: 467

Sequence: 1 MARMVECVKLNKEAEQMKFP.....QMEQYFFGADAVQGVVFQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

A_Geneseq_21: *
1: geneseqp1980s: *
2: geneseqp1990s: *
3: geneseqp2000s: *
4: geneseqp2001s: *
5: geneseqp2002s: *
6: geneseqp2003as: *
7: geneseqp2003bs: *
8: geneseqp2004s: *
9: geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78171 Amino aci
2	467	100.0	88	5	ABB78172 Amino aci
3	467	100.0	88	5	ABB78173 Amino aci
4	467	100.0	88	6	ABP77219 N. gonorr
5	339	72.6	87	5	ABB78175 Amino aci
6	333	71.3	87	5	ABB78174 Amino aci
7	294	63.0	87	5	ABB78176 Amino aci
8	290	62.1	87	5	ABB78148 Amino aci
9	290	62.1	87	5	ABB78147 Amino aci
10	272.5	58.4	86	5	ABB78149 Amino aci
11	271	58.0	89	9	AEB41576 L. pneumo
12	271	58.0	95	9	AEB38294 L. pneumo
13	258	55.2	88	5	ABB78178 Amino aci
14	243	52.0	87	5	ABB78177 Amino aci
15	240	51.4	90	5	ABB78155 Amino aci
16	235	50.3	87	5	ABB78153 Amino aci
17	230	49.3	88	5	ABB78154 Amino aci
18	228	48.8	91	5	ABB78150 Amino aci
19	227	48.6	87	5	ABB78152 Amino aci
20	227	48.6	107	7	ABO65445 Klebsiell
21	225.5	48.3	92	6	ADA34169 Acinetoba
22	221	47.3	93	7	ADF05158 Bacteri
23	219	46.9	87	5	ABB78169 Amino aci
24	217	46.5	87	5	ABB78151 Amino aci

25	213	45.6	91	5	ABB78158 Amino aci
26	213	45.6	91	5	ABB78157 Amino aci
27	213	45.6	91	5	ABB78156 Amino aci
28	211	45.2	88	5	ABB78160 Amino aci
29	211	45.2	91	5	ABB78161 Amino aci
30	211	45.2	91	5	ABB78159 Amino aci
31	211	45.2	91	5	ABB78162 Amino aci
32	210	45.0	78	5	ABB78164 Amino aci
33	207	44.3	87	5	ABB78170 Amino aci
34	207	44.3	122	7	ABO74609 Pseudomon
35	202	43.3	91	5	ABB78163 Amino aci
36	198	42.4	90	5	ABB78165 Amino aci
37	198	42.4	90	5	ABB78168 Amino aci
38	193.5	41.4	90	5	ABB78167 Amino aci
39	182	39.0	110	8	ADL05173 M. catarr
40	158	33.8	76	5	ABB78166 Amino aci
41	74	15.8	1122	6	ABU22044 Protein e
42	70	15.0	202	7	ABM90380 Rice abio
43	70	15.0	1079	8	ADN19463 Bacterial
44	69	14.8	774	4	ABG29304 Novel hum
45	68.5	14.7	361	7	ABO76259 Pseudomon
46	68	14.6	189	9	ADM18357 Pinus rad
47	67.5	14.5	466	7	ABO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221 Protein e
49	66	14.1	418	7	ABO66638 Klebsiell
50	65.5	14.0	649	7	ADC94671 E. faeciu
51	65.5	14.0	1443	7	ADJ68530 Human hea
52	65.5	14.0	1935	7	ADJ70260 Human hea
53	65.5	14.0	3830	5	ABB81168 TRRAP pro
54	65.5	14.0	3830	8	ADJ78499 PAF/TRRAP
55	65.5	14.0	3830	8	ADQ19749 Human sof
56	65.5	14.0	3830	8	ADQ89826 Antagonis
57	65.5	14.0	3859	7	ADJ68548 Human hea
58	65.5	14.0	3859	8	ADS88242 Human pro
59	65	13.9	255	7	ADM27073 Hyperther
60	65	13.9	296	4	AU35611 Haemophil
61	65	13.9	296	6	ABU30521 Protein e
62	65	13.9	438	2	AA11015 H. pylori
63	65	13.9	442	2	AAW20830 H. pylori
64	65	13.9	465	2	AAW20303 H. pylori
65	64.5	13.8	207	6	ABM73508 Staphyloc
66	64.5	13.8	207	9	ADV16859 Staphyloc
67	64.5	13.8	207	9	ADM94758 Prolifera
68	64.5	13.8	362	7	ADF89476 Human ery
69	64.5	13.8	362	8	ADK48858 Human tra
70	64.5	13.8	362	8	ADP12457 Protein e
71	64	13.7	260	4	AAW38702 Human pol
72	64	13.7	378	4	AAW40488 Human pol
73	64	13.7	656	4	ABU53239 Human tes
74	64	13.7	656	8	ADJ28417 Human nuc
75	64	13.7	2426	2	ADH11285 Vertebrat

ALIGNMENTS

RESULT 1	ABB78171	standard; protein; 88 AA.
ID	ABB78171	
XX		
AC	ABB78171;	
XX		
DT	29-AUG-2003	(revised)
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Neisseria gonorrhoeae.	
XX		
PN	US2002072118-A1.	

XX 13-JUN-2002.
PD 18-SEP-2001; 2001US-00955502.
XX 22-SEP-2000; 2000US-0234588P.
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues. (Updated on 29-AUG-2003 to
CC standardise OS field)
XX
SQ Sequence 88 AA;

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAEGMKPPPLPNEIGKRIFENVSQEAWAAMTRHQTMLINENRLSLADP 60
1 MARMVFCVKLNKEAEGMKPPPLPNEIGKRIFENVSQEAWAAMTRHQTMLINENRLSLADP 60
DB 61 RAREYLAQQMEQYFFGDDGADAVQGYVPQ 88
61 RAREYLAQQMEQYFFGDDGADAVQGYVPQ 88

RESULT 2
ID ABB78172 standard; protein; 88 AA.
XX
AC ABB78172;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YgX homologue.
XX
KW Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
OS Neisseria meningitidis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PS (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX

PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX

Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCVKLNKEAEGMKPPPLPNEIGKRIFENVSQEAWAAMTRHQTMLINENRLSLADP 60
1 MARMVFCVKLNKEAEGMKPPPLPNEIGKRIFENVSQEAWAAMTRHQTMLINENRLSLADP 60
DB 61 RAREYLAQQMEQYFFGDDGADAVQGYVPQ 88
61 RAREYLAQQMEQYFFGDDGADAVQGYVPQ 88

RESULT 3
ID ABB78173 standard; protein; 88 AA.
XX
AC ABB78173;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YgX homologue.
XX
KW Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
OS Neisseria meningitidis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PS (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-27

Perfect score: 467
Sequence: 1 MARMVFCVKLNKAEAGMKFP.....QMEQYFFGDGADAVQGYVPQ 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	2 H81014	conserved hypothet
2	240	51.4	90	2 C82320	conserved hypothet
3	227	48.6	90	2 C64013	hypothetical prote
4	213	45.6	91	2 A85954	hypothetical prote
5	213	45.6	91	2 A65082	hypothetical prote
6	213	45.6	91	2 F91108	hypothetical prote
7	211	45.2	91	2 AH0879	conserved hypothet
8	207	44.3	90	2 H83003	conserved hypothet
9	201	43.0	105	2 C82624	conserved hypothet
10	198	42.4	90	2 A10116	conserved hypothet
11	158	33.8	93	2 E84994	hypothetical prote
12	72	15.4	1041	2 A81960	probable DNA helic
13	70	15.0	1079	2 T38913	translation initia
14	68.5	14.7	338	2 A83389	probable permease
15	68.5	14.7	549	2 A11457	ABC transporter ol
16	68	14.6	195	2 S74714	hypothetical prote
17	67.5	14.5	899	2 A83019	conserved hypothet
18	66.5	14.2	401	2 C70159	translation elonga
19	66	14.1	598	1 RGEENX	nitrate/nitrite se
20	66	14.1	598	2 F85702	nitrate/nitrite se
21	66	14.1	598	2 G90844	nitrate/nitrite se
22	65	13.9	296	2 A64110	cell division inh
23	65	13.9	465	2 C71870	hypothetical prote
24	65	13.9	590	2 E85057	probable transposo
25	64.5	13.8	207	2 E89952	conserved hypothet
26	64.5	13.8	362	2 T45072	erythroid Kruppel-
27	64.5	13.8	400	2 A39254	inositol-1,4-bisph
28	64.5	13.8	1553	2 S67483	adenosinetriphosph
29	64	13.7	676	2 A45984	sperm-binding glyco

30	64	13.7	677	2 S33664	flagella-associate
31	63.5	13.6	288	2 H95018	transcription regu
32	63.5	13.6	301	2 F82446	DNA replication regu
33	63	13.5	282	2 D97138	cellulase (EC 3.2.
34	63	13.5	388	1 JC5461	cellulase (EC 3.2.
35	63	13.5	388	1 S43920	cellulase (EC 3.2.
36	62	13.3	120	2 G97833	hypothetical prote
37	62	13.3	200	2 B82203	transcription regu
38	62	13.3	259	2 S55033	transcription init
39	62	13.3	570	2 D83177	probable phosphot
40	62	13.3	2314	2 T38645	hypothetical prote
41	61.5	13.2	211	2 T38645	transcription regu
42	61.5	13.2	288	2 B95122	probable phosphot
43	61.5	13.2	374	2 A96502	hypothetical prote
44	61.5	13.2	412	2 G81581	transcription regu
45	61.5	13.2	422	2 G86535	probable phosphot
46	61.5	13.2	422	2 D72088	hypothetical prote
47	61.5	13.2	589	2 AE3530	transcription regu
48	61	13.1	425	2 T50184	probable acyl-acyl
49	61	13.1	563	2 F97028	tyrosyl-tRNA synth
50	61	13.1	969	2 T33156	tyrosyl-tRNA synth
51	61	13.1	1639	2 T50119	tyrosine-tRNA liga
52	60.5	13.0	186	1 WMRZ19	mammalian swi/snf
53	60.5	13.0	186	2 JC4784	arginyl-tRNA synth
54	60.5	13.0	261	2 S14875	hypothetical prote
55	60.5	13.0	357	2 F82892	probable sensory t
56	60.5	13.0	448	2 T45145	19K globulin precu
57	60.5	13.0	1888	2 T39009	alpha-globulin pre
58	60	12.8	292	2 A10422	dnak-type molecula
59	60	12.8	306	2 A97249	heat-inducible tra
60	60	12.8	309	2 D95843	glutamate-ammonia
61	60	12.8	323	2 T35734	hypothetical prote
62	60	12.8	335	2 D83142	conserved hypothet
63	60	12.8	397	2 A75503	Zn-binding lipopro
64	60	12.8	410	2 T39115	probable transcrip
65	60	12.8	508	2 T02486	hypothetical prote
66	60	12.8	615	2 E81451	hypothetical prote
67	60	12.8	655	2 E75206	formamidase-like p
68	60	12.8	859	2 T29630	1-deoxyxylulose-5-
69	60	12.8	1006	2 A59384	alpha-amylase (or
70	60	12.8	1021	2 AC2202	hypothetical prote
71	60	12.8	1025	2 A59383	oxytocinase/insuli
72	60	12.8	3788	2 T30851	lysosomal traffick
73	59.5	12.7	157	1 HHPM17	heat shock protein
74	59.5	12.7	237	2 A55218	sfp homolog gsp -
75	59.5	12.7	295	2 T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
R/Accession: H81014; F81958
C/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
xi, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEF>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:J
A/Experimental source: serogroup B, strain MC58
R/Parhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
R.; Holroyd, S.; Jørgensen, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000


```

A/Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: F81958
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <PAR>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A/Experimental source: serogroup A, strain Z2491
C/Genetics:
A/Gene: NME2021; MMA0419
C/Superfamily: fe(II) trafficking protein YggX

Query Match      100.0%; Score 467; DB 2; Length 88;
Best Local Similarity 100.0%; Pred. No. 2.7e-46;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MARWFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
    |||||
Db 1 MARWFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
    |||||

Oy 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
    |||||
Db 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
    |||||

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein YggX

Query Match      51.4%; Score 240; DB 2; Length 90;
Best Local Similarity 50.6%; Pred. No. 2.5e-20;
Matches 44; Conservative 14; Mismatches 29; Indels 0; Gaps 0;

Oy 1 MARWFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
    |||||
Db 1 MARTVFCCTRLQKEADGLDQYLPGLGKRIFDNIKCEAWAQWTKQTMLINEKKNMMDP 60
    |||||

Oy 61 RAREYLAQOMEQYFFGDGADAVQGYVP 87
    |||||
Db 61 EHRKLLQEGEMVNFLEFGKEVHIIEGYTP 87
    |||||

RESULT 3
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

```

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A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64013
A;/Status: nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-90 <TIGR>
A;/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023;-NID:g15
C;/Superfamily: fe(II) trafficking protein YggX

Query Match          48.6%; Score 227; DB 2; Length 90;
Best Local Similarity 50.0%; Pred. No. 7.8e-19;
Matches      44; Conservative   17; Mismatches    25; Indels       2; Gaps       2;

QY      1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAWTRHQTMLINENRLSLADP 60
        ||| ||| | : ||||| : | | ||||| : ||||| : | | : ||||| : ||||| : 
DB      1 MARTVFCEYLKKAEGLDFQLYPGELGKRIFDSVSKAQAGEWIKKQTM LVNEKLLNMNA 60

QY      61 RAREYLAQQOMEQYFFGDGADA-VQGYP 87
        | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      61 EHRKLLEQEMVNFLF-EGKDVIIEGYTP 87

RESULT 4
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933
C;/Species: Escherichia coli
C;/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
A;/Accession: A85954
R;/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;/Reference number: A85480; MUID:21074935; PMID:11206551
A;/Accession: A85954
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <STO>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A;/Experimental source: strain O157:H7, substrain EDL933
C;/Genetics:
A;/Gene: yggX
C;/Superfamily: fe(II) trafficking protein YggX

Query Match          45.6%; Score 213; DB 2; Length 91;
Best Local Similarity 44.3%; Pred. No. 3.1e-17;
Matches      39; Conservative   16; Mismatches    33; Indels       0; Gaps       0;

QY      1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAWTRHQTMLINENRLSLADP 60
        ||| ||| | : ||||| : | | ||||| : ||||| : | | : ||||| : ||||| : 
DB      1 MSRTIFCTFLGREAEQGFQLYPGELGKRITYNEISKEAWAQWHKQTM LINEKLLNMNA 60

QY      61 RAREYLAQQOMEQYFFGDGADVQGYVP 88
        | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB      61 EHRKLLEQEMVNFLFEGKEVHIIEGYTP 88

RESULT 5
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;/Species: Escherichia coli
C;/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
A;/Accession: A65082
R;/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;/Title: The complete genome sequence of Escherichia coli K-12.
A;/Reference number: A64720; MUID:97426617; PMID:9278503
A;/Accession: A65082
A;/Status: preliminary; nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-91 <BLAT>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g3
A;/Experimental source: strain K-12, substrain MG1655
C;/Superfamily: fe(II) trafficking protein YggX

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-27

Perfect score: 467
Sequence: 1 MARWVFCVKLNKEABGMKRP.....QMEQYFFGDGADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	467	100.0	88 1	FETP_NEIG1 Q5F553 neisseria g
2	467	100.0	88 1	FETP_NEIMA P67615 neisseria m
3	467	100.0	88 1	FETP_NEIMA P67615 neisseria m
4	354	75.8	91 1	FETP_RALSO Q8Y010 ralsstonia s
5	348	74.5	91 2	Q4LS19 9BURK Q4LS19 burkholderi
6	339	72.6	91 1	FETP_BURMA Q621u9 burkholderi
7	339	72.6	91 1	FETP_BURMA Q621u9 burkholderi
8	335	71.7	90 1	FETP_BURVO Q638j4 burkholderi
9	319	68.3	90 1	FETP_NITEU Q82xf2 nitrosomona
10	290	62.1	90 1	FETP_BORBR Q7wh06 bordetella
11	290	62.1	90 1	FETP_BORBR Q7wh06 bordetella
12	290	62.1	90 1	FETP_BORBR Q7wh06 bordetella
13	275	58.9	89 1	FETP_LEGPA Q5wvc4 legionella
14	271	58.0	89 1	FETP_LEGPA Q5x3x9 legionella
15	271	58.0	89 1	FETP_LEGPA Q5x3x9 legionella
16	258	55.2	90 1	FETP_COXBU Q83d06 coxiella bu
17	254	54.4	90 1	FETP_VIBF1 Q5e7c0 vibrio fisc
18	252	54.0	92 2	Q4NWQ4_9DELT Q4nwq4 anaeromyxob
19	243	52.0	90 1	FETP_METCA Q60aj7 methylcocc
20	242	51.8	90 1	FETP_IDILO Q5qy58 idiomarina
21	240	51.4	90 1	FETP_VIBCH Q9kura4 vibrio chol
22	239	51.2	90 1	FETP_VIBPA Q87115 vibrio para
23	239	51.2	90 1	FETP_VIBVU Q8dccc5 vibrio vuln
24	239	51.2	90 1	FETP_VIBVU Q8dccc5 vibrio vuln
25	235	50.3	91 1	FETP_XANAC Q8bjh7 xanthomonas
26	235	50.3	91 1	FETP_XANAC Q8bjh7 xanthomonas
27	233	49.9	92 1	FETP_XANOR Q5gy22 xanthomonas
28	230	49.3	92 1	FETP_SHEON Q8ebx6 shewanella
29	227	48.6	90 1	FETP_HAEIN P44048 haemophilus
30	227	48.6	90 2	Q4QMD9 HAEI8 Q4qmd9 haemophilus
31	225	48.2	92 1	FETP_XANCP Q8p829 xanthomonas

32	225	48.2	92 2	Q4UW14_XANCP Q4uw14 xanthomonas
33	224	48.0	91 1	FETP_MANSW Q65vt7 manheimia
34	220.5	47.2	90 1	FETP_AC1AD Q6ifb3 acinetobact
35	220	47.1	90 1	FETP_PHOPR Q6lmk7 photobacter
36	219	46.9	90 1	FETP_PSEPK Q88r49 pseudomonas
37	217	46.5	90 1	FETP_PASMU Q9c1b9 pasteurella
38	217	46.5	90 1	FETP_PASMU Q9c1b9 pasteurella
39	211	45.2	90 2	Q6T7F6_PSEFL Q6t7f6 pseudomonas
40	209	44.8	90 1	FETP_XYLFT Q87d06 xylella fas
41	208	44.5	87 1	FETP_FRATF Q5uhj8 francisella
42	208	44.5	90 1	FETP_ECO57 P0a8p4 escherichia
43	208	44.5	90 1	FETP_ECOLI P0a8p3 escherichia
44	208	44.5	90 1	FETP_ECOLI P0a8p3 escherichia
45	208	44.5	90 1	FETP_ERWCT P0a8p5 shigella car
46	207	44.3	90 1	FETP_PSEAE Q9nu36 pseudomonas
47	207	44.3	90 2	Q4KJT2_PSEF5 Q4ktj2 pseudomonas
48	206	44.1	90 1	FETP_SALCH Q57k04 salmonella
49	206	44.1	90 1	FETP_SALPA Q5pmn1 salmonella
50	206	44.1	90 1	FETP_SALTI P67618 salmonella
51	206	44.1	90 1	FETP_SALTY P67617 salmonella
52	206	44.1	90 1	FETP_YERPS Q66m3 yersinia ps
53	206	44.1	96 2	Q4FVU7_9GAMM Q4fvu7 psychrobact
54	204	43.7	90 1	FETP_ECOL6 Q8fe19 escherichia
55	201	43.0	90 1	FETP_XYLFA Q9pc73 xylella fas
56	198	42.4	90 1	FETP_PSESM Q87u5 pseudomonas
57	198	42.4	90 1	FETP_YERPE Q8zhe7 yersinia pe
58	198	42.4	90 2	Q4ZLP3_PSESY Q4zlp3 pseudomonas
59	196	42.0	90 2	Q4J228_AZOV1 Q4j228 azotobacter
60	186	39.8	79 1	FETP_CANBF Q7yr9 candidatus
61	167	35.8	78 1	FETP_BUCAP Q8K925 buchnera ap
62	167	35.8	78 1	FETP_WIGBR Q8d3c5 wigleswort
63	158	33.8	77 1	FETP_BUCAI P57618 buchnera ap
64	127	27.2	87 1	FETP_BUCBP Q89a44 buchnera ap
65	75	16.1	359 2	Q7VKN4_HAEIU Q7vkn4 haemophilus
66	74	15.8	453 2	Q4PBL1_USTMA Q4pbl1 ustilago ma
67	74	15.8	1598 2	Q62CB0_BUDMA Q62cb0 burkholderi
68	74	15.8	1599 2	Q63KS1_BURPS Q63ks1 burkholderi
69	73	15.6	820 2	Q521A7_MAGGR Q521a7 magnaporthe
70	72.5	15.5	301 2	Q6LNI9_PHOPR Q6lni9 photobacter
71	72	15.4	203 2	Q568W6_BRARE Q568w6 brachydanio
72	72	15.4	1041 2	Q9JWD5_NEIMA Q9jwd5 neisseria m
73	71	15.2	346 2	Q8EP42_SHEON Q8ef42 shewanella
74	70.5	15.1	320 2	Q6PKY5_XENIA Q6pkys xenopus lae
75	70	15.0	1079 1	IF2P_SCHPO Q10251 schizosacch

ALIGNMENTS

RESULT 1
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ID FETP_NEIG1 STANDARD; PRT; 88 AA.
AC Q5F553;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Ordered locus names=NGO2083;
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=242231;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RA Lewis L.A., Gillapay A.F., McLaughlin R.E., Gipson M., Ducey T.F.,
RA Ombeley T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;
RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
RL "The complete genome sequence of Neisseria gonorrhoeae";
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-27
Perfect score: 467
Sequence: 1 MARWFCVKNKEAGMKP.....QMEQYFPGDADAVGGYVQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RG_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	48.6	107	US-09-489-039A-11962	Sequence 11962, A
2	225.5	48.3	92	US-09-328-352-5456	Sequence 5456, Ap
3	221	47.3	93	US-09-543-681A-5443	Sequence 5443, Ap
4	207	44.3	122	US-09-252-991A-23355	Sequence 23355, A
5	182	39.0	110	US-09-540-236-2859	Sequence 2859, Ap
6	68.5	14.7	361	US-09-252-991A-25005	Sequence 25005, A
7	67.5	14.5	466	US-09-252-991A-32761	Sequence 32761, A
8	66	14.1	418	US-09-489-039A-13155	Sequence 13155, A
9	65.5	14.0	649	US-09-107-532A-4298	Sequence 4298, Ap
10	65.5	14.0	3838	US-09-949-016-10853	Sequence 10853, A
11	64.5	13.8	361	US-08-874-569B-21	Sequence 21, Appl
12	64.5	13.8	361	US-09-955-518-21	Sequence 21, Appl
13	63	13.5	351	US-09-248-796A-19129	Sequence 19129, A
14	63	13.5	461	US-08-672-571A-3	Sequence 3, Appl
15	63	13.5	490	US-08-672-571A-1	Sequence 1, Appl
16	62.5	13.4	263	US-09-252-991A-22230	Sequence 22230, A
17	62	13.3	360	US-09-543-681A-7067	Sequence 7067, Ap
18	62	13.3	671	US-09-252-991A-18020	Sequence 18020, A
19	61.5	13.2	422	US-09-198-452A-377	Sequence 377, App
20	61.5	13.2	423	US-09-438-185A-363	Sequence 363, App
21	60.5	13.0	478	US-09-489-039A-7300	Sequence 7300, Ap
22	60.5	13.0	596	US-09-902-540-10121	Sequence 10121, A
23	60	12.8	621	US-09-489-039A-10378	Sequence 10378, A
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26	59.5	12.7	315	US-09-461-325-297	Sequence 297, App
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28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
29	59.5	12.7	346	2	US-09-808-701A-32	Sequence 32, Appl
30	59.5	12.7	420	2	US-09-902-540-16463	Sequence 16463, A
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32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
33	59.5	12.7	431	2	US-09-311-021-178	Sequence 178, App
34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	848	2	US-09-538-092-33	Sequence 33, Appl
36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-31958	Sequence 31958, A
39	59	12.6	563	2	US-09-583-110-4195	Sequence 4195, Ap
40	59	12.6	577	2	US-09-107-433-3424	Sequence 3424, Ap
41	59	12.6	5069	2	US-10-042-665A-5	Sequence 5, Appl
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49	58.5	12.5	340	2	US-09-270-767-42358	Sequence 42358, A
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51	58.5	12.5	397	2	US-09-079-030-123	Sequence 123, App
52	58.5	12.5	401	2	US-09-252-991A-17272	Sequence 17272, A
53	58	12.4	303	2	US-09-543-681A-7924	Sequence 7924, Ap
54	58	12.4	318	2	US-09-489-039A-8369	Sequence 8369, Ap
55	58	12.4	331	2	US-08-849-751-4	Sequence 4, Appl
56	58	12.4	331	2	US-09-478-816-4	Sequence 4, Appl
57	58	12.4	486	2	US-08-906-743-4	Sequence 4, Appl
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70	57.5	12.3	451	2	US-09-543-681A-7401	Sequence 7401, Ap
71	57.5	12.3	879	2	US-09-107-433-4058	Sequence 4058, Ap
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73	57	12.2	157	2	US-09-902-540-15203	Sequence 15203, A
74	57	12.2	384	2	US-10-094-944-19	Sequence 19, Appl
75	57	12.2	412	2	US-09-538-092-709	Sequence 709, App

ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 55.5262 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-27

Perfect score: 467
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Scoring table: BLOSUM62
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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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16	227	48.6	87	3	US-09-955-502-7
17	219	46.9	87	3	US-09-955-502-24
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24	211	45.2	91	3	US-09-955-502-16
25	210	45.0	91	3	US-09-955-502-17
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27	207	44.3	87	3	US-09-955-502-25

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46	65.5	14.0	3830	5	US-10-723-860-2568	Sequence 2568, Ap
47	65.5	14.0	3830	5	US-10-745-237-256	Sequence 256, App
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55	65	13.9	465	4	US-10-335-977-8913	Sequence 8913, Ap
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63	63.5	13.6	288	5	US-10-472-928-132	Sequence 132, App
64	63	13.5	417	4	US-10-156-761-8759	Sequence 8759, Ap
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72	62	13.3	835	4	US-10-087-887-67	Sequence 67, Appl
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75	62	13.3	1025	4	US-10-424-599-149485	Sequence 149485,

ALIGNMENTS

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Sequence 26, Application US/099555502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 26
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

GenCore version 5.1.7
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Title: US-09-955-502A-27

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7	57.5	12.3	200	US-10-793-626-2390	Sequence 2390, Ap
8	57.5	12.3	204	US-11-098-686-10498	Sequence 10498, A
9	57.5	12.3	655	US-11-098-686-10464	Sequence 10464, A
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11	57	12.2	620	US-10-131-826A-324	Sequence 324, App
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13	56.5	12.1	688	US-11-165-226-124	Sequence 124, App
14	56	12.0	1124	US-11-090-617-688	Sequence 688, App
15	56	12.0	1376	US-10-995-561-809	Sequence 809, App
16	56	12.0	1376	US-11-100-640-32	Sequence 32, Appl
17	55.5	11.9	403	US-11-009-658-14	Sequence 14, Appl
18	55.5	11.9	408	US-10-821-234-1100	Sequence 1100, Ap
19	55.5	11.9	449	US-11-098-686-10535	Sequence 10535, A
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21	55	11.8	261	US-10-467-657-400	Sequence 400, App
22	55	11.8	611	US-10-454-437-54	Sequence 54, Appl
23	55	11.8	633	US-11-193-561-13	Sequence 13, Appl
24	55	11.8	633	US-11-193-771-13	Sequence 13, Appl
25	55	11.8	633	US-11-193-789-13	Sequence 13, Appl

26	55	11.8	633	7	US-11-193-806-13	Sequence 13, Appl
27	55	11.8	633	7	US-11-193-857-13	Sequence 13, Appl
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33	54	11.6	685	7	US-11-098-686-10574	Sequence 10574, A
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35	53.5	11.5	291	6	US-10-883-512-103	Sequence 103, App
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42	53	11.3	288	6	US-10-467-657-3426	Sequence 3426, App
43	53	11.3	291	7	US-11-120-308-24	Sequence 24, Appl
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55	52.5	11.2	1476	6	US-10-647-956A-4	Sequence 4, Appl1
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57	52	11.1	223	7	US-11-018-868-140	Sequence 140, App
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59	52	11.1	390	7	US-11-019-711-65	Sequence 65, Appl
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71	51	10.9	326	7	US-11-098-686-10173	Sequence 10173, A
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74	50.5	10.8	347	6	US-10-853-807A-45	Sequence 45, Appl
75	50.5	10.8	352	6	US-10-878-556A-40	Sequence 40, Appl

ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

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Title: US-09-955-502A-28

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	5	ABB78171 Amino aci
2	467	100.0	88	5	ABB78172 Amino aci
3	467	100.0	88	5	ABB78173 Amino aci
4	467	100.0	88	6	ABP77219 N. gonorr
5	339	72.6	87	5	ABB78175 Amino aci
6	333	71.3	87	5	ABB78174 Amino aci
7	294	63.0	87	5	ABB78176 Amino aci
8	290	62.1	87	5	ABB78147 Amino aci
9	290	62.1	87	5	ABB78148 Amino aci
10	272.5	58.4	86	5	ABB78149 Amino aci
11	271	58.0	89	9	AEBA41576 L. pneumo
12	271	58.0	89	9	AEBA41576 L. pneumo
13	258	55.2	88	5	ABB78178 Amino aci
14	243	52.0	87	5	ABB78177 Amino aci
15	240	51.4	90	5	ABB78155 Amino aci
16	235	50.3	87	5	ABB78153 Amino aci
17	230	49.3	88	5	ABB78154 Amino aci
18	228	48.8	91	5	ABB78150 Amino aci
19	227	48.6	87	5	ABB78152 Amino aci
20	227	48.6	107	7	ABO65445 Klebsiell
21	225.5	48.3	92	6	ADA34169 Acinetoba
22	221	47.3	93	7	ADF05158 Bacteri
23	219	46.9	87	5	ABB78169 Amino aci
24	217	46.5	87	5	ABB78151 Amino aci

25	213	45.6	91	5	ABB78158 Amino aci
26	213	45.6	91	5	ABB78157 Amino aci
27	213	45.6	91	5	ABB78156 Amino aci
28	211	45.2	88	5	ABB78160 Amino aci
29	211	45.2	91	5	ABB78161 Amino aci
30	211	45.2	91	5	ABB78159 Amino aci
31	211	45.2	91	5	ABB78162 Amino aci
32	210	45.0	78	5	ABB78164 Amino aci
33	207	44.3	87	5	ABB78170 Amino aci
34	207	44.3	122	7	ABO74609 Pseudomon
35	202	43.3	91	5	ABB78163 Amino aci
36	198	42.4	90	5	ABB78165 Amino aci
37	198	42.4	90	5	ABB78168 Amino aci
38	193.5	41.4	90	5	ABB78167 Amino aci
39	182	39.0	110	8	ADL05173 M. catarr
40	158	33.8	76	5	ABB78166 Amino aci
41	74	15.8	1122	6	ABU22044 Protein e
42	70	15.0	202	7	ABM90380 Rice abio
43	70	15.0	1079	8	ADN19463 Bacterial
44	69	14.8	774	4	ABG29304 Novel hum
45	68.5	14.7	361	7	ABO76259 Pseudomon
46	68	14.6	189	9	ADM18357 Pinus rad
47	67.5	14.5	466	7	ABO84015 Pseudomon
48	66.5	14.2	401	6	ABU19221 Protein e
49	66	14.1	418	7	ABO66638 Klebsiell
50	65.5	14.0	649	7	ADC94671 E. faeciu
51	65.5	14.0	1443	7	ADJ68530 Human hea
52	65.5	14.0	1935	7	ADJ70260 Human hea
53	65.5	14.0	3830	5	ABB81168 TRRAP pro
54	65.5	14.0	3830	8	ADJ78499 PAF/TRRAP
55	65.5	14.0	3830	8	ADQ19749 Human sof
56	65.5	14.0	3830	8	ADQ89826 Antagonis
57	65.5	14.0	3859	7	ADJ68548 Human hea
58	65.5	14.0	3859	8	ADS88242 Human pro
59	65	13.9	255	7	ADM27073 Hyperther
60	65	13.9	296	4	AAU35611 Haemophil
61	65	13.9	296	6	ABU30521 Protein e
62	65	13.9	438	2	AAV11015 H. pylori
63	65	13.9	442	2	AAW20830 H. pylori
64	65	13.9	465	2	AAW20303 H. pylori
65	64.5	13.8	207	6	ABM73508 Staphyloc
66	64.5	13.8	207	9	ADV16859 Staphyloc
67	64.5	13.8	207	9	ADM94758 Prolifera
68	64.5	13.8	362	7	ADF89476 Human ery
69	64.5	13.8	362	8	ADK48858 Human tra
70	64.5	13.8	362	8	ADP12457 Protein e
71	64	13.7	260	4	AAW38702 Human pol
72	64	13.7	378	4	AAW40488 Human pol
73	64	13.7	656	4	ABU53239 Human tes
74	64	13.7	656	8	ADL28417 Human nuc
75	64	13.7	2426	2	ADH11285 Vertebrat

ALIGNMENTS

RESULT 1	ABB78171	standard; protein; 88 AA.
ID	ABB78171	
XX		
AC	ABB78171;	
XX		
DT	29-AUG-2003	(revised)
DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue.	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX		
OS	Neisseria gonorrhoeae.	
XX		
PN	US2002072118-A1.	

XX PD 13-JUN-2002.
XX 18-SEP-2001; 2001US-00955502.
XX PF 22-SEP-2000; 2000US-0234588P.
XX PR
XX
XX (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX PI
XX PI Downs D, Gralnick JA;
XX DR WPI; 2002-589476/63.
XX DR
XX WPI; 2002-589476/63.
XX
XX
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX PS Example; Fig 1A; 16pp; English.
XX
XX CC The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from Salmonella
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues. (Updated on 29-AUG-2003 to
XX CC standardise OS field)
XX
XX SQ Sequence 88 AA;
SQ
Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
QY 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
Db 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
RESULT 2
ABB78172
ID ABB78172 standard; protein; 88 AA.
XX
XX AC ABB78172;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Amino acid sequence of a YggX homologue.
XX
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Neisseria meningitidis.
XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.
XX
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX CC

PI Downs D, Gralnick JA;
XX
XX DR WPI; 2002-589476/63.
XX
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX PS Example; Fig 1A; 16pp; English.
XX
XX CC The specification describes a method for reducing superoxide damage to a
XX CC cell. The method comprises engineering the cell to produce more than the
XX CC native amount of YggX protein (a protein identified from Salmonella
XX CC enterica serovar typhimurium) or its homolog, where the cells are
XX CC rendered more resistant to superoxide damage. YggX reduces the oxidation
XX CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
XX CC clusters. The resulting decrease in free-iron levels generates fewer
XX CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
XX CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 88 AA;
SQ
Query Match 100.0%; Score 467; DB 5; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.8e-54;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSGEAWAAMTRHQTMLINENRLSLADP 60
QY 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
Db 61 RAREYLAQOMEQYFFGDGADAVQGYVPQ 88
RESULT 3
ABB78173
ID ABB78173 standard; protein; 88 AA.
XX
XX AC ABB78173;
XX
XX DT 05-NOV-2002 (first entry)
XX
XX DE Amino acid sequence of a YggX homologue.
XX
XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX OS Neisseria meningitidis.
XX
XX PN US2002072118-A1.
XX
XX PD 13-JUN-2002.
XX
XX PF 18-SEP-2001; 2001US-00955502.
XX
XX PR 22-SEP-2000; 2000US-0234588P.
XX
XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.
XX
XX PI Downs D, Gralnick JA;
XX
XX DR WPI; 2002-589476/63.
XX
XX PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
XX PT cell, comprises engineering the cell to produce more YggX protein, a
XX PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX PS Example; Fig 1A; 16pp; English.
XX
XX CC The specification describes a method for reducing superoxide damage to a

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:17:30 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-28
Perfect score: 467
Sequence: 1 MARMVFCVKLNKEAEGMKFP.....QMEGYFFGDGADAVGGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467	100.0	88	2 H81014	conserved hypothet
2	240	51.4	90	2 C82320	conserved hypothet
3	227	48.6	90	2 C64013	hypothetical prote
4	213	45.6	91	2 A85954	hypothetical prote
5	213	45.6	91	2 A65082	hypothetical prote
6	213	45.6	91	2 F91108	hypothetical prote
7	211	45.2	91	2 AH0879	conserved hypothet
8	207	44.3	90	2 H83003	conserved hypothet
9	201	43.0	105	2 C82624	conserved hypothet
10	198	42.4	90	2 AI0116	conserved hypothet
11	158	33.8	93	2 E84994	hypothetical prote
12	72	15.4	1041	2 A81960	probable DNA helic
13	70	15.0	1079	2 T38913	translation initia
14	68.5	14.7	338	2 A83389	probable permease
15	68.5	14.7	549	2 AI1457	ABC transporter ol
16	68	14.6	195	2 S74714	hypothetical prote
17	67.5	14.5	899	2 A83019	conserved hypothet
18	66.5	14.2	401	2 C70159	translation elonga
19	66	14.1	598	1 RGEENX	nitrate/nitrite se
20	66	14.1	598	2 F85702	nitrate/nitrite se
21	66	14.1	598	2 G90844	nitrate/nitrite se
22	65	13.9	296	2 A64110	cell division inh
23	65	13.9	465	2 C71870	hypothetical prote
24	65	13.9	590	2 E85057	probable transpos
25	64.5	13.8	207	2 E89952	conserved hypothet
26	64.5	13.8	362	2 T45072	erythroid Kruppel-
27	64.5	13.8	400	2 A39254	inositol-1,4-bisph
28	64.5	13.8	1553	2 S67483	adenosinetriphosph
29	64	13.7	676	2 A45984	sperm-binding glyc

30	64	13.7	677	2 S33664	flagella-associate
31	63.5	13.6	288	2 H95018	transcription regu
32	63.5	13.6	301	2 F82446	transcription regu
33	63	13.5	282	2 D97138	DNA replication pr
34	63	13.5	388	1 JC5461	cellulase (EC 3.2.
35	63	13.5	388	1 S43920	cellulase (EC 3.2.
36	62	13.3	120	2 G97833	hypothetical prote
37	62	13.3	200	2 E82203	transcription regu
38	62	13.3	259	2 S55033	transcription init
39	62	13.3	570	2 D83177	probable phosphotr
40	62	13.3	2314	2 T28698	hypothetical prote
41	61.5	13.2	211	2 T38645	hypothetical prote
42	61.5	13.2	288	2 B95122	transcription regu
43	61.5	13.2	374	2 A96502	probable acyl-acyl
44	61.5	13.2	412	2 G81581	tyrosyl-tRNA synth
45	61.5	13.2	422	2 G86535	tyrosyl tRNA synth
46	61.5	13.2	422	2 D72088	tyrosine-tRNA liga
47	61.5	13.2	589	2 AE3530	flagellar biosynth
48	61	13.1	425	2 T50184	mammalian swi/snf
49	61	13.1	563	2 F97028	arginyl-tRNA synth
50	61	13.1	969	2 T33156	hypothetical prote
51	61	13.1	1639	2 T50119	probable sensory t
52	60.5	13.0	186	1 WMR219	19K globulin precu
53	60.5	13.0	186	2 JC4784	alpha-globulin pre
54	60.5	13.0	261	2 S14875	dark-type molecula
55	60.5	13.0	357	2 F82892	heat-inducible tra
56	60.5	13.0	448	2 T45145	glutamate-ammonia
57	60.5	13.0	1888	2 T39009	hypothetical prote
58	60	12.8	292	2 AI0422	conserved hypothet
59	60	12.8	306	2 A97249	Zn-binding lipopro
60	60	12.8	309	2 D95843	probable transcrip
61	60	12.8	323	2 T35734	probable aminopept
62	60	12.8	335	2 D83142	hypothetical prote
63	60	12.8	397	2 A75503	hypothetical prote
64	60	12.8	410	2 T39115	formamidase-like p
65	60	12.8	508	2 T02486	hypothetical prote
66	60	12.8	615	2 E81451	1-deoxyxylulose-5-
67	60	12.8	655	2 E75206	alpha-amylase (or
68	60	12.8	859	2 T29630	hypothetical prote
69	60	12.8	1006	2 A59384	oxotocinase/insuli
70	60	12.8	1021	2 AC2202	hypothetical prote
71	60	12.8	1025	2 A59383	oxotocinase/insuli
72	60	12.8	3788	2 T30851	lysosomal traffick
73	59.5	12.7	157	1 HHPM17	heat shock protein
74	59.5	12.7	237	2 A55218	sfp homolog gsp -
75	59.5	12.7	295	2 T35330	probable RNA polym

ALIGNMENTS

RESULT 1
H81014
Conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58 ;
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tettelin, H.; Saunderson, N.J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
Li, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizzi, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: A81000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TR>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:G7227279; PIDN:J
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
J.; Holroyd, S.; Jags, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 64.9476 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-28

Perfect score: 467
Sequence: 1 MARMVFCVKLNKEABGMKRP.....QMEQYFPGDADAVQGYVPQ 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	467	100.0	88	1	FETP_NEIG1
2	467	100.0	88	1	FETP_NEIMA
3	467	100.0	88	1	FETP_NEIMA
4	354	75.8	91	1	FETP_RALSO
5	348	74.5	91	2	Q4LS19_9BURK
6	339	72.6	91	1	FETP_BURMA
7	339	72.6	91	1	FETP_BURMA
8	335	71.7	90	1	FETP_CHRVO
9	319	68.3	90	1	FETP_NITEU
10	290	62.1	90	1	FETP_BORBR
11	290	62.1	90	1	FETP_BORBR
12	290	62.1	90	1	FETP_BORBR
13	275	58.9	89	1	FETP_LEGPA
14	271	58.0	89	1	FETP_LEGPA
15	271	58.0	89	1	FETP_LEGPA
16	258	55.2	90	1	FETP_COXBU
17	254	54.4	90	1	FETP_VIBF1
18	252	54.0	92	2	Q4NM04_9DELT
19	243	52.0	90	1	FETP_METCA
20	242	51.8	90	1	FETP_IDILO
21	240	51.4	90	1	FETP_VIBCH
22	239	51.2	90	1	FETP_VIBPA
23	239	51.2	90	1	FETP_VIBVU
24	239	51.2	90	1	FETP_VIBVU
25	235	50.3	91	1	FETP_VIBVU
26	235	50.3	91	1	FETP_XANAC
27	233	49.9	92	1	FETP_XANOR
28	230	49.3	92	1	FETP_SHEON
29	227	48.6	90	1	FETP_HAEIN
30	227	48.6	90	2	Q4QMD9_HAEI8
31	225	48.2	92	1	FETP_XANCP

32	225	48.2	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
33	224	48.0	91	1	FETP_MANSM	Q65vt7 manheimia
34	220.5	47.2	90	1	FETP_ACIAD	Q6f1b3 acinetobact
35	220	47.1	90	1	FETP_PHOPR	Q6lmk7 photobacter
36	219	46.9	90	1	FETP_PSEPK	Q88r49 pseudomonas
37	217	46.5	90	1	FETP_PASMU	Q9clb9 pasteurella
38	217	46.5	90	1	FETP_PASMU	Q7n711 photorhabdu
39	211	45.2	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
40	209	44.8	90	1	FETP_XYLF1	Q87d06 xyliella fas
41	208	44.5	87	1	FETP_PRAIT	Q5nhj8 francisella
42	208	44.5	90	1	FETP_ECO57	Q0a8p4 escherichia
43	208	44.5	90	1	FETP_ECOLI	Q0a8p3 escherichia
44	208	44.5	90	1	FETP_ERWCT	Q6d8j9 erwina car
45	208	44.5	90	1	FETP_SHIFL	Q0a8p5 shigella fl
46	207	44.3	90	1	FETP_PSEAE	Q9hu36 pseudomonas
47	207	44.3	90	2	Q4KJ72_PSEF5	Q4kjt2 pseudomonas
48	206	44.1	90	1	FETP_SALCH	Q57k04 salmoneilla
49	206	44.1	90	1	FETP_SALPA	Q5pmn1 salmoneilla
50	206	44.1	90	1	FETP_SALTI	Q67618 salmoneilla
51	206	44.1	90	1	FETP_SALTY	Q67617 salmoneilla
52	206	44.1	90	1	FETP_YERPS	Q66m3 yersinia ps
53	206	44.1	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
54	204	43.7	90	1	FETP_ECOL6	Q8fe19 escherichia
55	201	43.0	90	1	FETP_XYLFA	Q9pc73 xyliella fas
56	198	42.4	90	1	FETP_PSESM	Q87uf5 pseudomonas
57	198	42.4	90	1	FETP_YERPE	Q8zhe7 yersinia pe
58	198	42.4	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
59	196	42.0	90	2	Q4J228_AZOV1	Q4j228 azotobacter
60	186	39.8	79	1	FETP_CANBF	Q7vrg9 candidatus
61	167	35.8	78	1	FETP_BUCAP	Q8k925 buchnera ap
62	167	35.8	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
63	158	33.8	77	1	FETP_BUCAI	P57618 buchnera ap
64	127	27.2	87	1	FETP_BUCBP	Q89a44 buchnera ap
65	75	16.1	359	2	Q7VKN4_HAEDU	Q7vkn4 haemophilus
66	74	15.8	453	2	Q4PBL1_USTMA	Q4pbl1 ustilago ma
67	74	15.8	1598	2	Q62CB0_BURMA	Q62cb0 burkholderi
68	74	15.8	1599	2	Q63KS1_BURPS	Q63ks1 burkholderi
69	73	15.6	820	2	Q521A7_MAGGR	Q521a7 magnaporthe
70	72.5	15.5	301	2	Q6LNI9_PHOPR	Q6lni9 photobacter
71	72	15.4	203	2	Q568W6_BRAPR	Q568w6 brachydanio
72	72	15.4	1041	2	Q9JWD5_NEIMA	Q9jwd5 neisseria m
73	71	15.2	346	2	Q8BF42_SHEON	Q8bf42 shewanella
74	70.5	15.1	320	2	Q6PKY5_XENLA	Q6pky5 xenopus lae
75	70	15.0	1079	1	IF2P_SCHPO	Q10251 schizosacch

ALIGNMENTS

RESULT 1	
FETP_NEIG1	
ID FETP_NEIG1	STANDARD; PRT; 88 AA.
AC Q5F553;	
DT 13-SEP-2005 (Rel. 48, Created)	
DT 13-SEP-2005 (Rel. 48, Last sequence update)	
DT 13-SEP-2005 (Rel. 48, Last annotation update)	
DE Probable Fe(2+) trafficking protein.	
GN OrderedLocusNames=NGO2083;	
OS Neisseria gonorrhoeae (strain ATCC 700825 / FA 1090).	
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC Neisseriaceae; Neisseria.	
OX NCBI_TaxID=242231;	
RN [1]	
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	
RA Lewis L.A., Gillaespy A.F., McLaughlin R.E., Gipson M., Ducey T.F.,	
RA Ombey T., Hartman K., Nydick C., Carson M.B., Vaughn J., Thomson C.,	
RA Song L., Lin S., Yuan X., Najjar F., Zhan M., Ren Q., Zhu H., Qi S.,	
RA Kenton S.M., Lai H., White J.D., Clifton S., Roe B.A., Dyer D.W.;	
RT "The complete genome sequence of Neisseria gonorrhoeae."	
RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.	
CC -1- FUNCTION: Could be a mediator in iron transactions between iron	
CC acquisition and iron-requiring processes, such as synthesis and/or	
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).	

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CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE004969; AAW90684.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best Local Similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MARMVFCVKLNKEAEGMKFPPLPNELGKRIFENVSOEAWAAMTRHQTMLINENRLSLADP 60

QY 61 RAREYLAQOMEQYFFGDDADAVQGYVPQ 88
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Db 61 RAREYLAQOMEQYFFGDDADAVQGYVPQ 88

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ID PETP_NEIMA STANDARD; PRT; 88 AA.
AC P67615; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 25-OCT-2004 (Rel. 45, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=MMA0419;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Davies R.M., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Jagsels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrrell B.G.;
RA "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."
RL Nature 404:502-506(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL162753; CAB83718.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.

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KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best local similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60
    |||
    1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60

DB 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60

OY 61 RAREYLAQOMEQYFFGDDADAVQGYVPQ 88
    |||
    61 RAREYLAQOMEQYFFGDDADAVQGYVPQ 88

DB 61 RAREYLAQOMEQYFFGDDADAVQGYVPQ 88

RESULT 3
FETP_NEIMB STANDARD; PRT; 88 AA.
ID FETP_NEIMB
AC P67616; Q9JQP5;
DT 10-OCT-2003 (Rel. 42, last Created)
DT 10-OCT-2003 (Rel. 42, last sequence update)
DT 13-SEP-2005 (Rel. 48, last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=NMB2021;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Ciftone H., Clark E.B., Cotton M.D., Uteback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scariato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RT Science 287:1809-1815(2000).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; AB002098; AAF42344.1; -; Genomic_DNA.
CC TIGR; NMB2021; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 88 AA; 10180 MW; EBC6F2FBF097F2F1 CRC64;

Query Match 100.0%; Score 467; DB 1; Length 88;
Best local similarity 100.0%; Pred. No. 1e-45;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60
    |||
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DB 1 MARMVFCVTLNKEAEGMKFPPLPNELGKRIFENVSQEAWAATRHQTMLINENRLSLADP 60

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-28

Perfect score: 467

Sequence: 1 MARMVFCVKLNKEAGMKFP.....OMEQYFPGDGADAVGGYVFG 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	225.5	48.3	92	2	US-09-328-352-5456
3	221	47.3	93	2	US-09-543-681A-5443
4	207	44.3	122	2	US-09-252-991A-23355
5	182	39.0	110	2	US-09-540-236-2859
6	68.5	14.7	361	2	US-09-252-991A-25005
7	67.5	14.5	466	2	US-09-252-991A-32761
8	66	14.1	418	2	US-09-489-039A-13155
9	65.5	14.0	649	2	US-09-107-532A-4298
10	65.5	14.0	3838	2	US-09-949-016-10853
11	64.5	13.8	361	2	US-08-874-569B-21
12	64.5	13.8	361	2	US-09-955-518-21
13	63	13.5	351	2	US-09-248-796A-19129
14	63	13.5	461	1	US-08-672-571A-3
15	63	13.5	490	1	US-08-672-571A-1
16	62.5	13.4	263	2	US-09-252-991A-22230
17	62	13.3	360	2	US-09-543-681A-7067
18	62	13.3	671	2	US-09-198-452A-377
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22	60.5	13.0	596	2	US-09-489-039A-10378
23	60	12.8	621	2	US-08-822-445-2
24	60	12.8	2186	1	US-09-396-540-2
25	59.5	12.7	315	2	US-09-461-325-297
26	59.5	12.7	315	2	US-10-012-542-297
27	59.5	12.7	315	2	US-10-012-542-297

28	59.5	12.7	315	2	US-10-115-123-297	Sequence 297, App
29	59.5	12.7	346	2	US-09-808-701A-32	Sequence 32, Appl
30	59.5	12.7	420	2	US-09-902-540-16463	Sequence 16463, A
31	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
32	59.5	12.7	431	2	US-10-012-542-146	Sequence 146, App
33	59.5	12.7	431	2	US-09-311-021-178	Sequence 178, App
34	59.5	12.7	431	2	US-10-115-123-146	Sequence 146, App
35	59.5	12.7	848	2	US-09-538-092-33	Sequence 33, Appl
36	59.5	12.7	977	2	US-08-335-844A-22	Sequence 22, Appl
37	59.5	12.7	977	2	US-09-129-366-22	Sequence 22, Appl
38	59	12.6	366	2	US-09-252-991A-31958	Sequence 31958, A
39	59	12.6	563	2	US-09-583-110-4195	Sequence 4195, Ap
40	59	12.6	577	2	US-09-107-433-3424	Sequence 3424, Ap
41	59	12.6	5069	2	US-10-042-665A-5	Sequence 5, Appl
42	58.5	12.5	213	2	US-09-959-873B-16	Sequence 16, Appl
43	58.5	12.5	213	2	US-09-949-016-5955	Sequence 5955, Ap
44	58.5	12.5	284	1	US-08-061-889-2	Sequence 2, Appl
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46	58.5	12.5	284	2	US-08-623-428D-2	Sequence 2, Appl
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48	58.5	12.5	284	4	PCT-US94-05378-2	Sequence 2, Appl
49	58.5	12.5	340	2	US-09-270-767-42358	Sequence 42358, A
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51	58.5	12.5	397	2	US-09-079-030-123	Sequence 123, App
52	58.5	12.5	401	2	US-09-352-991A-17272	Sequence 17272, A
53	58	12.4	303	2	US-09-543-681A-7924	Sequence 7924, Ap
54	58	12.4	318	2	US-09-489-039A-8369	Sequence 8369, Ap
55	58	12.4	331	2	US-08-849-751-4	Sequence 4, Appl
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61	58	12.4	720	2	US-10-101-080-2	Sequence 2, Appl
62	58	12.4	1178	2	US-09-489-039A-9944	Sequence 9944, Ap
63	57.5	12.3	163	2	US-09-198-452A-103	Sequence 103, App
64	57.5	12.3	180	2	US-09-640-211A-834	Sequence 834, App
65	57.5	12.3	200	2	US-09-710-279-1186	Sequence 1186, Ap
66	57.5	12.3	200	2	US-09-710-279-2390	Sequence 2390, Ap
67	57.5	12.3	208	2	US-09-134-001C-3785	Sequence 3785, Ap
68	57.5	12.3	210	2	US-09-438-185A-88	Sequence 88, Appl
69	57.5	12.3	282	2	US-09-543-681A-4715	Sequence 4715, Ap
70	57.5	12.3	451	2	US-09-543-681A-7401	Sequence 7401, Ap
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72	57.5	12.3	890	2	US-09-583-110-4739	Sequence 4739, Ap
73	57	12.2	157	2	US-09-902-540-15203	Sequence 15203, A
74	57	12.2	384	2	US-10-094-944-19	Sequence 19, Appl
75	57	12.2	412	2	US-09-538-092-709	Sequence 709, App

ALIGNMENTS

RESULT 1
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Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 55.5262 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-28

Perfect score: 467

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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9	272.5	58.4	86	3	US-09-955-502-4
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13	235	50.3	87	3	US-09-955-502-8
14	230	49.3	88	3	US-09-955-502-9
15	228	48.8	91	3	US-09-955-502-5
16	227	48.6	87	3	US-09-955-502-7
17	219	46.9	87	3	US-09-955-502-24
18	217	46.5	87	3	US-09-955-502-6
19	213	45.6	91	3	US-09-955-502-11
20	213	45.6	91	3	US-09-955-502-12
21	213	45.6	91	3	US-09-955-502-13
22	211	45.2	88	3	US-09-955-502-15
23	211	45.2	91	3	US-09-955-502-14
24	211	45.2	91	3	US-09-955-502-16
25	210	45.0	91	3	US-09-955-502-17
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29	201	43.0	89	3	US-09-955-502-22	Sequence 20, Appl
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35	69	14.8	774	5	US-10-450-763-59663	Sequence 191747, A
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37	66.5	14.2	401	4	US-10-282-122A-47145	Sequence 131308, A
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57	64.5	13.8	361	3	US-09-955-518-21	Sequence 21, Appl
58	64.5	13.8	361	4	US-10-289-152-21	Sequence 22706, A
59	64.5	13.8	1501	5	US-10-732-923-22706	Sequence 22705, A
60	64.5	13.8	1553	5	US-10-732-923-22705	Sequence 22584, A
61	64.5	13.8	1555	5	US-10-732-923-22584	Sequence 281438, A
62	63.5	13.6	94	4	US-10-425-115-281438	Sequence 132, App
63	63.5	13.6	288	5	US-10-472-928-132	Sequence 8759, App
64	63	13.5	417	4	US-10-156-761-8759	Sequence 172448, A
65	62.5	13.4	126	4	US-10-437-963-172448	Sequence 68811, A
66	62	13.3	360	4	US-10-282-122A-68811	Sequence 4727, Ap
67	62	13.3	519	4	US-10-369-493-4727	Sequence 7486, Ap
68	62	13.3	532	4	US-10-369-493-7486	Sequence 11951, A
69	62	13.3	570	3	US-09-815-242-11951	Sequence 66545, A
70	62	13.3	570	4	US-10-282-122A-66545	Sequence 7, Appli
71	62	13.3	835	4	US-10-273-680-7	Sequence 67, Appl
72	62	13.3	835	4	US-10-087-887-67	Sequence 74, Appl
73	62	13.3	835	4	US-10-087-887-74	Sequence 7, Appli
74	62	13.3	835	5	US-10-889-340-7	Sequence 149485, A
75	62	13.3	1025	4	US-10-424-599-149485	

ALIGNMENTS

RESULT 1
US-09-955-502-26
; Sequence 26, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 26
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-18
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFEKDVHIEGYPTEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 segs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	488	100.0	91	5	ABB78163
2	474	97.1	91	5	ABB78161
3	474	97.1	91	5	ABB78159
4	474	97.1	91	5	ABB78162
5	458	93.9	88	5	ABB78160
6	455	93.2	91	5	ABB78158
7	455	93.2	91	5	ABB78157
8	455	93.2	91	5	ABB78156
9	431	88.3	107	7	ABO65445
10	386	79.1	78	5	ABB78164
11	379	77.7	90	5	ABB78165
12	378	77.5	87	5	ABB78152
13	375	76.8	90	5	ABB78155
14	370	75.8	87	5	ABB78151
15	369.5	75.7	91	5	ABB78150
16	369	75.6	93	7	ADF05158
17	364	74.6	87	5	ABB78153
18	326	66.8	88	5	ABB78154
19	259	53.1	76	5	ABB78166
20	242	49.6	87	5	ABB78148
21	242	49.6	87	5	ABB78147
22	241	49.4	86	5	ABB78149
23	224.5	46.0	89	9	AEB41576
24	224.5	46.0	95	9	AEB38294

25	221	45.3	87	5	ABB78170	Abb78170 Amino aci
26	221	45.3	122	7	ABO74609	AbO74609 Pseudomon
27	220.5	45.2	90	5	ABB78167	Abb78167 Amino aci
28	214	43.9	88	5	ABB78178	Abb78178 Amino aci
29	212	43.4	90	5	ABB78168	Abb78168 Amino aci
30	211	43.2	87	5	ABB78169	Abb78169 Amino aci
31	202	41.4	88	5	ABB78171	Abb78171 Amino aci
32	202	41.4	88	5	ABB78172	Abb78172 Amino aci
33	202	41.4	88	5	ABB78173	Abb78173 Amino aci
34	202	41.4	88	6	ABP77219	Abp77219 N. gonorr
35	199	40.8	87	5	ABB78175	Abb78175 Amino aci
36	193	39.5	87	5	ABB78174	Abb78174 Amino aci
37	190	38.9	87	5	ABB78176	Abb78176 Amino aci
38	188	38.5	87	5	ABB78177	Abb78177 Amino aci
39	187.5	38.4	92	6	ADA34169	Ada34169 Acinetoba
40	124	25.4	110	8	ADL05173	Adl05173 M. catarr
41	72	14.8	309	8	ADN46828	Adn46828 Thermococ
42	72	14.8	506	3	AAV74371	Aay74371 Neisseria
43	72	14.8	507	6	ABU40210	Abu40210 Protein e
44	71.5	14.7	184	3	AAI16290	Aab16290 Pinus rad
45	71	14.5	507	3	AAV74372	Aay74372 Neisseria
46	71	14.5	507	3	AAV74373	Aay74373 Neisseria
47	71	14.5	546	6	ABU38097	Abu38097 Protein e
48	71	14.5	548	4	AAE04737	Aae04737 Brugia ma
49	70.5	14.4	184	3	AAI16325	Aab16325 Pinus rad
50	70.5	14.4	184	4	AAE65734	Aab65734 Annexin-1
51	70.5	14.4	184	7	ADB94702	AdB94702 Programme
52	70.5	14.4	503	4	ABG16577	Abg16577 Novel hum
53	70	14.3	257	3	AAI31203	Aag31203 Arabidops
54	70	14.3	297	3	AAI31202	Aag31202 Arabidops
55	70	14.3	324	3	AAI31201	Aag31201 Arabidops
56	70	14.3	758	9	ADW71760	Adw71760 Salmonell
57	69.5	14.2	227	3	AAI38052	Aag38052 Arabidops
58	69.5	14.2	307	5	ABB49355	Abb49355 Listeria
59	69.5	14.2	869	8	ADW64441	Adw64441 Thermosta
60	69.5	14.2	1377	8	ADV81847	Adv81847 Streptoco
61	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
62	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
63	69	14.1	679	9	ADZ85056	Adz85056 Partial F
64	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
65	68	13.9	285	4	AAI92683	Aab92683 Human pro
66	68	13.9	414	6	ABU11747	Abu11747 Human MDD
67	68	13.9	614	9	ADX06837	Adx06837 Cyclin-de
68	68	13.9	614	9	ADY16108	Ady16108 PRO polyp
69	68	13.9	764	5	ABB77432	Abb77432 Human tum
70	68	13.9	764	7	ADC99062	Adc99062 Human KKP
71	68	13.9	817	4	AAI38657	Aam38657 Human pol
72	68	13.9	863	4	AAI38656	Aam38656 Human pol
73	68	13.9	1135	8	ADSI10706	Adsi10706 Human the
74	68	13.9	1181	8	ADSI10708	Adsi10708 Human the
75	68	13.9	1186	8	ADSI10709	Adsi10709 Human the

ALIGNMENTS

RESULT 1	
ABB78163	
ID	ABB78163 standard; protein; 91 AA.
XX	
AC	ABB78163;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	
KW	hydroxyl radical; DNA damage; YggX homologue.
XX	
OS	Salmonella typhimurium.
XX	
PN	US2002072118-A1.
XX	

PD 13-JUN-2002.
XX
PT 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmoneila
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 6.2e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAWQOHKQTMLINEKLNMMNA 60
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAWQOHKQTMLINEKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYPTEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYPTEDKK 91

RESULT 2
ABB78161 ID ABB78161 standard; protein; 91 AA.
XX
AC ABB78161;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmoneila enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmoneila
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 97.1%; Score 474; DB 5; Length 91;
Best Local Similarity 97.8%; Pred. No. 2.7e-47;
Matches 89; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAWQOHKQTMLINEKLNMMNA 60
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAMAWQOHKQTMLINEKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYPTEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYPTEDKK 91

RESULT 3
ABB78159 ID ABB78159 standard; protein; 91 AA.
XX
AC ABB78159;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmoneila enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmoneila

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-18
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFEGKDVHIEGYPTEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query Length	DB	ID	Description
1	474	97.1	91	2	AH0879	conserved hypothet
2	455	93.2	91	2	A85954	hypothetical prote
3	455	93.2	91	2	A65082	hypothetical prote
4	455	93.2	91	2	F91108	hypothetical prote
5	379	77.7	90	2	A10116	conserved hypothet
6	378	77.5	90	2	C64013	hypothetical prote
7	375	76.8	90	2	C82320	conserved hypothet
8	259	53.1	93	2	E84994	hypothetical prote
9	230	47.1	105	2	C82624	conserved hypothet
10	221	45.3	90	2	H83003	conserved hypothet
11	202	41.4	88	2	H81014	conserved hypothet
12	79.5	16.3	1638	2	D87749	protein unc-73b [i
13	79.5	16.3	2488	2	T42739	guanine nucleotide
14	73.5	15.1	495	2	AH0985	probable zinc-prot
15	71.5	14.7	209	2	I64172	hypothetical prote
16	71	14.5	507	2	C81063	fumarate hydratase
17	71	14.5	546	2	A81807	fumarate hydratase
18	71	14.5	548	2	A54510	63K antigen - nema
19	70	14.3	324	2	T05429	hypothetical prote
20	70	14.3	758	2	AD0763	thiosulfate reduct
21	70	14.3	758	2	A57143	thiosulfate-dithio
22	70	14.3	1260	2	T04440	hypothetical prote
23	69.5	14.2	307	2	AH1269	primosome componen
24	69.5	14.2	859	2	T29630	hypothetical prote
25	69	14.1	265	2	T46013	hypothetical prote
26	67.5	13.8	166	2	F70562	hypothetical prote
27	67.5	13.8	287	2	F82265	conserved hypothet
28	67	13.7	618	2	A71364	probable phosphoen
29	67	13.7	1111	2	T23047	hypothetical prote

30	66.5	13.6	410	1	KIIMSD	cathepsin D (EC 3.
31	66	13.5	703	2	B82148	ATP-dependent heli
32	66	13.5	1085	2	S62516	hypothetical coile
33	65.5	13.4	251	2	E90428	hypothetical prote
34	65.5	13.4	307	2	AB1632	primosome componen
35	65.5	13.4	365	2	B54128	Fe-binding protein
36	65	13.3	447	2	JC2076	alpha-1,3-mannosyl
37	65	13.3	507	2	A83105	probable fumalase
38	65	13.3	593	2	C64097	probable soluble l
39	65	13.3	1230	2	S56850	SMC1 protein homol
40	64.5	13.2	327	2	AD2129	transcription regu
41	64.5	13.2	511	2	A99574	ABC transporter at
42	64.5	13.2	544	2	T40058	probable chromatin
43	64	13.1	548	2	A28209	60K filarial antig
44	63.5	13.0	156	2	F70382	conserved hypothet
45	63.5	13.0	274	2	T16581	hypothetical prote
46	63.5	13.0	379	2	S70709	type II site-speci
47	63.5	13.0	438	2	T37786	probable RNA-bindi
48	63.5	13.0	2672	2	A48126	translation activa
49	63.5	13.0	2911	2	T20566	hypothetical prote
50	63	12.9	235	2	G65212	hypothetical prote
51	63	12.9	243	2	T29635	hypothetical prote
52	63	12.9	258	2	A97991	phosphoesterase, p
53	63	12.9	258	2	E95121	alpha-1,3-mannosyl
54	63	12.9	445	1	XUHUMB	hypothetical prote
55	63	12.9	447	2	T16527	hypothetical prote
56	63	12.9	472	2	A64576	hypothetical prote
57	63	12.9	483	2	G64799	ybeV protein - Bsc
58	63	12.9	543	2	T16015	hypothetical prote
59	63	12.9	549	2	T16016	hypothetical prote
60	63	12.9	1166	2	H71609	hypothetical prote
61	63	12.9	1209	2	T46027	hypothetical prote
62	63	12.9	1327	2	T14594	guanidine nucleoti
63	62.5	12.8	165	2	A81382	shikimate kinase (
64	62.5	12.8	214	1	KABOSB	alpha-s1-casein pr
65	62.5	12.8	259	2	G83203	conserved hypothet
66	62.5	12.8	305	2	A75211	asparaginase (EC 3
67	62.5	12.8	339	2	A90395	conserved hypothet
68	62.5	12.8	385	2	D87723	protein R06A10.2 [
69	62.5	12.8	401	2	AB1978	hypothetical prote
70	62.5	12.8	498	2	G91179	hypothetical prote
71	62.5	12.8	498	2	H86025	hypothetical prote
72	62.5	12.8	498	2	S47748	53.1K protein prec
73	62.5	12.8	906	2	G69531	alanyl-cRNA synthe
74	62.5	12.8	1141	2	T29185	hypothetical prote
75	62	12.7	226	1	G64211	formylmethionine d

ALIGNMENTS

RESULT 1
AH0879
C,Species: Salmonella enterica subsp. enterica
A,Note: this species has also been called Salmonella typhi
C,Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C,Accession: AH0879
R,Parikhil, J.; Dugan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, U.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A,Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A,Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A,Reference number: AB0502; MUID:21534947; PMID:11677608
A,Accession: AH0879
A,Status: preliminary
A,Molecule type: DNA
A,Residues: 1-91 <PAR>
A,Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
C,Genetics:
A,Gene: STY3266
C,Superfamily: fe(II) trafficking protein YggX

Query Match	97.1%;	Score 474;	DB 2;	Length 91;	
Best Local Similarity	97.8%;	Pred. No. 2.4e-41;			
Matches	89;	Conservative	0;	Mismatches 2;	Indels 0; Gaps 0;
OY	1	MSRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA	60		
Db	1	MSRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA	60		
OY	61	EHRKLLGEQEMVSLFEGKDVHIEGYPTEDKK	91		
Db	61	EHRKLLGEQEMVSLFEGKDVHIEGYTPEDKK	91		
RESULT 2					
A85954		hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93			
C/Species:	Escherichia coli				
C/Date:	16-Feb-2001	#sequence_revision 16-Feb-2001	#text_change 05-Oct-2004		
C/Accession:	A85954				
R;Perna, N.T.;	Plunkett III, G.;	Burland, V.;	Mau, B.;	Glasner, J.D.;	Rose, D.J.;
iller, L.;	Grobeck, E.J.;	Davis, N.W.;	Lim, A.;	Dimalanta, E.;	Potamoculis, K.;
Nature	409, 529-533,	2001			
A/Title:	Genome sequence of enterohemorrhagic Escherichia coli O157:H7.				
A/Reference number:	A85480;	MUID:21074935;	PMID:11206551		
A/Accession:	A85954				
A/Status:	preliminary				
A/Molecule type:	DNA				
A/Residues:	1-91 <STO>				
A/Cross-references:	UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F				
A/Experimental source:	strain O157:H7, substrain EDL933				
C/Genetics:					
A/Gene:	YggX				
C/Superfamily:	fe(II) trafficking protein YggX				
Query Match	93.2%;	Score 455;	DB 2;	Length 91;	
Best Local Similarity	92.3%;	Pred. No. 2e-39;			
Matches	84;	Conservative	5;	Mismatches 2;	Indels 0; Gaps 0;
OY	1	MSRTIFCTYLQRDAGGDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMMNA	60		
Db	1	MSRTIFCTFLQREAGGDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMMNA	60		
OY	61	EHRKLLGEQEMVSLFEGKDVHIEGYPTEDKK	91		
Db	61	EHRKLLGEQEMVNLFFEGKEVHIEGYTPEDKK	91		
RESULT 3					
A65082		hypothetical protein b2962 - Escherichia coli (strain K-12)			
C/Species:	Escherichia coli				
C/Date:	12-Sep-1997	#sequence_revision 17-Sep-1997	#text_change 05-Oct-2004		
C/Accession:	A65082				
R;Blatner, F.R.;	Plunkett III, G.;	Bloch, C.A.;	Perna, N.T.;	Burland, V.;	Riley, M.;
.A.;	Rose, D.J.;	Mau, B.;	Shao, Y.		
Science	277, 1453-1462,	1997			
A/Title:	The complete genome sequence of Escherichia coli K-12.				
A/Reference number:	A64720;	MUID:97426617;	PMID:9278503		
A/Accession:	A65082				
A/Status:	preliminary;	nucleic acid sequence not shown;	translation not shown		
A/Molecule type:	DNA				
A/Residues:	1-91 <BLAT>				
A/Cross-references:	UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9				
A/Experimental source:	strain K-12, substrain MG1655				
C/Superfamily:	fe(II) trafficking protein YggX				
Query Match	93.2%;	Score 455;	DB 2;	Length 91;	
Best Local Similarity	92.3%;	Pred. No. 2e-39;			
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OY	61	EHRKLLGEQEMVSLFEGKDVHIEGYPTEDKK	91		
Db	61	EHRKLLGEQEMVNLFFEGKEVHIEGYTPEDKK	91		
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F91108		hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI			
C/Species:	Escherichia coli				
C/Date:	18-Jul-2001	#sequence_revision 18-Jul-2001	#text_change 05-Oct-2004		
C/Accession:	F91108				
R;Hayashi, T.;	Makino, K.;	Ohnishi, M.;	Kurokawa, K.;	Ishii, K.;	Yokoyama, K.;
gasawara, N.;	Yasunaga, T.;	Kuhara, S.;	Shiba, T.;	Hattori, M.;	Shinagawa, H.
DNA Res.	8, 11-22,	2001			
A/Title:	Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno				
A/Reference number:	A99629;	MUID:21156231;	PMID:11258796		
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A/Status:	preliminary				
A/Molecule type:	DNA				
A/Residues:	1-91 <HAY>				
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A/Experimental source:	strain O157:H7, substrain RIMD 0509952				
C/Genetics:					
A/Gene:	ECs3838				
C/Superfamily:	fe(II) trafficking protein YggX				
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Db	61	EHRKLLGEQEMVNLFFEGKEVHIEGYTPEDKK	91		
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C/Species:	Yersinia pestis				
C/Date:	02-Nov-2001	#sequence_revision 02-Nov-2001	#text_change 05-Oct-2004		
C/Accession:	A10116				
R;Parkhill, J.;	Wren, B.W.;	Thomson, N.R.;	Titball, R.W.;	Holden, M.T.G.;	Prentice, M.B.
deno-Tarraga, A.M.;	Chillingworth, T.;	Cronin, A.;	Davies, R.M.;	Davis, P.;	Dougan, G.;
ll, M.;	Rutherford, K.;	Simmonds, M.;	Skelton, J.;	Stevens, K.;	Whitehead, S.;
Nature	413, 523-527,	2001			
A/Title:	Genome sequence of Yersinia pestis, the causative agent of plague.				
A/Reference number:	AB0001;	MUID:21470413;	PMID:11586360		
A/Accession:	A10116				
A/Status:	preliminary				
A/Molecule type:	DNA				
A/Residues:	1-90 <KUR>				
A/Cross-references:	UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;				
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A/Gene:	YPO0953				
C/Superfamily:	fe(II) trafficking protein YggX				
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Best Local Similarity	78.9%;	Pred. No. 1.1e-31;			
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Db	1	MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITTKOTMLINEKKLSMMNI	60		
OY	61	EHRKLLGEQEMVSLFEGKDVHIEGYPTEDK	90		
Db	61	EDRKLLGEQEMVNLFFEGQDVHLAGYTPPSK	90		

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-18
Perfect score: 488
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	469	96.1	90	1	FETP_SALPA Q5pmml salmonella
3	469	96.1	90	1	FETP_SALTI P67618 salmonella
4	469	96.1	90	1	FETP_SALTY P67617 salmonella
5	450	92.2	90	1	FETP_ECO57 P0A8P4 escherichia
6	450	92.2	90	1	FETP_ECOLI P0A8P3 escherichia
7	450	92.2	90	1	FETP_SHIFL P0A8P5 shigella fl
8	446	91.4	90	1	FETP_ECOL6 Q8fel9 escherichia
9	404	82.8	90	1	FETP_ERWCT Q6d8j9 erwinia car
10	387	79.3	90	1	FETP_YERPS Q66m3 yersinia ps
11	383	78.5	90	1	FETP_VIBPA Q87li5 vibrio para
12	379	77.7	90	1	FETP_YERPS Q8zhe7 yersinia pe
13	379	77.7	91	1	FETP_MANSM Q65vt7 manheimia
14	378	77.5	90	1	FETP_HAEIN P44048 haemophilus
15	378	77.5	90	2	Q4OMD9 HAEI8 Q4qmd9 haemophilus
16	376	77.0	90	1	FETP_PASMU Q9clb9 pasteurella
17	375	76.8	90	1	FETP_VIBCH Q9kur4 vibrio chol
18	375	76.8	90	1	FETP_VIBVU Q8dcs5 vibrio vuln
19	375	76.8	90	1	FETP_VIBVY Q7mbi4 vibrio vuln
20	369	75.6	90	1	FETP_PHOPR Q6lmk7 photobacter
21	364	74.6	94	1	FETP_HAEDU Q7vkb6 haemophilus
22	362	74.2	90	1	FETP_PHOLD Q7n7i1 photorhabdu
23	355	72.7	90	1	FETP_VIBF1 Q5e7c0 vibrio fisc
24	328.5	67.3	90	1	FETP_IDILO Q5qy58 idiomarina
25	327.5	67.1	92	1	FETP_SHEON Q8dbx6 sheuanaella
26	259	53.1	77	1	FETP_BUCAL P57618 buchnera ap
27	243	49.8	78	1	FETP_BUCAP Q8k925 buchnera ap
28	242	49.6	90	1	FETP_BORBR Q7wh06 bordetella
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30	242	49.6	90	1	FETP_XANAC Q7wvc4 bordetella
31	239	49.0	91	1	FETP_XANAC Q8pjh7 xanthomonas

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33	230	47.1	90	1	FETP_XYLFA	Q9pc73 xylella fas
34	228.5	46.8	89	1	FETP_LEGPL	Q5wvc4 legioneella
35	228	46.7	92	1	FETP_XANCP	Q8p829 xanthomonas
36	228	46.7	92	2	Q4UW14_XANCP	Q4uwl4 xanthomonas
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38	225	46.1	78	1	FETP_WIGBR	Q8d3c5 wigglewort
39	224.5	46.0	89	1	FETP_LEGPA	Q5x3x9 legioneella
40	224.5	46.0	89	1	FETP_LEGPH	Q5zu80 legioneella
41	221	45.3	90	1	FETP_PSEAB	Q9nu36 pseudomonas
42	218	44.7	90	2	Q4J228_AZOVI	Q4j228 azotobacter
43	214	43.9	90	1	FETP_COXBU	Q83d06 coxiella bu
44	212	43.4	79	1	FETP_CANBF	Q7vr99 candidatus
45	212	43.4	90	1	FETP_NITEU	Q82xf2 nitrosomona
46	212	43.4	90	1	FETP_PSEPK	Q88r49 pseudomonas
47	212	43.4	90	1	FETP_PSESM	Q87uf5 pseudomonas
48	212	43.4	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
49	210	43.0	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
50	207	42.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
51	202	41.4	88	1	FETP_NEIG1	Q5f553 neisseria g
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55	201.5	41.3	90	1	FETP_CHRVO	Q7nsr4 chromobacte
56	199	40.8	90	2	Q4KJ2_PSEFS	Q4kjt2 pseudomonas
57	199	40.8	91	1	FETP_BURMA	Q62iu9 burkholderi
58	199	40.8	91	1	FETP_BURPS	Q63ej4 burkholderi
59	198	40.6	91	1	FETP_RALSO	Q8y010 ralstonia s
60	191	39.1	87	1	FETP_FRATT	Q5nhj8 francisella
61	188	38.5	90	1	FETP_METCA	Q60aj7 methylococc
62	182.5	37.4	90	1	FETP_ACTIAD	Q6fjb3 acinetobact
63	142	29.1	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
64	132	27.0	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	82.5	16.9	482	2	Q5NUY1_9BURK	Q5nuyl ralstonia m
66	82.5	16.9	514	2	Q6AIZ9_DESPS	Q6aiz9 desulfotale
67	79.5	16.3	1638	2	Q7KPP4_CABEL	Q7kpp4 caenorhabdi
68	79.5	16.3	2140	2	Q6BEW2_CABEL	Q6bew2 caenorhabdi
69	79.5	16.3	2488	2	O61528_CABEL	O61528 caenorhabdi
70	78.5	16.1	337	2	O81AR8_BACCR	O81ar8 bacillus ce
71	76.5	15.7	486	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
72	75	15.4	385	2	Q734A2_BACCI	Q734a2 bacillus ce
73	75	15.4	508	2	Q7NSF0_CHRVO	Q7nsf0 chromobacte
74	74.5	15.3	1589	2	O516E7_ENTHI	O516e7 entamoeba h
75	73.5	15.1	495	1	YHJ0_SALTI	Q8z286 salmonella

ALIGNMENTS

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OS	Salmonella choleraesuis.				
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;				
OC	Enterobacteriaceae; Salmonella.				
OX	NCBI_TaxID=591;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].				
RC	STRAIN=SC-B67;				
RX	PubMed=15781495; DOI=10.1093/nar/gki297;				
RA	Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,				
RA	Wang H.-S., Lee Y.-S.;				
RT	"The genome sequence of Salmonella enterica serovar Choleraesuis, a				
RT	highly invasive and resistant zoonotic pathogen.";				
RL	Nucleic Acids Res. 33:1690-1698(2005).				
CC	-l- FUNCTION: Could be a mediator in iron transactions between iron				
CC	acquisition and iron-regulating processes, such as synthesis and/or				

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
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407.805 Million cell updates/sec

Title: US-09-955-502A-18

Perfect score: 488

Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFKGVHIEGYPTEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	431	88.3	107	2	US-09-489-039A-11962 Sequence 11962, A
2	369	75.6	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	221	45.3	122	2	US-09-252-991A-23355 Sequence 23355, A
4	187.5	38.4	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	124	25.4	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	14.5	548	2	US-09-167-299-3 Sequence 3, Appli
7	70.5	14.4	184	2	US-09-325-932A-66 Sequence 66, Appl
8	68.5	14.0	544	2	US-09-248-796A-18911 Sequence 18911, A
9	68	13.9	337	2	US-09-270-767-41746 Sequence 41746, A
10	68	13.9	1214	2	US-10-164-595-24 Sequence 24, Appl
11	67.5	13.8	192	2	US-08-545-573A-9 Sequence 9, Appli
12	66	13.5	292	2	US-09-328-352-5836 Sequence 5836, Ap
13	66	13.5	331	2	US-09-328-352-6400 Sequence 6400, Ap
14	65.5	13.4	125	2	US-08-545-573A-13 Sequence 13, Appl
15	65	13.3	474	2	US-09-252-991A-24473 Sequence 24473, A
16	64	13.1	1176	2	US-09-489-039A-8879 Sequence 8879, Ap
17	63.5	13.0	546	1	US-08-533-669A-2 Sequence 2, Appli
18	63.5	13.0	546	2	US-09-183-861-2 Sequence 2, Appli
19	63.5	13.0	546	2	US-09-022-765-2 Sequence 2, Appli
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22	63.5	13.0	546	2	US-09-639-206A-2 Sequence 2, Appli
23	63.5	13.0	546	2	US-09-874-923-2 Sequence 2, Appli
24	63.5	13.0	546	2	US-08-798-841-2 Sequence 2, Appli
25	63.5	13.0	982	2	US-09-551-974A-95 Sequence 95, Appl
26	63.5	13.0	982	2	US-09-565-501A-95 Sequence 95, Appl
27	63.5	13.0	982	2	US-09-639-206A-95 Sequence 95, Appl

28	63.5	13.0	982	2	US-09-874-923-95	Sequence 95, Appl
29	63.5	13.0	1427	2	US-09-551-974A-97	Sequence 97, Appl
30	63.5	13.0	1427	2	US-09-565-501A-97	Sequence 97, Appl
31	63.5	13.0	1427	2	US-09-639-206A-97	Sequence 97, Appl
32	63.5	13.0	1427	2	US-09-874-923-97	Sequence 97, Appl
33	63.5	13.0	1641	2	US-09-551-974A-96	Sequence 96, Appl
34	63.5	13.0	1641	2	US-09-565-501A-96	Sequence 96, Appl
35	63.5	13.0	1641	2	US-09-639-206A-96	Sequence 96, Appl
36	63.5	13.0	1641	2	US-09-874-923-96	Sequence 96, Appl
37	63	12.9	317	2	US-09-540-236-3449	Sequence 3449, Ap
38	63	12.9	569	2	US-09-107-532A-6689	Sequence 6689, Ap
39	62.5	12.8	199	2	US-08-545-573A-42	Sequence 42, Appl
40	62.5	12.8	199	2	US-09-066-330-9	Sequence 9, Appli
41	62.5	12.8	214	2	US-08-545-573A-41	Sequence 41, Appl
42	62.5	12.8	260	2	US-09-252-991A-17498	Sequence 17498, A
43	62.5	12.8	662	2	US-09-583-110-5119	Sequence 5119, Ap
44	62.5	12.8	664	2	US-09-107-433-2775	Sequence 2775, Ap
45	62	12.7	227	2	US-09-270-767-58283	Sequence 58283, A
46	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
47	62	12.7	898	2	US-09-583-110-3750	Sequence 3750, Ap
48	62	12.7	899	2	US-09-107-433-3196	Sequence 3196, Ap
49	61.5	12.6	526	2	US-09-071-035-84	Sequence 84, Appl
50	61.5	12.6	526	2	US-10-206-576-84	Sequence 84, Appl
51	61.5	12.6	528	2	US-09-071-035-44	Sequence 44, Appl
52	61.5	12.6	528	2	US-10-206-576-44	Sequence 44, Appl
53	61.5	12.6	546	2	US-09-071-035-82	Sequence 82, Appl
54	61.5	12.6	546	2	US-10-206-576-82	Sequence 82, Appl
55	61.5	12.6	547	2	US-09-071-035-42	Sequence 42, Appl
56	61.5	12.6	547	2	US-10-206-576-42	Sequence 42, Appl
57	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appli
58	61	12.5	143	2	US-09-270-767-45872	Sequence 45872, A
59	61	12.5	184	2	US-09-270-767-61671	Sequence 61671, A
60	61	12.5	325	2	US-09-134-000C-4346	Sequence 4346, Ap
61	61	12.5	389	2	US-09-270-767-46116	Sequence 46116, A
62	61	12.5	527	2	US-09-489-039A-10883	Sequence 10883, A
63	61	12.5	687	2	US-09-538-092-539	Sequence 539, App
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65	60.5	12.4	337	2	US-09-248-796A-14738	Sequence 14738, A
66	60.5	12.4	525	2	US-09-540-236-2250	Sequence 2250, Ap
67	60	12.3	139	2	US-08-545-573A-15	Sequence 15, Appl
68	60	12.3	124	2	US-09-513-999C-4802	Sequence 4802, Ap
69	60	12.3	230	2	US-09-248-796A-17807	Sequence 17807, A
70	60	12.3	251	2	US-09-248-796A-16794	Sequence 16794, A
71	60	12.3	258	2	US-09-513-999C-4800	Sequence 4800, Ap
72	60	12.3	264	2	US-09-949-016-6012	Sequence 6012, Ap
73	60	12.3	276	2	US-09-949-016-11703	Sequence 11703, A
74	60	12.3	421	2	US-09-489-039A-7512	Sequence 7512, Ap
75	60	12.3	1326	2	US-09-252-991A-17932	Sequence 17932, A

ALIGNMENTS

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Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity 86.8%; Pred. No. 1e-47;
Matches 79; Conservative 7; Mismatches 5; Indels 0; Gaps 0;

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DB      77 EHRKLLEQEMVGLFEGKDVHIEGYTPPEKQ 107


RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443


Query Match      75.6%; Score 369; DB 2; Length 93;
Best Local Similarity 75.6%; Pred. No. 8e-40;
Matches 68; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY      1 MSRTIFCTYLORDAEGODFQLYPGELGKRIYNESKDAAWAOHQOTMLINEKKLNMNNA 60
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DB      4 MSRTIFCTPLNKADGLDQLYPGELGKRIYNESKEAWAQOMAKQTMLINEKKLTMPN 63

QY      61 EHRKLLEQEMVSLFEGKDVHIEGYPTEDK 90
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DB      64 DDRKLLEQEMVRFLFEGHDVHIDGYTPPEK 93


RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355


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Best Local Similarity 52.3%; Pred. No. 1.3e-20;
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Db      33 MSRTVMCRKXHEELPGLDRPPYFGAKGEDIYNNVSRKAWDEWQKHQTMLINERRLNMMNA 92
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Db      93 EDRKFLQEMDKFL-SGEDYAKADGY 117

RESULT 4
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; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328.352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Matches 36; Conservative 15; Mismatches 37; Indels 1; Gaps 1;

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QY      61 EHRKLLQEMVSVLFEGKDVH-IEGYPT 88
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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540.236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

Query Match
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Matches 28; Conservative 13; Mismatches 40; Indels 0; Gaps 0;

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Db      25 VFCRKRYQQLPKLPNPPFPNAKGQEIQTISAKAWNAWLELQTMLINEKLSMIDPOAKK 84
QY      65 LLEQEMVSVLFEGKDVHIEGY 85
Db      85 YLNEQREKFLDNGDYEKPAY 105

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
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Title: US-09-955-502A-18

Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFEKDVHIEGYPTEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	474	97.1	91	3	US-09-955-502-14 Sequence 14, Appl
3	474	97.1	91	3	US-09-955-502-16 Sequence 16, Appl
4	474	97.1	91	3	US-09-955-502-17 Sequence 17, Appl
5	458	93.9	88	3	US-09-955-502-15 Sequence 15, Appl
6	455	93.2	91	3	US-09-955-502-11 Sequence 11, Appl
7	455	93.2	91	3	US-09-955-502-12 Sequence 12, Appl
8	455	93.2	91	3	US-09-955-502-13 Sequence 13, Appl
9	386	79.1	78	3	US-09-955-502-19 Sequence 19, Appl
10	379	77.7	90	3	US-09-955-502-20 Sequence 20, Appl
11	378	77.5	87	3	US-09-955-502-7 Sequence 7, Appl
12	375	76.8	90	3	US-09-955-502-10 Sequence 10, Appl
13	370	75.8	87	3	US-09-955-502-6 Sequence 6, Appl
14	369.5	75.7	91	3	US-09-955-502-5 Sequence 5, Appl
15	364	74.6	87	3	US-09-955-502-8 Sequence 8, Appl
16	326	66.8	88	3	US-09-955-502-9 Sequence 9, Appl
17	259	53.1	76	3	US-09-955-502-21 Sequence 21, Appl
18	242	49.6	87	3	US-09-955-502-2 Sequence 2, Appl
19	242	49.6	87	3	US-09-955-502-3 Sequence 3, Appl
20	241	49.4	86	3	US-09-955-502-4 Sequence 4, Appl
21	230	47.1	89	3	US-09-955-502-22 Sequence 22, Appl
22	221	45.3	87	3	US-09-955-502-25 Sequence 25, Appl
23	214	43.9	88	3	US-09-955-502-33 Sequence 33, Appl
24	212	43.4	90	3	US-09-955-502-23 Sequence 23, Appl
25	211	43.2	87	3	US-09-955-502-24 Sequence 24, Appl
26	202	41.4	88	3	US-09-955-502-26 Sequence 26, Appl
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30	199	40.8	87	3	US-09-955-502-30	Sequence 30, Appl
31	190	38.9	87	3	US-09-955-502-31	Sequence 31, Appl
32	188	38.5	87	3	US-09-955-502-32	Sequence 32, Appl
33	77	15.8	167	4	US-10-437-963-158697	Sequence 158697,
34	72	14.8	507	4	US-10-282-122A-68134	Sequence 68134, A
35	72	14.8	1261	4	US-10-437-963-189166	Sequence 189166,
36	71.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
37	71	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
38	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
39	70.5	14.4	184	4	US-10-393-840-118	Sequence 118, App
40	70.5	14.4	503	5	US-10-450-763-46936	Sequence 46936, A
41	69	14.1	679	5	US-10-805-684-105	Sequence 105, App
42	68.5	14.0	449	4	US-10-424-599-279212	Sequence 279212,
43	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, Ap
44	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
45	68	13.9	764	4	US-10-491-467-15	Sequence 15, Appl
46	68	13.9	1206	4	US-10-085-198-144	Sequence 144, App
47	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
48	67.5	13.8	166	5	US-10-482-706-269	Sequence 269, App
49	67.5	13.8	192	2	US-08-545-573A-9	Sequence 9, Appl
50	67	13.7	306	4	US-10-424-599-241560	Sequence 241560,
51	66.5	13.6	292	4	US-10-424-599-164588	Sequence 164588,
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54	66	13.5	321	4	US-10-282-122A-45018	Sequence 45018, A
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56	65.5	13.4	172	5	US-10-450-763-34132	Sequence 34132, A
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58	65.5	13.4	728	4	US-10-437-963-190117	Sequence 22160, A
59	65	13.3	1230	4	US-10-369-493-22160	Sequence 55, Appl
60	64.5	13.2	242	4	US-10-393-840-55	Sequence 4948, Ap
61	64.5	13.2	447	4	US-10-106-698-4948	Sequence 50306, A
62	64.5	13.2	593	5	US-10-450-763-50306	Sequence 2, Appl
63	64.5	13.2	1278	5	US-10-510-812-2	Sequence 19793, A
64	64	13.1	325	4	US-10-369-493-19793	Sequence 4885, Ap
65	64	13.1	786	5	US-10-732-923-4885	Sequence 768, App
66	63.5	13.0	102	3	US-09-864-408A-768	Sequence 346175,
67	63.5	13.0	176	4	US-10-425-115-346175	Sequence 10738, A
68	63.5	13.0	199	5	US-10-770-712-51	Sequence 6306, Ap
69	63.5	13.0	237	4	US-10-156-761-10738	Sequence 1906, Ap
70	63.5	13.0	239	6	US-11-097-143-6306	Sequence 1983, Ap
71	63.5	13.0	387	4	US-10-408-765A-1906	Sequence 9369, Ap
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75	63.5	13.0	546	3	US-09-991-496-2	

ALIGNMENTS

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; Sequence 18, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnicks, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955, 502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella typhimurium

GenCore version 5.1.7
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Perfect score: 488
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	65	13.3	593	7	US-11-194-246-317 Sequence 317, App
3	64.5	13.2	1432	6	US-10-510-386-218 Sequence 218, App
4	63	12.9	478	6	US-10-821-234-915 Sequence 915, App
5	62	12.7	251	7	US-11-054-515-1496 Sequence 1496, App
6	61	12.5	700	6	US-10-995-561-922 Sequence 922, App
7	61	12.5	700	6	US-10-995-561-924 Sequence 924, App
8	60	12.3	264	6	US-10-821-234-1555 Sequence 1555, App
9	60	12.3	834	6	US-10-453-372-658 Sequence 658, App
10	59.5	12.2	285	6	US-10-467-657-222 Sequence 222, App
11	59.5	12.2	285	6	US-10-467-657-8230 Sequence 8230, App
12	59.5	12.2	650	6	US-10-467-657-1948 Sequence 1948, App
13	59.5	12.2	1995	7	US-11-069-834-60 Sequence 60, Appl
14	59	12.1	257	7	US-11-054-515-1710 Sequence 1710, App
15	59	12.1	695	6	US-10-453-372-648 Sequence 648, App
16	59	12.1	697	6	US-10-485-517-202 Sequence 202, App
17	59	12.1	774	7	US-11-070-627-7 Sequence 7, Appli
18	59	12.1	1450	6	US-10-485-517-152 Sequence 152, App
19	58.5	12.0	177	6	US-10-467-657-1658 Sequence 1658, App
20	58.5	12.0	749	7	US-11-098-686-10505 Sequence 10505, A
21	58	11.9	336	6	US-10-453-372-640 Sequence 640, App
22	58	11.9	480	6	US-10-510-386-12 Sequence 12, Appl
23	58	11.9	775	6	US-10-453-372-656 Sequence 656, App
24	58	11.9	793	6	US-10-995-561-925 Sequence 925, App
25	58	11.9	804	6	US-10-453-372-650 Sequence 650, App

26	58	11.9	847	6	US-10-453-372-654	Sequence 654, App
27	58	11.9	857	6	US-10-453-372-652	Sequence 652, App
28	58	11.9	905	6	US-10-453-372-638	Sequence 638, App
29	58	11.9	905	6	US-10-453-372-662	Sequence 662, App
30	58	11.9	905	6	US-10-453-372-664	Sequence 664, App
31	58	11.9	963	6	US-10-995-561-923	Sequence 923, App
32	58	11.9	963	6	US-10-453-372-660	Sequence 660, App
33	58	11.9	1012	6	US-10-453-372-646	Sequence 646, App
34	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
35	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
36	57.5	11.8	782	6	US-10-793-626-2352	Sequence 2352, App
37	57	11.7	432	6	US-10-821-234-1463	Sequence 1463, App
38	57	11.7	504	7	US-11-072-512-3467	Sequence 3467, App
39	57	11.7	604	6	US-10-942-072-4	Sequence 4, Appli
40	57	11.7	1167	6	US-10-942-072-6	Sequence 6, Appli
41	56.5	11.6	647	7	US-11-000-463-722	Sequence 722, App
42	56.5	11.6	1254	6	US-10-528-031-47	Sequence 47, Appl
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49	56	11.5	3433	6	US-10-714-781A-67	Sequence 67, Appl
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51	55.5	11.4	250	7	US-11-098-686-11014	Sequence 11014, A
52	55.5	11.4	279	7	US-11-098-686-10812	Sequence 10812, A
53	55.5	11.4	577	7	US-11-072-175-187	Sequence 187, App
54	55	11.3	189	7	US-11-071-262-1	Sequence 1, Appli
55	55	11.3	692	6	US-10-793-626-198	Sequence 198, App
56	55	11.3	667	7	US-11-038-284-33	Sequence 33, Appl
57	55	11.3	873	7	US-11-038-284-35	Sequence 35, Appl
58	55	11.3	889	7	US-11-038-284-15	Sequence 15, Appl
59	55	11.3	1142	7	US-11-109-156-22	Sequence 22, Appl
60	55	11.3	2665	7	US-11-124-368A-214	Sequence 214, App
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62	54.5	11.2	317	6	US-10-523-503-74	Sequence 74, Appl
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65	54	11.1	251	7	US-11-009-658-36	Sequence 36, Appl
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67	54	11.1	3003	6	US-10-453-372-1080	Sequence 1080, App
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70	53.5	11.0	335	6	US-10-995-561-970	Sequence 970, App
71	53.5	11.0	345	6	US-10-995-561-971	Sequence 971, App
72	53.5	11.0	384	6	US-10-467-657-2024	Sequence 2024, App
73	53.5	11.0	1404	6	US-10-878-556A-169	Sequence 169, App
74	53.5	11.0	2214	7	US-11-080-991-94	Sequence 94, Appl
75	53	10.9	111	6	US-10-771-257-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIAGNI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	395	95.2	91	5	ABB78157 Amino aci
5	395	95.2	91	5	ABB78156 Amino aci
6	386	93.0	88	5	ABB78160 Amino aci
7	386	93.0	91	5	ABB78161 Amino aci
8	386	93.0	91	5	ABB78159 Amino aci
9	386	93.0	91	5	ABB78162 Amino aci
10	386	93.0	91	5	ABB78163 Amino aci
11	350	84.3	90	5	ABB78155 Amino aci
12	347	83.6	93	7	ADF05158 Bacterial
13	342	82.4	90	5	ABB78165 Amino aci
14	327	78.8	87	5	ABB78153 Amino aci
15	325	78.3	87	5	ABB78152 Amino aci
16	317	76.4	87	5	ABB78151 Amino aci
17	316	76.1	91	5	ABB78150 Amino aci
18	292	70.4	88	5	ABB78154 Amino aci
19	256	61.7	76	5	ABB78166 Amino aci
20	227	54.7	88	5	ABB78178 Amino aci
21	222	53.5	86	5	ABB78149 Amino aci
22	222	53.5	87	5	ABB78148 Amino aci
23	222	53.5	87	5	ABB78147 Amino aci
24	214.5	51.7	89	9	ABB41576 L. pneumo

25	214.5	51.7	95	9	AEB38294	Aeb38294 L. pneumo
26	211	50.8	87	5	ABB78170	Abb78170 Amino aci
27	211	50.8	122	7	ABO74609	AbO74609 Pseudomon
28	210	50.6	88	5	ABB78171	Abb78171 Amino aci
29	210	50.6	88	5	ABB78172	Abb78172 Amino aci
30	210	50.6	88	5	ABB78173	Abb78173 Amino aci
31	210	50.6	88	6	ABP77219	Abp77219 N. gonorr
32	209.5	50.5	90	5	ABB78167	Abb78167 Amino aci
33	197.5	47.6	87	5	ABB78175	Abb78175 Amino aci
34	197.5	47.6	87	5	ABB78169	Abb78169 Amino aci
35	196	47.2	87	5	ABB78176	Abb78176 Amino aci
36	195	47.0	90	5	ABB78168	Abb78168 Amino aci
37	191.5	46.1	87	5	ABB78174	Abb78174 Amino aci
38	189	45.5	87	5	ABB78177	Abb78177 Amino aci
39	187	45.1	92	6	ADA34169	Ada34169 Acinetoba
40	134	32.3	110	8	ADL05173	Adl05173 M. catarr
41	69.5	16.7	166	7	ADB80231	Adb80231 Mycobacte
42	68.5	16.5	167	2	AAR14362	Aar14362 E.histoly
43	68.5	16.5	507	6	ABU40210	Abu40210 Protein e
44	68.5	16.5	548	4	AAE04737	Aae04737 Brugia ma
45	67.5	16.3	641	6	ABM67978	Abm67978 Phototrab
46	67.5	16.3	2000	6	ABR52622	AbR52622 Protein S
47	67.5	16.3	2000	7	ADK62602	Adk62602 Disease t
48	66.5	16.0	102	5	ABP31411	Abp31411 Human ORF
49	66.5	16.0	193	8	ABM80636	Abm80636 Tumour-as
50	66.5	16.0	507	3	AAV74372	Aay74372 Neisseria
51	66.5	16.0	507	3	AAV74373	Aay74373 Neisseria
52	66.5	16.0	546	6	ABU38097	Abu38097 Protein e
53	65	15.7	679	9	ADZ85056	Adz85056 Partial F
54	64.5	15.5	506	3	AAV74371	Aay74371 Neisseria
55	64	15.4	285	4	AAB92683	Aab92683 Human PRO
56	64	15.4	414	6	ABU11747	Abu11747 Human MDD
57	64	15.4	614	9	ADX06837	Adx06837 Cyclin-de
58	64	15.4	614	9	ADY16108	Ady16108 PRO polyp
59	64	15.4	629	8	ADN46272	Adn46272 Thermococ
60	64	15.4	764	5	ABB77432	Abb77432 Human tum
61	64	15.4	764	7	ADC99062	Adc99062 Human KRP
62	64	15.4	817	4	AAH38657	Aam38657 Human pol
63	64	15.4	863	4	AAH38656	Aam38656 Human pol
64	64	15.4	1135	8	ADS10706	Adsl0706 Human the
65	64	15.4	1181	8	ADS10708	Adsl0708 Human the
66	64	15.4	1186	8	ADS10709	Adsl0709 Human the
67	64	15.4	1188	8	ADH45460	Adh45460 Human mol
68	64	15.4	1206	5	ADH48860	Adh48860 NOVG1 pro
69	64	15.4	1214	7	ADK65785	Adk65785 Angiogene
70	63.5	15.3	105	4	AAB70079	Aab70079 Human sec
71	63.5	15.3	105	5	ABG65513	Abg65513 Human alb
72	63.5	15.3	105	8	ADL78780	Adl78780 Albumin f
73	63.5	15.3	419	4	ABG20697	Abg20697 Novel hum
74	63.5	15.3	505	3	AAV53036	Aay53036 Human sec
75	63.5	15.3	505	8	ADN03608	Adn03608 Antipsori

ALIGNMENTS

RESULT 1	
ABB78164	
ID	ABB78164 standard; protein; 78 AA.
AC	ABB78164;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	hydroxyl radical; DNA damage; YggX homologue.
OS	Klebsiella pneumoniae.
XX	
PN	US2002072118-A1.
XX	

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YgX homologues
XX
SQ Sequence 78 AA;

Query Match 100.0%; Score 415; DB 5; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.5e-44;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGODFQLYPGELGKRITNEISKEAWAQWQHKTMLINEKLSMNP 60
|||
1 MSRTIFCTFLQREADGODFQLYPGELGKRITNEISKEAWAQWQHKTMLINEKLSMNP 60

Db 61 EHRKLEQEMVQFLFEGK 78
|||||
61 EHRKLEQEMVQFLFEGK 78

RESULT 2
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.

DR N-PSDB; ACH98996.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
XX The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 107 AA;

Query Match 100.0%; Score 415; DB 7; Length 107;
Best Local Similarity 100.0%; Pred. No. 5.2e-44;
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREADGODFQLYPGELGKRITNEISKEAWAQWQHKTMLINEKLSMNP 60
|||
17 MSRTIFCTFLQREADGODFQLYPGELGKRITNEISKEAWAQWQHKTMLINEKLSMNP 76

Db 61 EHRKLEQEMVQFLFEGK 78
|||||
77 EHRKLEQEMVQFLFEGK 94

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX
AC ABB78158;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YgX homologue.
XX
KW Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YgX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YgX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YgX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YgX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 8.52847 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-19
Perfect score: 415
Sequence: 1 MSRTIFCTFLQREADGQDFQ.....NPEHRKLLBQEMVQFLFEKG 78

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	395	95.2	91	2	A85954	hypothetical prote
2	395	95.2	91	2	A65082	hypothetical prote
3	395	95.2	91	2	F91108	hypothetical prote
4	386	93.0	91	2	AH0879	conserved hypothet
5	350	84.3	90	2	C82320	conserved hypothet
6	342	82.4	90	2	A10116	conserved hypothet
7	325	78.3	90	2	C64013	hypothetical prote
8	256	61.7	93	2	E84994	hypothetical prote
9	220	53.0	105	2	C82624	conserved hypothet
10	211	50.8	90	2	H83003	conserved hypothet
11	210	50.6	88	2	H81014	conserved hypothet
12	77.5	18.7	1638	2	D87749	protein unc-73b li
13	77.5	18.7	2488	2	T42739	guanine nucleotide
14	72	17.3	251	2	E90428	hypothetical prote
15	72	17.3	265	2	T46013	hypothetical prote
16	69.5	16.7	94	2	S17449	probable ligand-bi
17	69.5	16.7	166	2	F70562	hypothetical prote
18	68.5	16.5	495	2	AH0985	probable zinc-prot
19	68.5	16.5	548	2	A54510	63k antigen - nema
20	68	16.4	1111	2	T23047	hypothetical prote
21	67.5	16.3	2672	2	A48126	translation activa
22	67	16.1	544	2	T40058	probable chromatin
23	67	16.1	593	2	C64097	probable soluble l
24	66.5	16.0	507	2	C81063	fumarate hydratase
25	66.5	16.0	511	2	A99574	ABC transporter at
26	66.5	16.0	546	2	A81807	fumarate hydratase
27	65	15.7	245	2	B43814	helix-loop-helix p
28	65	15.7	278	2	A43814	helix-loop-helix p
29	65	15.7	278	2	S16678	Lyl-1 protein - mo

30	64.5	15.5	859	2	T29630	hypothetical prote
31	64	15.4	330	2	S74456	regulatory protein
32	63.5	15.3	91	2	H90521	hypothetical prote
33	63.5	15.3	197	2	T46344	hypothetical prote
34	63.5	15.3	821	2	A12417	hypothetical prote
35	63	15.2	159	2	F82675	transcription regu
36	63	15.2	401	2	A81978	hypothetical prote
37	63	15.2	438	2	T37786	probable RNA-bindi
38	63	15.2	703	2	B82148	ATP-dependent heli
39	63	15.2	1141	2	T29185	hypothetical prote
40	62.5	15.1	633	2	D75112	glu-tRNA amidotran
41	62.5	15.1	1206	2	E96507	hypothetical prote
42	62	14.9	153	2	C87301	hypothetical prote
43	62	14.9	552	2	S45886	hypothetical prote
44	62	14.9	743	2	S19437	hypothetical prote
45	62	14.9	758	2	F72363	hypothetical prote
46	61.5	14.8	485	2	A84043	chromosome replica
47	61.5	14.8	548	2	A28209	60K filarial antig
48	61.5	14.8	1011	2	T51399	DNA-directed RNA p
49	61	14.7	225	2	C88939	protein C05E4.8 li
50	61	14.7	241	2	T27636	hypothetical prote
51	61	14.7	292	2	F84463	hypothetical prote
52	61	14.7	330	1	B64561	ketol-acid reducto
53	61	14.7	507	2	A83105	probable fumaraase
54	61	14.7	561	2	T01950	hypothetical prote
55	61	14.7	859	2	S69700	hypothetical prote
56	61	14.7	946	2	T31488	hypothetical prote
57	60.5	14.6	500	2	T41385	betaine-aldehyde d
58	60.5	14.6	591	1	F0MVM4	gag polyprotein -
59	60.5	14.6	863	1	S51789	VLDL receptor prec
60	60.5	14.6	873	1	A49729	VLDL receptor prec
61	60.5	14.6	873	1	I48952	VLDL receptor prec
62	60.5	14.6	873	1	QRRBVD	VLDL receptor prec
63	60.5	14.6	1099	1	S31926	myosin IB heavy ch
64	60.5	14.6	1436	2	S67655	probable membrane
65	60.5	14.6	1935	2	A59286	myosin heavy chain
66	60	14.5	258	2	S58159	hypothetical prote
67	60	14.5	324	2	T05429	hypothetical prote
68	60	14.5	343	2	T02399	hypothetical prote
69	60	14.5	349	2	T30952	hypothetical prote
70	60	14.5	586	2	B84434	hypothetical prote
71	60	14.5	606	2	A72429	oligopeptide ABC t
72	60	14.5	728	2	A86453	CDS protein F9L11.
73	60	14.5	755	2	T46411	hypothetical prote
74	60	14.5	783	2	F84514	hypothetical prote
75	59.5	14.3	365	2	B54128	Fc-binding protein

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; P
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: yggx
C/Superfamily: fe(II) trafficking protein Yggx
Query Match 95.2%; Score 395; DB 2; Length 91;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 57.4784 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-19
Perfect score: 415
Sequence: 1 MSRTIFCTFLQREADGQDFQ.....NPEHRKLEQEMVQFLFECK 78

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	390	94.0	90	1	FETP_ECO57
2	390	94.0	90	1	FETP_ECOL6
3	390	94.0	90	1	FETP_ECOLI
4	390	94.0	90	1	FETP_SHIFL
5	381	91.8	90	1	FETP_SALCH
6	381	91.8	90	1	FETP_SALPA
7	381	91.8	90	1	FETP_SALTI
8	381	91.8	90	1	FETP_SALTY
9	362	87.2	90	1	FETP_ERWCT
10	350	84.3	90	1	FETP_VIBCH
11	350	84.3	90	1	FETP_YERPS
12	348	84.1	90	1	FETP_PHOLL
13	348	83.9	90	1	FETP_VIBVU
14	348	83.9	90	1	FETP_VIBVY
15	345	83.1	90	1	FETP_VIBPA
16	342	82.4	90	1	FETP_YERPE
17	337	81.2	90	1	FETP_VIBFI
18	327	78.8	94	1	FETP_HAEDU
19	326	78.6	91	1	FETP_MANSN
20	325	78.3	90	1	FETP_HAEIN
21	325	78.3	90	1	FETP_PHOPR
22	325	78.3	90	2	Q4QMD9_HAEI8
23	317	76.4	90	1	FETP_PASMU
24	304	73.3	90	1	FETP_IDILO
25	292	70.4	92	1	FETP_SHEON
26	256	61.7	77	1	FETP_BUCAL
27	240	57.8	78	1	FETP_BUCAP
28	232	55.9	91	1	FETP_XANAC
29	229	55.2	92	1	FETP_XANOR
30	227	54.7	90	1	FETP_COXBU
31	223	53.7	92	1	FETP_XANCP

32	223	53.7	92	2	Q4UW14_XANCP	Q4UW14 xanthomonas
33	222	53.5	90	1	FETP_BORBR	Q7wh06 bordetella
34	222	53.5	90	1	FETP_BORPA	Q7w9q2 bordetella
35	222	53.5	90	1	FETP_BORPE	Q7wvc4 bordetella
36	221	53.3	78	1	FETP_WIGBR	Q8d3c5 wigleswort
37	220	53.0	90	1	FETP_XYLFA	Q9pc73 xyella fas
38	217	52.3	90	1	FETP_XYLFT	Q87d06 xyella fas
39	214.5	51.7	89	1	FETP_LEGPA	Q5x3x9 legioneella
40	214.5	51.7	89	1	FETP_LEGPH	Q5zu80 legioneella
41	214.5	51.7	89	1	FETP_LEGPL	Q5wvc4 legioneella
42	211	50.8	90	1	FETP_PSEAB	Q9hu36 pseudomonas
43	210	50.6	88	1	FETP_NEIGI	Q5f553 neisseria g
44	210	50.6	88	1	FETP_NEIMA	P67615 neisseria m
45	210	50.6	88	1	FETP_NEIMB	P67616 neisseria m
46	205	49.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
47	204	49.2	90	2	Q4J228_AZOVI	Q4j228 azotobacter
48	201	48.4	87	1	FETP_FRATT	Q5nhj8 francisella
49	200	48.2	79	1	FETP_CANBF	Q7vrg9 candidatus
50	198	47.7	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
51	197.5	47.6	90	1	FETP_PSEBP	Q88r49 pseudomonas
52	197.5	47.6	91	1	FETP_BURMA	Q62iu9 burkholderi
53	197.5	47.6	91	1	FETP_BURPS	Q63sj4 burkholderi
54	197	47.5	90	1	FETP_CHRVO	Q7nsr4 chromobacte
55	195.5	47.1	90	1	FETP_NITEU	Q82xf2 nitrosomona
56	195	47.0	90	1	FETP_PSESM	Q87uf5 pseudomonas
57	195	47.0	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
58	189	45.5	90	1	FETP_METCA	Q60aj7 methylcoccc
59	188.5	45.4	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
60	188.5	45.4	90	2	QAKJT2_PSEFP5	Q4kjt2 pseudomonas
61	188.5	45.4	91	1	FETP_RALSO	Q8y010 ralstonia s
62	184	44.3	90	1	FETP_AC1AD	Q6fb3 acinetobact
63	156	37.6	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
64	140	33.7	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	88	21.2	482	2	Q5NUTY1_9BURK	Q5nuy1 ralstonia m
66	81.5	19.6	514	2	Q6A1Z9_DESPS	Q6aiz9 desulfotale
67	77.5	18.7	1638	2	Q7KPP4_CABEL	Q7kpp4 caenothabdi
68	77.5	18.7	2140	2	Q6BEW2_CABEL	Q6bew2 caenothabdi
69	77.5	18.7	2488	2	Q61528_CABEL	Q61528 caenothabdi
70	75.5	18.2	486	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
71	72.5	17.5	209	2	Q61A16_CAEBR	Q61a16 caenothabdi
72	72.5	17.5	508	2	Q7NSF0_CHRVO	Q7nsf0 chromobacte
73	72	17.3	251	2	Q97VQ8_SULSO	Q97vq8 sulfobus
74	72	17.3	265	2	Q9M2Q7_ARATH	Q9m2q7 arabidopsis
75	71.5	17.2	345	2	Q55821_9PLAV	Q55821 rocio virus

ALIGNMENTS

RESULT 1
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ID FETP_ECO57 STANDARD; PRT; 90 AA.
AC P0A8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=24307, ECs3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck B.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


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RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
  Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
  Rida T., Takami H., Honda T., Sasaki C., Ogasawara N., Yasunaga T.,
  Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
  O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC
CC EMBL; AE005174; AAG58093.1; -; Genomic DNA.
CC EMBL; BA000007; BAB37261.1; -; Genomic DNA.
CC PIR; A85954; A85954.
CC PIR; F91108; F91108.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe traffic_YggX; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC INIT MET 0 By similarity.
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match 94.0%; Score 390; DB 1; Length 90;
Best Local Similarity 94.8%; Pred. No. 2.8e-35;
Matches 73; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 SRTTCTFLQREAGDGFQLYPGBLGKRIYNEISKEAWAQWQHKTMLINEKLSMNP 60
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QY 62 HRKLEQEMVQFLFEKG 78
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RESULT 2
FETP_ECOL6 STANDARD; PRT; 90 AA.
AC Q8FEI9;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=c3550;
OS Escherichia coli O6.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=217992;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O6:H1 / CFT073 / ATCC 700928 / UPEC;
RX MEDLINE=22388234; PubMed=12471157; DOI=10.1073/pnas.252529799;
RA Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
  Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
  Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
  Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT "Extensive mosaic structure revealed by the complete genome sequence
  of uropathogenic Escherichia coli.";
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RL Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC
CC EMBL; AB016766; AAN81998.1; -; Genomic DNA.
CC SMR; Q8FEI9; 1-90.
CC HAMAP; MF_00686; -; 1.
CC InterPro; IPR007457; YggX.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe traffic_YggX; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC INIT MET 0 By similarity.
CC SEQUENCE 90 AA; 10805 MW; D7C66C2A35E63692 CRC64;

Query Match 94.0%; Score 390; DB 1; Length 90;
Best Local Similarity 94.8%; Pred. No. 2.8e-35;
Matches 73; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 SRTTCTFLQREAGDGFQLYPGBLGKRIYNEISKEAWAQWQHKTMLINEKLSMNP 60
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QY 62 HRKLEQEMVQFLFEKG 78
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Db 61 HRKLEQEMVNFLEKG 77

RESULT 3
FETP_ECOL1 STANDARD; PRT; 90 AA.
AC P0A8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
  Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
  Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
  Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
  in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:15:51 ; Search time 15.8132 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-19
Perfect score: 415
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	415	100.0	107	2	US-09-489-039A-11962 Sequence 11962, A
2	347	83.6	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	211	50.8	122	2	US-09-252-991A-23355 Sequence 23355, A
4	187	45.1	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	134	32.3	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	68.5	16.5	548	2	US-09-167-299-3 Sequence 3, Appli
7		64	15.4	2	US-10-164-595-24 Sequence 24, Appl
8		63	15.2	2	US-09-134-000C-4346 Sequence 4346, Ap
9		62	14.9	2	US-09-328-352-6400 Sequence 6400, Ap
10		62	14.9	2	US-09-902-540-11253 Sequence 11253, A
11		61	14.7	233	1 US-08-557-309B-40 Sequence 40, Appl
12		61	14.7	233	2 US-08-834-306-40 Sequence 40, Appl
13		61	14.7	233	2 US-08-993-674A-40 Sequence 40, Appl
14		61	14.7	233	2 US-09-256-976-40 Sequence 40, Appl
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21		61	14.7	546	2 US-09-639-206A-2 Sequence 2, Appli
22		61	14.7	546	2 US-09-874-923-2 Sequence 2, Appli
23		61	14.7	546	2 US-08-798-841-2 Sequence 2, Appli
24		61	14.7	859	2 US-09-538-092-206 Sequence 206, App
25		61	14.7	982	2 US-09-551-974A-95 Sequence 95, Appl
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28	61	14.7	982	2	US-09-874-923-95	Sequence 95, Appl
29	61	14.7	1427	2	US-09-551-974A-97	Sequence 97, Appl
30	61	14.7	1427	2	US-09-565-501A-97	Sequence 97, Appl
31	61	14.7	1427	2	US-09-639-206A-97	Sequence 97, Appl
32	61	14.7	1427	2	US-09-874-923-97	Sequence 97, Appl
33	61	14.7	1641	2	US-09-551-974A-96	Sequence 96, Appl
34	61	14.7	1641	2	US-09-565-501A-96	Sequence 96, Appl
35	61	14.7	1641	2	US-09-639-206A-96	Sequence 96, Appl
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42	60.5	14.6	846	1	US-08-451-883-4	Sequence 4, Appli
43	60.5	14.6	873	1	US-08-393-734-2	Sequence 2, Appli
44	60.5	14.6	873	2	US-08-894-489-2	Sequence 2, Appli
45	60.5	14.6	873	2	US-10-167-264-2	Sequence 2, Appli
46	60.5	14.6	904	2	US-09-949-016-9528	Sequence 9528, Ap
47	59	14.2	193	1	US-08-820-170A-4	Sequence 4, Appli
48	59	14.2	193	2	US-09-055-699-4	Sequence 4, Appli
49	59	14.2	193	2	US-09-273-565-4	Sequence 4, Appli
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53	59	14.2	258	2	US-09-949-016-7845	Sequence 7845, Ap
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56	59	14.2	565	2	US-09-800-960-2	Sequence 2, Appli
57	59	14.2	565	2	US-10-096-960-2	Sequence 2, Appli
58	59	14.2	637	2	US-09-540-236-2167	Sequence 2167, Ap
59	59	14.2	798	2	US-09-861-451A-12	Sequence 12, Appl
60	59	14.2	1003	2	US-09-991-181-33	Sequence 33, Appl
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63	59	14.2	1003	2	US-09-992-598-33	Sequence 33, Appl
64	58.5	14.1	57	2	US-09-562-737-124	Sequence 124, App
65	58.5	14.1	116	2	US-09-562-737-125	Sequence 125, App
66	58.5	14.1	401	2	US-09-328-352-4963	Sequence 4963, Ap
67	58.5	14.1	451	2	US-09-543-681A-7401	Sequence 7401, Ap
68	58.5	14.1	508	2	US-10-104-047-2186	Sequence 2186, Ap
69	58.5	14.1	896	2	US-09-949-016-6155	Sequence 6155, Ap
70	58.5	14.1	926	2	US-09-949-016-10683	Sequence 10683, A
71	58.5	14.1	1135	2	US-09-949-016-10393	Sequence 10393, A
72	58	14.0	292	2	US-09-328-352-5836	Sequence 5836, Ap
73	58	14.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 49.3941 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-19
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	395	95.2	91	3	US-09-955-502-11 Sequence 11, Appl
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4	395	95.2	91	3	US-09-955-502-13 Sequence 13, Appl
5	386	93.0	88	3	US-09-955-502-15 Sequence 15, Appl
6	386	93.0	91	3	US-09-955-502-14 Sequence 14, Appl
7	386	93.0	91	3	US-09-955-502-16 Sequence 16, Appl
8	386	93.0	91	3	US-09-955-502-17 Sequence 17, Appl
9	386	93.0	91	3	US-09-955-502-18 Sequence 18, Appl
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11	342	82.4	90	3	US-09-955-502-20 Sequence 20, Appl
12	327	78.8	87	3	US-09-955-502-8 Sequence 8, Appl
13	325	78.3	87	3	US-09-955-502-7 Sequence 7, Appl
14	317	76.4	87	3	US-09-955-502-6 Sequence 6, Appl
15	316	76.1	91	3	US-09-955-502-5 Sequence 5, Appl
16	292	70.4	88	3	US-09-955-502-9 Sequence 9, Appl
17	256	61.7	76	3	US-09-955-502-21 Sequence 21, Appl
18	227	54.7	88	3	US-09-955-502-33 Sequence 33, Appl
19	222	53.5	86	3	US-09-955-502-4 Sequence 4, Appl
20	222	53.5	87	3	US-09-955-502-2 Sequence 2, Appl
21	222	53.5	87	3	US-09-955-502-3 Sequence 3, Appl
22	220	53.0	89	3	US-09-955-502-22 Sequence 22, Appl
23	211	50.8	87	3	US-09-955-502-25 Sequence 25, Appl
24	210	50.6	88	3	US-09-955-502-26 Sequence 26, Appl
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26	210	50.6	88	3	US-09-955-502-28 Sequence 28, Appl
27	197.5	47.6	87	3	US-09-955-502-24 Sequence 24, Appl

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29	197.5	47.6	87	3	US-09-955-502-30	Sequence 30, Appl
30	196	47.2	87	3	US-09-955-502-31	Sequence 31, Appl
31	195	47.0	90	3	US-09-955-502-23	Sequence 23, Appl
32	189	45.5	87	3	US-09-955-502-32	Sequence 32, Appl
33	69.5	16.7	166	5	US-10-482-706-269	Sequence 269, App
34	68.5	16.5	449	4	US-10-424-599-279212	Sequence 279212,
35	68.5	16.5	507	4	US-10-282-122A-68134	Sequence 68134, A
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37	66.5	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
38	65	15.7	679	5	US-10-805-684-105	Sequence 105, App
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44	63.5	15.3	105	3	US-09-768-826-47	Sequence 47, Appl
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47	63.5	15.3	419	5	US-10-450-763-51056	Sequence 51056, A
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51	63.5	15.3	505	5	US-10-993-986-20	Sequence 20, Appl
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53	63	15.2	315	5	US-10-958-216-464	Sequence 464, App
54	63	15.2	315	5	US-10-958-216-466	Sequence 466, App
55	63	15.2	856	4	US-10-408-765A-2006	Sequence 2006, Ap
56	62.5	15.1	95	4	US-10-416-314-27	Sequence 27, Appl
57	62	14.9	258	4	US-10-468-091-1	Sequence 1, Appl
58	62	14.9	321	4	US-10-282-122A-45018	Sequence 45018, A
59	62	14.9	1293	4	US-10-697-036-41	Sequence 41, Appl
60	61.5	14.8	204	5	US-10-756-149-5207	Sequence 5207, Ap
61	61.5	14.8	242	4	US-10-393-840-55	Sequence 55, Appl
62	61.5	14.8	511	4	US-10-282-122A-50464	Sequence 50464, A
63	61.5	14.8	1242	3	US-09-791-254-2	Sequence 2, Appl
64	61	14.7	172	5	US-10-450-763-34132	Sequence 34132, A
65	61	14.7	176	4	US-10-425-115-346175	Sequence 346175,
66	61	14.7	330	3	US-09-815-242-11319	Sequence 11319, A
67	61	14.7	330	4	US-10-282-122A-58687	Sequence 58687, A
68	61	14.7	331	5	US-10-739-930-8330	Sequence 8330, Ap
69	61	14.7	487	4	US-10-425-115-358829	Sequence 358829,
70	61	14.7	545	5	US-10-732-923-9369	Sequence 9369, Ap
71	61	14.7	546	3	US-09-874-923-2	Sequence 2, Appl
72	61	14.7	546	3	US-09-991-496-2	Sequence 2, Appl
73	61	14.7	546	4	US-10-098-732A-71	Sequence 71, Appl
74	61	14.7	714	5	US-10-732-923-23069	Sequence 23069, A
75	61	14.7	926	3	US-09-991-496-128	Sequence 128, App

ALIGNMENTS

RESULT 1

US-09-955-502-19

Sequence 19, Application US/099555502

Patent No. US20020072118A1

GENERAL INFORMATION:

APPLICANT: Downs, Diana M.

APPLICANT: Gralnick, Jeff A.

TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

FILE REFERENCE: 960296.97559

CURRENT APPLICATION NUMBER: US/09/955,502

PRIOR FILING DATE: 2001-09-18

PRIOR APPLICATION NUMBER: 60/234,588

NUMBER OF SEQ ID NOS: 33

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 19

LENGTH: 78

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 4.35308 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502A-19
Perfect score: 415
Sequence: 1 MSRTIPCTPLQREADGQDFQ.....NPBHRKLEQEMVQFLPEGK 78

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*
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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	210	50.6	88	6	US-10-467-657-968 Sequence 968, App
2	67	16.1	593	7	US-11-194-246-317 Sequence 317, App
3	60.5	14.6	752	7	US-11-072-512-3003 Sequence 3003, App
4	59.5	14.3	834	6	US-10-453-372-658 Sequence 658, App
5	59.5	14.3	1088	7	US-11-098-686-10718 Sequence 10718, A
6	59	14.2	251	7	US-11-054-515-1496 Sequence 1496, App
7	58.5	14.1	508	7	US-11-072-512-2186 Sequence 2186, App
8	58.5	14.1	1432	6	US-10-510-386-218 Sequence 218, App
9	57.5	13.9	336	6	US-10-453-372-640 Sequence 640, App
10	57.5	13.9	695	6	US-10-453-372-648 Sequence 648, App
11	57.5	13.9	700	6	US-10-995-561-922 Sequence 922, App
12	57.5	13.9	700	6	US-10-995-561-924 Sequence 924, App
13	57.5	13.9	775	6	US-10-453-372-656 Sequence 656, App
14	57.5	13.9	793	6	US-10-995-561-925 Sequence 925, App
15	57.5	13.9	804	6	US-10-453-372-650 Sequence 650, App
16	57.5	13.9	847	6	US-10-453-372-654 Sequence 654, App
17	57.5	13.9	857	6	US-10-453-372-652 Sequence 652, App
18	57.5	13.9	905	6	US-10-453-372-638 Sequence 638, App
19	57.5	13.9	905	6	US-10-453-372-662 Sequence 662, App
20	57.5	13.9	905	6	US-10-453-372-664 Sequence 664, App
21	57.5	13.9	963	6	US-10-995-561-923 Sequence 923, App
22	57.5	13.9	963	6	US-10-453-372-660 Sequence 660, App
23	57.5	13.9	1012	6	US-10-453-372-646 Sequence 646, App
24	57	13.7	235	7	US-11-098-686-11270 Sequence 11270, A
25	57	13.7	395	7	US-11-009-658-46 Sequence 46, Appl

26	56.5	13.6	397	7	US-11-022-562-223	Sequence 223, App
27	56	13.5	257	7	US-11-054-515-1710	Sequence 1710, App
28	56	13.5	341	7	US-11-055-822-1054	Sequence 1054, App
29	55.5	13.4	1995	7	US-11-069-834-60	Sequence 60, Appl
30	55	13.3	264	6	US-10-821-234-1555	Sequence 1555, App
31	55	13.3	404	7	US-11-009-658-48	Sequence 48, Appl
32	55	13.3	893	7	US-11-072-512-3504	Sequence 3504, App
33	54.5	13.1	524	7	US-11-118-809-4	Sequence 4, Appl1
34	54	13.0	103	6	US-10-467-657-4178	Sequence 4178, App
35	54	13.0	187	6	US-10-793-626-2226	Sequence 2226, App
36	54	13.0	480	6	US-10-510-386-12	Sequence 12, Appl
37	53.5	12.9	166	7	US-11-175-690-104	Sequence 104, App
38	53.5	12.9	774	7	US-11-070-627-7	Sequence 7, Appl1
39	53.5	12.9	1299	6	US-10-821-234-1145	Sequence 1145, App
40	53.5	12.9	1404	6	US-10-878-556A-169	Sequence 169, App
41	53	12.8	189	7	US-11-071-262-1	Sequence 1, Appl1
42	52.5	12.7	415	7	US-11-072-512-2624	Sequence 2624, App
43	52.5	12.7	504	7	US-11-072-512-3467	Sequence 3467, App
44	52.5	12.7	1098	7	US-11-072-512-3280	Sequence 3280, App
45	52	12.5	898	7	US-11-099-691-7	Sequence 7, Appl1
46	52	12.5	898	7	US-11-124-367A-330	Sequence 330, App
47	52	12.5	898	7	US-11-124-367A-333	Sequence 333, App
48	51.5	12.4	285	6	US-10-467-657-222	Sequence 222, App
49	51.5	12.4	285	6	US-10-467-657-8230	Sequence 8230, App
50	51.5	12.4	336	7	US-11-165-226-125	Sequence 125, App
51	51.5	12.4	571	7	US-11-072-512-3814	Sequence 3814, App
52	51.5	12.4	635	7	US-11-098-686-10433	Sequence 10433, A
53	51.5	12.4	654	7	US-11-110-082-24	Sequence 24, Appl1
54	51	12.3	117	7	US-11-004-590-178	Sequence 178, App
55	51	12.3	117	7	US-11-004-590-179	Sequence 179, App
56	51	12.3	117	7	US-11-004-590-188	Sequence 188, App
57	51	12.3	117	7	US-11-004-590-210	Sequence 210, App
58	51	12.3	166	7	US-11-132-722-45	Sequence 45, Appl
59	51	12.3	166	7	US-11-176-830-186	Sequence 186, App
60	51	12.3	166	7	US-11-172-409-2	Sequence 2, Appl1
61	51	12.3	189	7	US-11-147-492-6	Sequence 6, Appl1
62	51	12.3	189	7	US-11-147-492-22	Sequence 22, Appl
63	51	12.3	194	7	US-11-072-512-2906	Sequence 2906, App
64	51	12.3	251	7	US-11-009-658-36	Sequence 36, Appl
65	51	12.3	311	7	US-11-156-084-307	Sequence 307, App
66	51	12.3	317	7	US-11-156-084-295	Sequence 295, App
67	51	12.3	332	6	US-10-793-626-550	Sequence 550, App
68	51	12.3	456	7	US-11-069-642-8	Sequence 8, Appl1
69	51	12.3	488	7	US-11-169-041-197	Sequence 197, App
70	51	12.3	600	7	US-11-072-512-3845	Sequence 3845, App
71	51	12.3	618	7	US-11-110-082-25	Sequence 25, Appl
72	51	12.3	1034	7	US-11-072-512-2343	Sequence 2343, App
73	51	12.3	1501	6	US-10-793-626-2850	Sequence 2850, App
74	51	12.3	2665	7	US-11-124-368A-214	Sequence 214, App
75	51	12.3	2668	7	US-11-124-368A-215	Sequence 215, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 73.9066 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-20

Perfect score: 473
Sequence: 1 MSRTIFCTFLKDAERQDPQ.....VNFLFEGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
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4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	473	100.0	90	5	ABB78165
2	400	84.6	107	7	ABO65445
3	396	83.7	91	5	ABB78158
4	396	83.7	91	5	ABB78157
5	396	83.7	91	5	ABB78156
6	393	83.1	91	5	ABB78161
7	393	83.1	91	5	ABB78159
8	393	83.1	91	5	ABB78162
9	389	82.2	88	5	ABB78160
10	389	82.2	93	7	ADF05158
11	379	80.1	91	5	ABB78163
12	366	77.4	90	5	ABB78155
13	363	76.7	87	5	ABB78152
14	357	75.5	91	5	ABB78150
15	351	74.2	87	5	ABB78153
16	346	73.2	87	5	ABB78151
17	342	72.3	78	5	ABB78164
18	308	65.1	88	5	ABB78154
19	256	54.1	76	5	ABB78166
20	233	49.3	88	5	ABB78178
21	226	47.8	87	5	ABB78148
22	226	47.8	87	5	ABB78147
23	221	46.7	122	7	ABO74609
24	218.5	46.2	89	9	ABB41576

25	218.5	46.2	95	9	ABB38294	Aeb38294 L. pneumo
26	212	44.8	86	5	ABB78149	Abb78149 Amino aci
27	210	44.4	87	5	ABB78170	Abb78170 Amino aci
28	206	43.6	90	5	ABB78168	Abb78168 Amino aci
29	199	42.1	87	5	ABB78175	Abb78175 Amino aci
30	198	41.9	88	5	ABB78171	Abb78171 Amino aci
31	198	41.9	88	5	ABB78172	Abb78172 Amino aci
32	198	41.9	88	5	ABB78173	Abb78173 Amino aci
33	198	41.9	88	5	ABB77219	Abp77219 N. gonorr
34	194.5	41.1	90	5	ABB78167	Abb78167 Amino aci
35	193	40.8	87	5	ABB78174	Abb78174 Amino aci
36	188	39.7	87	5	ABB78169	Abb78169 Amino aci
37	186	39.3	87	5	ABB78177	Abb78177 Amino aci
38	186	39.3	87	5	ABB78176	Abb78176 Amino aci
39	176.5	37.3	92	6	ADA34169	Ada34169 Acinetoba
40	143	30.2	110	8	ADL05173	Adl05173 M. catarr
41	81	17.1	102	5	ABP31411	Abp31411 Human ORF
42	81	17.1	2000	6	ABR52622	AbR52622 Protein s
43	81	17.1	2000	7	ADK62602	Adk62602 Disease t
44	74	15.6	397	4	ABB11207	Abb11207 Human PI-
45	74	15.6	403	6	ABM71645	Abm71645 Staphyloc
46	74	15.6	506	4	AAU79180	Aau79180 Human par
47	74	15.6	576	4	ABG19914	Abg19914 Novel hum
48	74	15.6	589	5	AAAB47871	Aab47871 ISIGP-1.
49	74	15.6	1116	4	AAAG67293	Aag67293 Amino aci
50	74	15.6	1116	4	AAU79181	Aau79181 Human pro
51	74	15.6	1116	8	ADM87230	Adm87230 Human pro
52	73.5	15.5	641	6	ABM67978	Abm67978 Photorhab
53	73	15.4	397	8	ADM87687	Adm87687 Human EST
54	70.5	14.9	635	4	ABB69129	Abb69129 Drosophil
55	70	14.8	184	3	AAAB16290	Aab16290 Pinus rad
56	70	14.8	869	8	ADM64441	Adm64441 Thermosta
57	69.5	14.7	867	6	ABU41082	Abu41082 Protein e
58	69.5	14.7	870	7	ADF04483	Adf04483 Bacterial
59	69.5	14.7	1589	4	ABG08898	Abg08898 Novel hum
60	69.5	14.7	1589	4	ABG22603	Abg22603 Novel hum
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64	69	14.6	209	7	ABO72159	AbO72159 Pseudomon
65	68	14.4	256	6	ABU25179	Abu25179 Protein e
66	68	14.4	344	7	ABO23534	AbO23534 Borrelia
67	68	14.4	506	3	AAAY74371	Aay74371 Neisseria
68	67.5	14.3	617	5	AAAM49439	Aam49439 Pyrococcu
69	67.5	14.3	701	7	ABO74542	AbO74542 Pseudomon
70	67	14.2	415	2	AAW22982	Aaw22982 Canine he
71	67	14.2	415	2	AAW72649	Aaw72649 Canine he
72	67	14.2	415	4	AAAB51306	Aab51306 Canine he
73	67	14.2	415	7	AAE39123	Aae39123 CHV PCgG
74	66.5	14.1	184	4	ABG04791	Abg04791 Novel hum
75	66.5	14.1	758	8	ADS21214	Ads21214 Bacterial

ALIGNMENTS

RESULT 1
ID ABB78165 standard; protein; 90 AA.
AC ABB78165;
DT 05-NOV-2002 (first entry)
DE Amino acid sequence of a YggX homologue.
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;

Query Match 100.0%; Score 473; DB 5; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.3e-48;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60
|||
Db 1 MSRTTCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60

QY 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
|||
Db 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90

RESULT 2
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.

DR N-PSDB; ACH98996.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
CC The invention describes a new isolated nucleic acid encoding a Klebsiella
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against Klebsiella pneumoniae. This is the amino acid sequence of a
CC Klebsiella pneumoniae polypeptide of the invention
XX
SQ Sequence 107 AA;

Query Match 84.6%; Score 400; DB 7; Length 107;
Best Local Similarity 83.3%; Pred. No. 1.5e-39;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTTCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNNI 60
|||
Db 17 MSRTTCTFLQREADGQDFQLYPGEIGKRIYNEISKEAWAQMOKQTMLINEKLSMNP 76

QY 61 EDRKLEQEMVNFLEGGQDVHIAGYTPPSK 90
|||
Db 77 EHRKLEQEMVQFLFEGKDVHIEGYTPPEK 106

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX
AC ABB78158;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.84055 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-20
Perfect score: 473
Sequence: 1 MSRTIFCTFLKKDAERQDFQ.....VNPLFEGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	473	100.0	90	2 A10116	conserved hypothet
2	396	83.7	91	2 A85954	hypothetical prote
3	396	83.7	91	2 A65082	hypothetical prote
4	396	83.7	91	2 F91108	hypothetical prote
5	393	83.1	91	2 AH0879	conserved hypothet
6	374	79.1	90	2 C64013	hypothetical prote
7	366	77.4	90	2 C82320	conserved hypothet
8	256	54.1	93	2 B84994	hypothetical prote
9	221	46.7	90	2 H83003	conserved hypothet
10	203	42.9	105	2 C82624	conserved hypothet
11	198	41.9	88	2 H81014	conserved hypothet
12	81	17.1	2672	2 A48126	translation activa
13	76.5	16.2	511	2 A99574	ABC transporter at
14	74	15.6	403	2 B89808	hypothetical prote
15	71.5	15.1	1008	2 H72310	conserved hypothet
16	70	14.8	265	2 T46013	hypothetical prote
17	70	14.8	1119	2 T18491	hypothetical prote
18	69.5	14.7	996	2 A71080	hypothetical prote
19	69	14.6	1386	1 RMTVC2	DNA-directed RNA p
20	68.5	14.5	165	2 A81382	shikimate kinase (
21	68	14.4	344	2 D70126	hypothetical prote
22	68	14.4	583	2 T48365	hypothetical prote
23	68	14.4	820	2 G88996	protein C17B7.5 [i
24	67.5	14.3	160	2 E70416	hypothetical prote
25	67.5	14.3	336	2 C64468	hypothetical prote
26	67.5	14.3	617	2 B71071	probable prollyl en
27	67.5	14.3	629	2 B83107	chemotactic transd
28	67	14.2	394	2 B70206	hypothetical prote
29	66.5	14.1	139	2 B97709	hypothetical prote

30	66.5	14.1	420	2 A25876	vitellogenin III p
31	66.5	14.1	648	2 A71647	glycine-tRNA ligas
32	66	14.0	705	2 T47949	hypothetical prote
33	66	14.0	799	2 T02656	probable salt-indu
34	65.5	13.8	91	2 H90521	hypothetical prote
35	65.5	13.8	688	2 S57131	hypothetical prote
36	65	13.7	118	2 G64302	hypothetical prote
37	65	13.7	411	2 A48946	aspartate kinase (
38	65	13.7	738	2 B69863	two-component sens
39	65	13.7	2101	2 A42184	nuclear mitotic ap
40	64.5	13.6	245	2 AG2300	hypothetical prote
41	64	13.5	158	2 A59102	hypothetical prote
42	64	13.5	235	2 AD1735	hypothetical prote
43	64	13.5	346	2 F97871	uroporphyrinogen d
44	64	13.5	1611	1 WMTMPV	183k protein - pep
45	63.5	13.4	548	2 A54510	63k antigen - nema
46	63.5	13.4	548	2 A28209	60k filarial antig
47	63.5	13.4	715	2 D84480	Mutator-like trans
48	63.5	13.4	884	1 RNBPT3	DNA-directed RNA p
49	63.5	13.4	1010	2 F75134	hypothetical prote
50	63.5	13.4	1119	2 T15842	hypothetical prote
51	63	13.3	254	2 A64437	hypothetical prote
52	63	13.3	264	2 G89808	hypothetical prote
53	63	13.3	269	2 AE1286	hypothetical prote
54	63	13.3	507	2 C81063	hypothetical prote
55	63	13.3	546	2 A81807	fumarate hydratase
56	63	13.3	821	1 A39616	fumarate hydratase
57	63	13.3	974	2 A40580	protein kinase RAD
58	63	13.3	1027	2 T27970	iodestar maternal-
59	62.5	13.2	173	2 H86869	hypothetical prote
60	62.5	13.2	259	2 D63998	hypothetical prote
61	62.5	13.2	477	2 B61378	leukotoxin secreti
62	62.5	13.2	674	2 D97864	glycine-tRNA ligas
63	62.5	13.2	869	2 T22422	hypothetical prote
64	62.5	13.2	1939	2 T18372	repeat organellar
65	62	13.1	143	2 B83688	hypothetical prote
66	62	13.1	212	2 B71853	probable biotin ac
67	62	13.1	224	2 C64240	mobilization prote
68	62	13.1	353	1 FOMVGR	gag polypeptide -
69	62	13.1	375	2 A36898	maspin - human
70	62	13.1	498	2 C90413	dihydropterocyste
71	62	13.1	593	2 C64097	probable soluble l
72	62	13.1	1030	2 T37868	probable helicase
73	61.5	13.0	222	2 S62001	ME15 protein - yea
74	61.5	13.0	287	2 F82265	conserved hypothet
75	61.5	13.0	339	2 A90395	conserved hypothet

ALIGNMENTS

RESULT 1
A10116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: A10116
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: A10116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UP100000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;
C/Genetics:
A/Gene: YPO0953
C/Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 473; DB 2; length 90;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 66.3212 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-20
Perfect score: 473
Sequence: 1 MSRTIFCTPLKKDAERQDFQ.....VNFLFEGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	473	100.0	90	1	FETP_YERPE	Q8zhe7 yersinia pe
2	466	98.5	90	1	FETP_YERPS	Q66m3 yersinia ps
3	412	87.1	90	1	FETP_ERWCT	Q6d8j9 yersinia car
4	391	82.7	90	1	FETP_ECO57	P0a8p4 escherichia
5	391	82.7	90	1	FETP_ECOLI	P0a8p3 escherichia
6	391	82.7	90	1	FETP_SHIFL	P0a8p5 shigella fl
7	388	82.0	90	1	FETP_SALCH	Q57k04 salmonella
8	388	82.0	90	1	FETP_SALPA	O5pmu1 salmonella
9	388	82.0	90	1	FETP_SALTI	P67618 salmonella
10	388	82.0	90	1	FETP_SALTY	P67617 salmonella
11	387	81.8	90	1	FETP_ECOL6	Q8fe19 escherichia
12	379	80.1	90	1	FETP_PHOL6	Q7n711 photorhabdu
13	377	79.7	90	1	FETP_PHOPR	Q6lmk7 photobacter
14	374	79.1	90	1	FETP_HA8IN	P44048 haemophilus
15	374	79.1	90	2	Q4QMD9_HAB18	Q4qmd9 haemophilus
16	366	77.4	90	1	FETP_VIBCH	Q9kur4 vibrio chol
17	362	76.5	90	1	FETP_VIBPA	Q871i5 vibrio para
18	357	75.5	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
19	357	75.5	90	1	FETP_VIBVY	Q7mh14 vibrio vuln
20	355	75.1	90	1	FETP_PASMU	Q9c1b9 pasteurella
21	354	74.8	91	1	FETP_MANSU	Q65vt7 mannheimia
22	351	74.2	94	1	FETP_HA8DU	Q7vkb6 haemophilus
23	330	69.8	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
24	308	65.1	92	1	FETP_SHEON	Q8ebx6 shewanella
25	305	64.5	90	1	FETP_IDILO	Q5qy58 idiomarina
26	256	54.1	77	1	FETP_BUCAI	P57618 buchnera ap
27	240	50.7	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
28	237	50.1	90	1	FETP_BORBR	Q7wh06 bordetella
29	237	50.1	90	1	FETP_BORPA	Q7w9q2 bordetella
30	237	50.1	90	1	FETP_BORPB	Q7wvc4 bordetella
31	234	49.5	78	1	FETP_BUCAP	Q8k925 buchnera ap

32	233	49.3	90	1	FETP_COXBU	Q83d06 coxiella bu
33	228	48.2	90	1	FETP_NITEU	Q82xf2 nitrosomona
34	222.5	47.0	89	1	FETP_LEGPL	Q5wvc4 legionella
35	221	46.7	90	1	FETP_PSEAB	Q9hu36 pseudomonas
36	220	46.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
37	218.5	46.2	89	1	FETP_LEGPA	Q5x3x9 legionella
38	218.5	46.2	89	1	FETP_LEGPH	Q5zu80 legionella
39	216	45.7	87	1	FETP_BUCBP	Q89a44 buchnera ap
40	216	45.7	92	1	FETP_XANOR	Q5gy22 xanthomona
41	213	45.0	90	1	FETP_CHRVO	Q7nsr4 chromobacte
42	210	44.4	92	1	FETP_XANCP	Q8p829 xanthomonas
43	210	44.4	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
44	208	44.0	90	2	Q4J228_AZOV1	Q4j228 azotobacter
45	208	44.0	91	1	FETP_BURMA	Q62iu9 burkholderi
46	208	44.0	91	1	FETP_BURPS	Q63sj4 burkholderi
47	207	43.8	90	1	FETP_XYLFT	Q87d06 xyella fas
48	206	43.6	90	1	FETP_PSESM	Q87uf5 pseudomonas
49	206	43.6	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
50	206	43.6	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
51	206	43.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
52	203	42.9	90	1	FETP_XYLFA	Q9pc73 xyella fas
53	203	42.9	91	1	FETP_RALSO	Q8y010 ralstonia s
54	199	42.1	79	1	FETP_CANBF	Q7vrg9 candidatus
55	198	41.9	88	1	FETP_NEIG1	Q5f553 neisseria g
56	198	41.9	88	1	FETP_NEIMA	P67615 neisseria m
57	198	41.9	88	1	FETP_NEIMB	P67616 neisseria m
58	197	41.6	90	1	FETP_PSEBK	Q88r49 pseudomonas
59	193	40.8	90	1	FETP_METCA	Q60aj7 methylococc
60	188	39.7	90	2	Q4KJ12_PSEFP5	Q4kj12 pseudomonas
61	184	38.9	87	1	FETP_FRATT	Q5nhj8 francisella
62	167.5	35.4	90	1	FETP_ACTIAD	Q6fbf3 acinetobact
63	148	31.3	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	138	29.2	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	82	17.3	1555	2	Q9U0N0_PLAF7	Q9u0n0 plasmodium
66	81	17.1	2672	1	GCN1_YEAST	P33892 saccharomyc
67	78.5	16.6	502	2	Q4T6I6_TETNG	Q4t6i6 tetraodon n
68	77.5	16.4	452	2	Q8F6U1_LEPIN	Q8f6u1 leptospira
69	77.5	16.4	464	2	Q72PI4_LEPIC	Q72pi4 leptospira
70	77	16.3	2248	2	Q4UB40_THEAN	Q4ub40 theileria a
71	76.5	16.2	511	2	Q98Q71_MYCPV	Q98q71 mycoplasma
72	76	16.1	2249	2	Q4MYU4_THEPA	Q4myu4 theileria p
73	75	15.9	1032	2	Q4XV2_PLACH	Q4xv2 plasmodium
74	74	15.6	330	2	Q8XKS4_CLOPE	Q8xks4 clostridium
75	74	15.6	403	2	Q5HIP0_STAAC	Q5hip0 staphylococ

ALIGNMENTS

RESULT 1
FETP_YERPE
ID FETP_YERPE STANDARD; PRT; 90 AA.
AC Q8ZHE7;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
OS OrderedLocustNames=YPO0953, Y3340, YP3488;
GN Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360; DOI=10.1038/35097083;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebatia M., James K.D., Churcher C.M., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.-M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltswell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
RA Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.M.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;


```
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RX DOI=10.1128/JB.184.16.4601-4611.2002;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.B., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RT "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=91001 / Biovar Mediaevalis;
RX PubMed=15368893;
RA Song Y., Tong Z., Wang J., Wang L., Guo Z., Han Y., Zhang J., Pei D.,
RA Zhou D., Qin H., Pang X., Han Y., Zhai J., Li M., Cui B., Qi Z.,
RA Jin L., Dai R., Chen F., Li S., Ye C., Du Z., Lin W., Wang J., Yu J.,
RA Yang H., Wang J., Huang P., Yang R.;
RT "Complete genome sequence of Yersinia pestis strain 91001, an isolate
RT avirulent to humans.";
RL DNA Res. 11:179-197(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AJ141415; CAC89796.1; -; Genomic DNA.
DR EMBL; AE013935; AAM86890.1; -; Genomic DNA.
DR EMBL; AE017140; AAS63643.1; -; Genomic_DNA.
DR SMR; Q8ZHE7; 1-90.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
FT CONFLICT 16 16 R -> G (in Ref. 3).
SQ SEQUENCE 90 AA; 10707 MW; C7374E6855653F65 CRC64;

Query Match 100.0%; Score 473; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 6.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLKDAERODFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60
   |||||
Db 1 MSRTIFCTFLKDAERODFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60
   |||||

QY 61 EDRKLLQEEMVNFLEGGDVHIAGYTPPSK 90
   |||||
Db 61 EDRKLLQEEMVNFLEGGDVHIAGYTPPSK 90
   |||||

RESULT 2
FETP_YERPS STANDARD; PRT; 90 AA.
AC Q666M3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocuNames=YPTB3225;
OS Yersinia pseudotuberculosis.
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OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Scoutland P.O.,
RA Regala W.M., Georgescu A.M., Vergez L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinebush J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX936398; CAH22463.1; -; Genomic_DNA.
DR SMR; Q666M3; 1-90.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10608 MW; C7375E7954752E64 CRC64;

Query Match 98.5%; Score 466; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 3.4e-40;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLKDAERODFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60
   |||||
Db 1 MSRTIFCTFLKDAERODFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKLSMNI 60
   |||||

QY 61 EDRKLLQEEMVNFLEGGDVHIAGYTPPSK 90
   |||||
Db 61 EDRKLLQEEMVNFLEGGDVHIAGYTPPSK 90
   |||||

RESULT 3
FETP_ERWCT STANDARD; PRT; 90 AA.
ID FETP_ERWCT
AC Q6D8U9;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocuNames=BCA0975;
OS Brwinia carotovora (subsp. atroseptica) (Pectobacterium atrosepticum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=29471;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SCRI 1043 / ATCC BAA-672;
RX PubMed=15263089; DOI=10.1073/pnas.0402424101;
RA Bell K.S., Sebahia M., Pritchard L., Holden M.T.G., Hyman L.J., Mungall K.,
RA Holeva M.C., Thomson N.R., Bentley S.D., Churcher L.J.C., Mungall K.,
RA Atkin R., Bason N., Brooks K., Chillingworth T., Clark K., Doggett J.,
RA Fraser A., Hance Z., Hauser H., Jagels K., Moule S., Norbertczak H.,
RA Ormond D., Price C., Quail M.A., Sanders M., Walker D., Whitehead S.,
RA Salmond G.P.C., Birch P.R.J., Parkhill J., Toth I.K.;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.246 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-20

Perfect score: 473
Sequence: 1 MSRTIFCTFLKKDAERQDFQ.....VNFLREGQDVHIAGYTPPSK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	400	84.6	107	2	US-09-489-039A-11962 Sequence 11962, A
2	389	82.2	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	221	46.7	122	2	US-09-252-991A-23355 Sequence 23355, A
4	176.5	37.3	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	143	30.2	110	2	US-09-540-236-2859 Sequence 2859, Ap
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62	60	12.7	837	2	US-10-015-393A-253	Sequence 253, App
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72	59.5	12.6	796	2	US-09-757-014-2	Sequence 2, Appli
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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RESULT 3
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; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
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; TYPE: PRT
; ORGANISM: Versinia pectis

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SUMMARIES

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43	54	11.4	248	7	US-11-024-959-401	Sequence 401, App
44	54	11.4	480	6	US-10-510-386-12	Sequence 12, Appl
45	54	11.4	574	6	US-10-763-712A-6	Sequence 6, Appli
46	54	11.4	626	6	US-10-467-657-6426	Sequence 6426, Ap
47	54	11.4	626	6	US-10-467-657-7618	Sequence 7618, Ap
48	54	11.4	1011	7	US-11-098-686-10257	Sequence 10257, A
49	53.5	11.3	177	6	US-10-467-657-1658	Sequence 1658, Ap
50	53.5	11.3	206	6	US-10-793-626-832	Sequence 832, App
51	53.5	11.3	233	5	US-09-978-360A-417	Sequence 417, App
52	53.5	11.3	279	7	US-11-098-686-10812	Sequence 10812, A
53	53.5	11.3	508	7	US-11-072-512-2186	Sequence 2186, Ap
54	53.5	11.3	690	7	US-11-052-554A-232	Sequence 232, App
55	53.5	11.3	702	6	US-10-510-386-214	Sequence 214, App
56	53.5	11.3	1813	6	US-10-495-083-10	Sequence 10, Appl
57	53	11.2	271	6	US-10-793-626-678	Sequence 678, App
58	53	11.2	2335	6	US-10-821-234-1610	Sequence 1610, App
59	52.5	11.1	264	6	US-10-821-234-1555	Sequence 1555, Ap
60	52.5	11.1	319	6	US-10-793-626-2760	Sequence 2760, Ap
61	52.5	11.1	388	7	US-11-046-668-7	Sequence 7, Appli
62	52.5	11.1	398	7	US-11-046-668-9	Sequence 9, Appli
63	52.5	11.1	886	6	US-10-821-234-1329	Sequence 1329, Ap
64	52	11.0	241	7	US-11-072-512-2203	Sequence 2203, Ap
65	52	11.0	296	7	US-11-087-227-10	Sequence 10, Appl
66	52	11.0	384	7	US-11-219-282-19	Sequence 19, Appl
67	52	11.0	395	7	US-11-009-658-46	Sequence 46, Appl
68	52	11.0	456	7	US-11-069-642-8	Sequence 8, Appli
69	52	11.0	497	6	US-10-454-437-410	Sequence 410, App
70	52	11.0	588	7	US-11-052-554A-339	Sequence 339, App
71	52	11.0	599	7	US-11-109-157A-3	Sequence 3, Appl1
72	52	11.0	600	7	US-11-072-512-3845	Sequence 3845, Ap
73	52	11.0	1145	6	US-10-793-626-1432	Sequence 1432, Ap
74	52	11.0	1613	7	US-11-108-528-84	Sequence 84, Appl
75	52	11.0	1613	7	US-11-108-528-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 62.41 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-21

Perfect score: 406
Sequence: 1 MNRRIIFCTPFKKKSGQDFQ.....MFNLEHRKIEKYMKLFLFK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	406	100.0	76	5	ABB78166
2	265	65.3	91	5	ABB78158
3	265	65.3	91	5	ABB78157
4	265	65.3	91	5	ABB78156
5	259	63.8	88	5	ABB78160
6	259	63.8	91	5	ABB78161
7	259	63.8	91	5	ABB78159
8	259	63.8	91	5	ABB78162
9	259	63.8	91	5	ABB78163
10	256	63.1	78	5	ABB78164
11	256	63.1	87	5	ABB78165
12	256	63.1	90	5	ABB78165
13	256	63.1	107	7	ABO65445
14	248	61.1	87	5	ABB78151
15	247	60.8	87	5	ABB78153
16	246	60.6	91	5	ABB78150
17	236	58.1	93	7	ADF05158
18	231	56.9	90	5	ABB78155
19	216	53.2	88	5	ABB78154
20	200	49.3	86	5	ABB78149
21	200	49.3	87	5	ABB78148
22	200	49.3	87	5	ABB78147
23	184	45.3	89	9	AEB41576
24	184	45.3	95	9	AEB38294

25	182	44.8	92	6	ADA34169	Ada34169 Acinetoba
26	181	44.6	87	5	ABB78175	Abb78175 Amino aci
27	175	43.1	87	5	ABB78170	Abb78170 Amino aci
28	175	43.1	87	5	ABB78174	Abb78174 Amino aci
29	175	43.1	122	7	ABO74609	Abc074609 Pseudomon
30	174.5	43.0	90	5	ABB78167	Abb78167 Amino aci
31	166	40.9	87	5	ABB78176	Abb78176 Amino aci
32	165	40.6	90	5	ABB78168	Abb78168 Amino aci
33	164	40.4	88	5	ABB78178	Abb78178 Amino aci
34	159	39.2	87	5	ABB78169	Abb78169 Amino aci
35	158	38.9	88	5	ABB78171	Abb78171 Amino aci
36	158	38.9	88	5	ABB78172	Abb78172 Amino aci
37	158	38.9	88	5	ABB78173	Abb78173 Amino aci
38	158	38.9	88	6	ABP77219	Abp77219 N. gonorr
39	154	37.9	87	5	ABB78177	Abb78177 Amino aci
40	128	31.5	110	8	ADL05173	Adl05173 M. catarr
41	75	18.5	903	8	ADN18395	Adn18395 Bacterial
42	73.5	18.1	319	9	AEA61809	Aea61809 Streptoco
43	73.5	18.1	321	6	ABU25343	Abu25343 Protein e
44	73	18.0	918	4	AAM79789	Aam79789 Human pro
45	73	18.0	1096	6	AAW78805	Aaw78805 Human pro
46	70	17.2	817	4	ABU22957	Abu22957 Protein e
47	69.5	17.1	81	7	ADC97424	Adc97424 E. faeciu
48	69.5	17.1	523	7	ADD72115	Add72115 Human end
49	69.5	17.1	2184	4	AAE00425	Aae00425 P. falcip
50	69	17.0	341	6	ABU18904	Abu18904 Protein e
51	69	17.0	954	6	ADR16190	Adr16190 Streptoco
52	69	17.0	2206	3	AAB18254	Aab18254 Plasmodiu
53	68.5	16.9	648	7	ADF16091	Adf16091 Human alb
54	68.5	16.9	648	7	ADF16086	Adf16086 Human alb
55	68	16.7	279	3	AAB05947	Aab05947 Protein d
56	67	16.5	447	8	ADR16238	Adr16238 Streptoco
57	67	16.5	577	4	AAU35662	Aau35662 Haemophil
58	67	16.5	577	6	ABU30623	Abu30623 Protein e
59	67	16.5	1657	2	AAW18822	Aaw18822 Human IQG
60	67	16.5	1657	7	ADU68688	Adj68688 Human hea
61	67	16.5	1657	8	ADQ30538	Adq30538 Pancreas
62	67	16.5	1657	8	ADU04997	Adu04997 Amino aci
63	66.5	16.4	1140	4	ABB69065	Abb69065 Drosophil
64	66	16.3	251	6	ABU48870	Abu48870 Protein e
65	65.5	16.1	399	6	ABU24107	Abu24107 Protein e
66	65	16.0	240	3	AAG32199	Aag32199 Arabidops
67	65	16.0	240	5	ABB91142	Abb91142 Herbicida
68	65	16.0	320	4	AAQ90768	Aaq90768 C glutami
69	64.5	15.9	109	8	ADR08542	Adr08542 Human pro
70	64.5	15.9	205	7	ADH87009	Adh87009 Enterococ
71	64.5	15.9	358	8	ADV89039	Adv89039 Streptoco
72	64.5	15.9	358	8	ADV80292	Adv80292 Streptoco
73	64.5	15.9	358	8	ADV82414	Adv82414 Moraxella
74	64.5	15.9	767	2	AAW46272	Aaw46272 Moraxella
75	64.5	15.9	768	2	ADR51505	Adr51505 Moraxella

ALIGNMENTS

RESULT 1	
ABB78166	ABB78166 standard; protein; 76 AA.
XX	
AC	ABB78166;
XX	
DT	05-NOV-2002 (first entry)
XX	
DS	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	
OS	hydroxyl radical; DNA damage; YggX homologue.
XX	
PN	Unidentified.
XX	
XX	US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
PA
XX
PI Downs D, Gralnick JA;
PI
XX
XX WPI; 2002-589476/63.
DR
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
PS
XX
XX Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent yggx homologues
XX
SQ Sequence 76 AA;

```

Query Match          100.0%; Score 406; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.3e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MNRIIFCTPFKKKSEGQDFQSYPGKLGGKIYDQISKAWEKWIEKQTILINEENTLNMFNL 60
        |||||||
Db       1 MNRIIFCTPFKKKSEGQDFQSYPGKLGGKIYDQISKAWEKWIEKQTILINEENTLNMFNL 60

OY      61 EHRKKIEKYMKLFLFK 76
        |||||||
Db       61 EHRKKIEKYMKLFLFK 76

RESULT 2
ABB78158
ID      ABB78158 standard; protein; 91 AA.
XX
AC      ABB78158;
XX
DT      05-NOV-2002 (first entry)
XX
DE      Amino acid sequence of a YggX homologue.
XX
KW      Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM      hydroxyl radical; DNA damage; YggX homologue.
XX
OS      Unidentified.
XX
PN      US2002072118-A1.
XX
PD      13-JUN-2002.
XX
PF      18-SEP-2001; 2001US-00955502.
XX
PR      22-SEP-2000; 2000US-0234588P.
XX
PA      (DOWN/) DOWNS D.
PA      (GRAL/) GRALNICK J A.
XX
PI      Downs D, Gralnick JA;
XX
```

DR WPI, 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT cell, comprises engineering the cell to produce more YggX protein, a

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

XX

PS Example; Fig 1A; 16pp; English.

XX

CC The specification describes a method for reducing superoxide damage to a

CC cell. The method comprises engineering the cell to produce more than the

CC native amount of YggX protein (a protein identified from *Salmonella*

CC enterica serovar typhimurium) or its homolog, where the cells are

CC rendered more resistant to superoxide damage. YggX reduces the oxidation

CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from

CC clusters. The resulting decrease in free-iron levels generates fewer

CC hydroxyl radicals and thus reduced DNA damage. The method is useful for

CC reducing superoxide damage in a bacterial, yeast, mammalian or plant

CC cell. ABB78147-78 represent YggX homologues

XX

SQ Sequence 91 AA;

```

Query Match          65.3%; Score 265; DB 5; Length 91;
Best Local Similarity 61.8%; Pred. No. 3.3e-23;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

QY      1 MNRIIFCTPFKKKSEGODFQSYPGKLGGKIYDQISKRAWEMKIEKOTILINEENINMFNL 60
       |:||||| ::::||||| |||::|::|::|::|: | |||:|||| |
Db      1 MSRTI FCTPLQREAGEGDFQLYPGELGRIRYNESKEAWAQWQHKTMLINEKNLNNNA 60

QY      61 EHRKKIKETMKLFLFK 76
       ||||| :|: |||:
Db      61 EHRLLEOEMVNFLE 76

```

RESULT 3
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX
AC ABB78157;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 8.3098 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-21
Perfect score: 406
Sequence: 1 MNRIIFCTPFKKKSEGQDFQ.....MFNLEHRRKKIEKMKLFLFK 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	406	100.0	93	2	B84994	hypothetical prote
2	265	65.3	91	2	A85954	hypothetical prote
3	265	65.3	91	2	A65082	hypothetical prote
4	265	65.3	91	2	F91108	hypothetical prote
5	259	63.8	91	2	AH0879	conserved hypot
6	256	63.1	90	2	AI0116	conserved hypot
7	256	63.1	90	2	C64013	hypothetical prote
8	231	56.9	90	2	C82320	conserved hypot
9	183	45.1	105	2	C82624	conserved hypot
10	175	43.1	90	2	H83003	conserved hypot
11	158	38.9	88	2	H81014	conserved hypot
12	75	18.5	903	1	C64444	cell division cont
13	69.5	17.1	193	2	D97157	stage III sporulat
14	69	17.0	2206	2	G71611	hypothetical prote
15	68.5	16.9	128	2	C59096	hypothetical prote
16	68.5	16.9	323	2	D90527	glycerol-3-phospha
17	67	16.5	356	2	G72386	conserved hypot
18	67	16.5	577	2	A64131	arginine-tRNA liga
19	67	16.5	1657	2	A54854	Ras GTPase activat
20	66	16.3	151	2	D64319	probable formate d
21	66	16.3	251	2	E82911	hypothetical prote
22	65.5	16.1	399	2	F97156	exonuclease VII, 1
23	65.5	16.1	634	2	A32241	lactose transport
24	65	16.0	240	2	D86395	T2P11.5 protein -
25	65	16.0	604	2	F64081	isomerase fucil (EC
26	65	16.0	731	2	T14231	NADH2 dehydrogenas
27	64.5	15.9	258	2	S26762	DNA endonuclease I
28	64.5	15.9	320	2	D90478	conserved hypot
29	64.5	15.9	403	2	C72396	hypothetical prote

30	64.5	15.9	510	2	A96735	hypothetical prote
31	64.5	15.9	556	1	QXBY34	DNA endonuclease I
32	64	15.8	128	2	T28294	ORF MSV133 hypothe
33	64	15.8	213	2	D69409	conserved hypot
34	64	15.8	250	2	G64709	hypothetical prote
35	64	15.8	265	2	T46013	hypothetical prote
36	64	15.8	286	2	D90609	conserved hypot
37	64	15.8	530	2	G64480	hypothetical prote
38	64	15.8	624	2	G82508	hypothetical prote
39	64	15.8	1024	2	T41415	probable leucine p
40	63.5	15.6	282	2	F96689	hypothetical prote
41	63.5	15.6	283	2	E84787	translin-like prot
42	63.5	15.6	529	2	T48253	myb-like protein -
43	63.5	15.6	1115	2	T41342	probable coiled-co
44	63.5	15.6	1304	2	T14073	dynein 1b heavy ch
45	63	15.5	174	2	S73113	hypothetical prote
46	63	15.5	300	2	H72326	conserved hypot
47	63	15.5	315	2	B59093	hypothetical prote
48	63	15.5	344	2	D70126	hypothetical prote
49	63	15.5	359	2	F84513	hypothetical prote
50	62.5	15.4	125	2	T22338	hypothetical prote
51	62.5	15.4	313	2	B90093	hypothetical prote
52	62.5	15.4	538	2	S67766	RNA-export mediato
53	62	15.3	183	2	T37599	hypothetical prote
54	62	15.3	253	2	C81393	probable transcrip
55	62	15.3	356	2	C97010	3-dehydroquinatase
56	62	15.3	601	2	H81282	probable translati
57	62	15.3	889	2	AD2215	two-component hybr
58	61.5	15.1	100	2	D71632	hypothetical prote
59	61.5	15.1	137	2	A84072	hypothetical prote
60	61.5	15.1	220	2	F70223	conserved hypot
61	61.5	15.1	233	2	T18453	hypothetical prote
62	61.5	15.1	424	2	T25803	hypothetical prote
63	61.5	15.1	490	2	G70108	hypothetical prote
64	61.5	15.1	599	2	H86227	hypothetical prote
65	61.5	15.1	1092	2	T18354	adhesin - Mycoplas
66	61.5	15.1	1549	2	T11974	glutamate synthase
67	61.5	15.1	2401	2	T28676	thoptry protein -
68	61	15.0	103	2	I51248	ACBP/DBI - duck
69	61	15.0	215	2	C81410	hypothetical prote
70	61	15.0	227	2	B70438	hypothetical prote
71	61	15.0	351	2	D82930	SRP family of GTP-
72	61	15.0	382	2	C90407	conserved hypot
73	61	15.0	390	2	I38202	leupin precursor -
74	61	15.0	664	2	T71106	hypothetical prote
75	61	15.0	2166	2	G70163	hypothetical prote

ALIGNMENTS

RESULT 1
E84994
hypothetical protein [imported] - Buchnera sp. (strain APS)
C:Species: Buchnera sp.
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 05-Oct-2004
C:Accession: E84994
R:Shigenobu, S.; Watanabe, H.; Hattori, M.; Sakaki, Y.; Ishikawa, H.
Nature 407, 81-86, 2000
A:Title: Genome sequence of the endocellular bacterial symbiont of aphids Buchnera sp. A
A:Reference number: A84930; MUID:20445173; PMID:10993077
A:Accession: E84994
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-93 <STO>
A:Cross-references: UNIPARC:UPI000005B610; GB:AP000398; GSPDB:GN00144
A:Experimental source: strain APS
C:Genetics:
A:Gene: yggX; BU553
C:Superfamily: fe(II) trafficking protein yggX
Query Match 100.0%; Score 406; DB 2; Length 93;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;

Matches	76;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;
Qy	1	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	60				
Db	17	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	76				
Qy	61	EHRKKIEKYMKLFLFK	76						
Db	77	EHRKKIEKYMKLFLFK	92						
RESULT 2									
A85954									
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93									
C/Species: Escherichia coli									
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004									
C/Accession: A85954									
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew									
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,									
Nature 409, 529-533, 2001									
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.									
A/Reference number: A85480; MUID:21074935; PMID:11206551									
A/Accession: A85954									
A/Status: preliminary									
A/Molecule type: DNA									
A/Residues: 1-91 <STO>									
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:g12517511; F									
A/Experimental source: strain O157:H7, substrain EDL933									
C/Genetics:									
A/Gene: yggX									
C/Superfamily: fe(II) trafficking protein YggX									
Query Match	65.3%;	Score 265;	DB 2;	Length 91;					
Best Local Similarity	61.8%;	Pred. No. 1.7e-19;							
Matches	47;	Conservative	16;	Mismatches	13;	Indels	0;	Gaps	0;
Qy	1	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	60				
Db	1	MSRTICTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLN	MWNA	60					
Qy	61	EHRKKIEKYMKLFLFK	76						
Db	61	EHRKLLQEMVNFLE	76						
RESULT 3									
A65082									
hypothetical protein b2962 - Escherichia coli (strain K-12)									
C/Species: Escherichia coli									
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004									
C/Accession: A65082									
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co									
.A.; Rose, D.J.; Mau, B.; Shao, Y.									
Science 277, 1453-1462, 1997									
A/Title: The complete genome sequence of Escherichia coli K-12.									
A/Reference number: A64720; MUID:97426617; PMID:9278503									
A/Accession: A65082									
A/Status: preliminary; nucleic acid sequence not shown; translation not shown									
A/Molecule type: DNA									
A/Residues: 1-91 <BLAT>									
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB000378; GB:U00096; NID:g									
A/Experimental source: strain K-12, substrain MG1655									
C/Superfamily: fe(II) trafficking protein YggX									
Query Match	65.3%;	Score 265;	DB 2;	Length 91;					
Best Local Similarity	61.8%;	Pred. No. 1.7e-19;							
Matches	47;	Conservative	16;	Mismatches	13;	Indels	0;	Gaps	0;
Qy	1	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	60				
Db	1	MSRTICTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLN	MWNA	60					
Qy	61	EHRKKIEKYMKLFLFK	76						
Db	61	EHRKLLQEMVNFLE	76						

Db	61	EHRKLLQEMVNFLE	76						
RESULT 4									
F91108									
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI									
C/Species: Escherichia coli									
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004									
C/Accession: F91108									
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.									
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.									
DNA Res. 8, 11-22, 2001									
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno									
A/Reference number: A99629; MUID:21156231; PMID:11258796									
A/Accession: F91108									
A/Status: preliminary									
A/Molecule type: DNA									
A/Residues: 1-91 <HAY>									
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;									
A/Experimental source: strain O157:H7, substrain RIMD 0509952									
C/Genetics:									
A/Gene: ECs3838									
C/Superfamily: fe(II) trafficking protein YggX									
Query Match	65.3%;	Score 265;	DB 2;	Length 91;					
Best Local Similarity	61.8%;	Pred. No. 1.7e-19;							
Matches	47;	Conservative	16;	Mismatches	13;	Indels	0;	Gaps	0;

Qy	1	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	60				
Db	1	MSRTICTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLN	MWNA	60					
Qy	61	EHRKKIEKYMKLFLFK	76						
Db	61	EHRKLLQEMVNFLE	76						

RESULT 5									
AH0879									
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica									
C/Species: Salmonella enterica subsp. enterica serovar Typhi									
A/Note: this species has also been called Salmonella typhi									
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004									
C/Accession: AH0879									
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,									
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,									
.S.; Moule, S.; O'Gaora, P.									
Nature 413, 848-852, 2001									
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;									
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov									
A/Reference number: AB0502; MUID:21534947; PMID:11677608									
A/Accession: AH0879									
A/Status: preliminary									
A/Molecule type: DNA									
A/Residues: 1-91 <PAR>									
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;									
C/Genetics:									
A/Gene: STY3266									
C/Superfamily: fe(II) trafficking protein YggX									
Query Match	63.8%;	Score 259;	DB 2;	Length 91;					
Best Local Similarity	60.5%;	Pred. No. 6.8e-19;							
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Qy	1	MNRRIICTFPFKKSGQDFQSYPGKLGKKIYDQISKKAWKEWIEKQITILINEENL	MFN	L	60				
Db	1	MSRTICTFLQREAGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLN	MWNA	60					
Qy	61	EHRKKIEKYMKLFLFK	76						
Db	61	EHRKLLQEMVNFLE	76						

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 56.0046 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-21
Perfect score: 406
Sequence: 1 MNRITCTPFPKKGQDPQ.....MFLNHRKKIKYMKLFLFK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	406	100.0	77	1	FETP_BUCAI	P57618 buchnera ap
2	300	73.9	78	1	FETP_BUCAP	Q8k925 buchnera ap
3	264	65.0	90	1	FETP_YERPS	Q666m3 yersinia ps
4	260	64.0	90	1	FETP_ECO57	P0a8p4 escherichia
5	260	64.0	90	1	FETP_ECOL6	Q8fe19 escherichia
6	260	64.0	90	1	FETP_ECOL1	P0a8p3 escherichia
7	260	64.0	90	1	FETP_SHIFL	P0a8p5 shigella fl
8	256	63.1	90	1	FETP_HAEIN	P44048 haemophilus
9	256	63.1	90	1	FETP_YERPE	Q8zhe7 yersinia pe
10	256	63.1	90	2	Q4QMD9_HAEI8	Q4qmd9 haemophilus
11	254	62.6	90	1	FETP_SALCH	Q57k04 salmonella
12	254	62.6	90	1	FETP_SALPA	Q5pmu1 salmonella
13	254	62.6	90	1	FETP_SALTI	P67618 salmonella
14	254	62.6	90	1	FETP_SALTY	P67617 salmonella
15	251	61.8	91	1	FETP_MANSM	Q65vt7 manheimia
16	248	61.1	90	1	FETP_PASMU	Q9clb9 pasteurella
17	247	60.8	90	1	FETP_PHOPR	Q6lmk7 photobacter
18	247	60.8	94	1	FETP_HAEDU	Q7vkb6 haemophilus
19	243	59.9	90	1	FETP_PHOL1	Q7n711 photorhabdu
20	241	59.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
21	239	58.9	90	1	FETP_VIBPA	Q871i5 vibrio para
22	238	58.6	90	1	FETP_BRWCT	Q6d8j9 erwinia car
23	232	57.1	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
24	231	56.9	90	1	FETP_VIBCH	Q9kuc4 vibrio chol
25	231	56.9	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
26	231	56.9	90	1	FETP_VIBVY	Q7mhl4 vibrio vuln
27	223	54.9	90	1	FETP_IDILO	Q5qy58 idiomarina
28	218	53.7	78	1	FETP_WIGBR	Q8d3c5 wigleswort
29	216	53.2	92	1	FETP_SHEON	Q8ebx6 shewanella
30	206	50.7	79	1	FETP_CANBF	Q7vrg9 candidatus
31	200	49.3	90	1	FETP_BORBR	Q7wh06 bordetella

32	200	49.3	90	1	FETP_BORPA	Q7w9q2 bordetella
33	200	49.3	90	1	FETP_BORPE	Q7wvc4 bordetella
34	188	46.3	90	1	FETP_XYLET	Q87d06 xylella fas
35	186	45.8	90	1	FETP_ACIAD	Q6ffb3 acinetobact
36	185	45.6	91	1	FETP_XANAC	Q8pjh7 xanthomonas
37	184	45.3	89	1	FETP_LEGPA	Q5x3x9 legionella
38	184	45.3	89	1	FETP_LEGPH	Q5zu80 legionella
39	184	45.3	89	1	FETP_LEGPL	Q5pc73 xylella fas
40	183	45.1	90	1	FETP_XYLEFA	Q82xf2 nitrosomonas
41	182	44.8	90	1	FETP_NITEU	Q62iu9 burkholderi
42	181	44.6	91	1	FETP_BURMA	Q63sj4 burkholderi
43	181	44.6	91	1	FETP_BURPS	Q41819 burkholderi
44	180	44.3	91	2	Q4LS19_9BURK	Q8p829 xanthomonas
45	179	44.1	92	1	FETP_XANCP	Q5gy22 xanthomonas
46	179	44.1	92	1	FETP_XANOR	Q4uw14 xanthomonas
47	179	44.1	92	2	Q4UW14_XANCP	Q8y010 ralsconia s
48	176	43.3	91	1	FETP_RALSO	Q9hu36 pseudomonas
49	175	43.1	90	1	FETP_PSEAE	Q4j228 azotobacter
50	175	43.1	90	2	Q4J228_AZOVI	Q6t7f6 pseudomonas
51	170	41.9	90	2	Q6T7P6_PSEFL	Q5nhj8 francisella
52	166	40.9	87	1	FETP_FRATY	Q87uf5 pseudomonas
53	165	40.6	90	1	FETP_PSESM	Q4zlp3 pseudomonas
54	165	40.6	90	2	Q4ZLP3_PSESY	Q83d06 coxiella bu
55	164	40.4	90	1	FETP_COXBU	Q7nsr4 chromobacte
56	163	40.1	90	1	FETP_CHRVO	Q88r49 pseudomonas
57	159	39.2	90	1	FETP_PSEPK	Q5f553 neisseria g
58	158	38.9	88	1	FETP_NEIG1	P67615 neisseria m
59	158	38.9	88	1	FETP_NEIMA	P67616 neisseria m
60	158	38.9	88	1	FETP_NEIMB	Q4kjt2 pseudomonas
61	158	38.9	90	2	Q4KJT2_PSEF5	Q60aj7 methylococc
62	154	37.9	90	1	FETP_METCA	Q4fvj7 psychrobact
63	126	31.0	96	2	Q4FVJ7_9GAMM	Q4nwq4 anaeromyxob
64	115	28.3	92	2	Q4NWQ4_9DELT	Q736m4 bacillus ce
65	87.5	21.6	540	2	Q736M4_BACC1	Q63aa2 bacillus ce
66	85.5	21.1	540	2	Q63AA2_BACC2	Q84ev3 mycoplasma
67	82	20.2	186	2	Q84EV3_MYCGA	Q9kx69 mycoplasma
68	82	20.2	186	2	Q9KX69_MYCGA	Q7nak4 mycoplasma
69	82	20.2	186	2	Q7NAK4_MYCGA	Q4xxz8 plasmodium
70	81.5	20.1	178	2	Q4XZX8_PLACH	Q4mp87 bacillus ce
71	80.5	19.8	540	2	Q4MP87_BACCH	Q6hhp3 bacillus th
72	80.5	19.8	540	2	Q6HHP3_BACCH	Q81cc5 bacillus ce
73	80.5	19.8	540	2	Q81CC5_BACCR	Q81pf9 bacillus an
74	80.5	19.8	540	2	Q81PF9_BACAN	
75	80	19.7	1629	2	Q9U0K9_PLAF7	Q9u0k9 plasmodium

ALIGNMENTS

RESULT 1
FETP_BUCAI STANDARD; PRT; 77 AA.
ID FETP_BUCAI
AC P57618;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=BUS53;
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum)
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077; DOI=10.1038/35024074;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
Buchnera sp. APS.";
RL Nature 407:81-86(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or


```
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BA000003; BAB13245.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 77 AA; 9511 MW; 00B049027CF480BF CRC64;

Query Match          100.0%; Score 406; DB 1; Length 77;
Best Local Similarity 100.0%; Pred. No. 8.3e-34;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNRIIFCTPFKKKSEGQDFQSYPGKLGKKIYDQISKKAWKWIIEKQTLINENLNMFNL 60
Db 1 MNRIIFCTPFKKKSEGQDFQSYPGKLGKKIYDQISKKAWKWIIEKQTLINENLNMFNL 60

OY 61 EHRKKIEKYMKLFLFK 76
Db 61 EHRKKIEKYMKLFLFK 76

RESULT 2
FETP_BUCAP
ID FETP_BUCAP STANDARD; PRT; 78 AA.
AC Q8K925;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=Bugs535;
OS Buchnera aphidicola (subsp. Schizaphis graminum).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22084549; PubMed=12089438; DOI=10.1126/science.1071278;
RA Tamas I., Klasson L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstroem J.P., Moran N.A., Andersson S.G.B.;
RT "50 million years of genomic stasis in endosymbiotic bacteria.";
RL Science 296:2376-2379(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE014127; AAM68076.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 78 AA; 9564 MW; ABB7086986777F44 CRC64;
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Query Match          73.9%; Score 300; DB 1; Length 78;
Best Local Similarity 76.0%; Pred. No. 5.7e-23;
Matches 57; Conservative 7; Mismatches 11; Indels 0; Gaps 0;

OY 1 MNRIIFCTPFKKKSEGQDFQSYPGKLGKKIYDQISKKAWKWIIEKQTLINENLNMFNL 60
Db 1 MNRIIFCTPFKKKSEGQDFQSYPGKLGKKIYDQISKKAWKWIIEKQTLINENLNMFNL 60

OY 61 EHRKKIEKYMKLFLF 75
Db 61 NDRKKIEKYMKLFLF 75

RESULT 3
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ID FETP_YERPS STANDARD; PRT; 90 AA.
AC Q666M3;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=YPTB3225;
OS Yersinia pseudotuberculosis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=IP32953 / Serotype I;
RX PubMed=15358858; DOI=10.1073/pnas.0404012101;
RA Chain P.S.G., Carniel E., Larimer F.W., Lamerdin J., Stoutland P.O.,
RA Regala W.M., Georgescu A.M., Verges L.M., Land M.L., Motin V.L.,
RA Brubaker R.R., Fowler J., Hinebusch J., Marceau M., Medigue C.,
RA Simonet M., Chenal-Francois V., Souza B., Dacheux D., Elliott J.M.,
RA Derbise A., Hauser L.J., Garcia E.;
RT "Insights into the evolution of Yersinia pestis through whole-genome
RT comparison with Yersinia pseudotuberculosis.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX936398; CAH22463.1; -; Genomic_DNA.
DR SMR; Q666M3; 1-90.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR Prodom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10608 MW; C7375E7954752E64 CRC64;
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Query Match          65.0%; Score 264; DB 1; Length 90;
Best Local Similarity 61.8%; Pred. No. 3.1e-19;
Matches 47; Conservative 16; Mismatches 13; Indels 0; Gaps 0;

OY 1 MNRIIFCTPFKKKSEGQDFQSYPGKLGKKIYDQISKKAWKWIIEKQTLINENLNMFNL 60
Db 1 MSRTIFCTPLKDDAGQDFQLYPGEIGKRIYNISKEAWSQWITKQTMLINEKLSMNNI 60

OY 61 EHRKKIEKYMKLFLFK 76
Db 61 EDRKLLIQEWMVNLFE 76
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 15.4077 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-21

Perfect score: 406
Sequence: 1 MNRILCTFPKKGSGQDFQ.....MFNLHRKIKIKMKLFLPK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	ID	Description
1	256	63.1	107	2	US-09-489-039A-11962
2	236	58.1	93	2	US-09-543-681A-5443
3	182	44.8	92	2	US-09-328-352-5456
4	175	43.1	122	2	US-09-252-991A-23355
5	128	31.5	110	2	US-09-540-236-2859
6	69.5	17.1	81	2	US-09-107-532A-7051
7	69.5	17.1	2184	2	US-09-417-485D-6
8	68	16.7	279	2	US-09-861-451A-28
9	67	16.5	1657	1	US-08-287-959-1
10	67	16.5	1657	2	US-09-949-016-6427
11	67	16.5	1678	2	US-09-949-016-9445
12	66.5	16.4	666	2	US-09-270-767-62249
13	66.5	16.4	721	2	US-09-270-767-46645
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32	60.5	14.9	85	2	US-09-107-433-4296	Sequence 4296, Ap
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37	60.5	14.9	591	2	US-09-370-368-8	Sequence 8, Appli
38	60.5	14.9	885	2	US-09-074-579-5	Sequence 5, Appli
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40	60	14.8	192	2	US-09-540-236-3508	Sequence 3508, Ap
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55	59	14.5	110	2	US-09-774-639-112	Sequence 112, App
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66	58	14.3	187	2	US-09-248-796A-16987	Sequence 16987, A
67	58	14.3	221	2	US-09-543-681A-8222	Sequence 8222, Ap
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69	58	14.3	284	2	US-09-949-016-11051	Sequence 11051, A
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ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 48.1276 Seconds
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659.810 Million cell updates/sec

Title: US-09-955-502A-21

Perfect score: 406
Sequence: 1 MNRIFTFFKKKSEGQDFQ.....MFNLHRKKIEKYMCLFLFK 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*

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and is derived by analysis of the total score distribution.

SUMMARIES

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74	63	15.5	917	6	US-11-034-275-27	Sequence 27, Appl
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ALIGNMENTS

RESULT 1
US-09-955-502-21
Sequence 21, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 76
TYPE: PRT
ORGANISM: Buchnera sp. APS

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Title: US-09-955-502A-21

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Post-processing: Minimum Match 0%

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SUMMARIES

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4	58	14.3	124	7	US-11-072-512-2018 Sequence 2018, Ap
5	58	14.3	805	6	US-10-927-641-77 Sequence 77, Appl
6	57	14.0	296	7	US-11-102-978-7 Sequence 7, Appl
7	57	14.0	552	7	US-11-072-512-3426 Sequence 3426, Ap
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9	57	14.0	629	7	US-11-072-512-3405 Sequence 3405, Ap
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14	56	13.8	369	7	US-11-156-084-45 Sequence 45, Appl
15	56	13.8	619	7	US-11-156-084-24 Sequence 24, Appl
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22	54	13.3	390	7	US-11-019-711-65 Sequence 65, Appl
23	54	13.3	390	7	US-11-219-282-12 Sequence 12, Appl
24	54	13.3	438	7	US-11-124-367A-331 Sequence 331, Appl
25	54	13.3	574	7	US-11-098-686-11000 Sequence 11000, A

26	54	13.3	898	7	US-11-099-691-7	Sequence 7, Appl
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ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR APPLICATION NUMBER: 2003-08-11
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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Perfect score: 483

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Database :

- 1: _Geneseq_21:*
- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	472.5	97.8	90 5 ABB78167	Abb78167 Amino aci
2	246	50.9	87 5 ABB78153	Abb78153 Amino aci
3	238	49.3	107 7 ABO65445	ABO65445 Klebsiell
4	237	49.1	87 5 ABB78151	Abb78151 Amino aci
5	237	49.1	87 5 ABB78152	Abb78152 Amino aci
6	234	48.4	91 5 ABB78150	Abb78150 Amino aci
7	232	48.0	91 5 ABB78161	Abb78161 Amino aci
8	232	48.0	91 5 ABB78159	Abb78159 Amino aci
9	232	48.0	91 5 ABB78162	Abb78162 Amino aci
10	230	47.6	91 5 ABB78163	Abb78163 Amino aci
11	229	47.4	88 5 ABB78160	Abb78160 Amino aci
12	228	47.2	90 5 ABB78155	Abb78155 Amino aci
13	227	47.0	93 7 ADF05158	Adf05158 Bacterial
14	226	46.8	91 5 ABB78158	Abb78158 Amino aci
15	226	46.8	91 5 ABB78157	Abb78157 Amino aci
16	226	46.8	91 5 ABB78156	Abb78156 Amino aci
17	220	45.5	78 5 ABB78164	Abb78164 Amino aci
18	215	44.5	87 5 ABB78176	Abb78176 Amino aci
19	214	44.3	88 5 ABB78178	Abb78178 Amino aci
20	209	43.3	89 9 AEB41576	Aeb41576 L. pneumo
21	209	43.3	95 9 AEB38294	Aeb38294 L. pneumo
22	205	42.4	87 5 ABB78148	Abb78148 Amino aci
23	205	42.4	87 5 ABB78147	Abb78147 Amino aci
24	203.5	42.1	92 6 ADA34169	Ada34169 Acinetoba

25	203	42.0	90 5 ABB78165	Abb78165 Amino aci
26	201	41.6	87 5 ABB78177	Abb78177 Amino aci
27	201	41.6	88 5 ABB78171	Abb78171 Amino aci
28	201	41.6	88 5 ABB78172	Abb78172 Amino aci
29	201	41.6	88 5 ABB78173	Abb78173 Amino aci
30	201	41.6	88 6 ABB77219	Abp77219 N. gonorr
31	200	41.4	90 5 ABB78168	Abb78168 Amino aci
32	198	41.0	87 5 ABB78169	Abb78169 Amino aci
33	198	41.0	122 7 ABO74609	ABO74609 Pseudomon
34	197	40.8	87 5 ABB78175	Abb78175 Amino aci
35	196	40.6	88 5 ABB78154	Abb78154 Amino aci
36	195	40.4	86 5 ABB78149	Abb78149 Amino aci
37	192	39.8	87 5 ABB78170	Abb78170 Amino aci
38	191	39.5	87 5 ABB78174	Abb78174 Amino aci
39	183	37.9	76 5 ABB78166	Abb78166 Amino aci
40	150	31.1	110 8 ADL05173	Adl05173 M. catarr
41	71	14.7	582 8 ADY10873	Ady10873 Plant ful
42	67.5	14.0	272 5 ABU05512	Abu05512 M. tuberc
43	67	13.9	87 3 AAB54259	Aab54259 Human pan
44	67	13.9	302 4 AAU35741	Aau35741 Helicobac
45	67	13.9	302 6 ABU30804	Abu30804 Protein e
46	67	13.9	305 7 ADM25449	Adm25449 Hypertther
47	66	13.7	379 4 AA97562	Aay97562 Mouse wnt
48	66	13.7	379 6 ABG71361	Abg71361 Mouse wnt
49	66	13.7	379 7 ADD90585	Add90585 WIF domai
50	66	13.7	379 7 ADD90566	Add90566 Mouse WIF
51	66	13.7	379 7 ADD90583	Add90583 WIF domai
52	66	13.7	379 7 ADD90581	Add90581 WIF domai
53	66	13.7	379 7 ADD90579	Add90579 WIF domai
54	66	13.7	379 8 ADP95945	Adp95945 Murine WI
55	64.5	13.4	327 3 AAB16535	Aab16535 Bacteriop
56	64	13.3	208 2 AAY41660	Aay41660 Triflicum
57	64	13.3	365 7 ADD90570	Add90570 Rat WIF-1
58	64	13.3	64 8 ADN20509	Adn20509 Bacterial
59	63	13.0	305 7 ADM25966	Adm25966 Hypertther
60	63	13.0	544 3 AAG40947	Aag40947 Zea may
61	62.5	12.9	219 8 ADM57215	Adm57215 A thalian
62	62.5	12.9	314 6 ABU44876	Abu44876 Protein e
63	62.5	12.9	363 7 ADE55261	Ades55261 Rat Prote
64	62.5	12.9	389 7 ADM04329	Adm04329 Human pro
65	62.5	12.9	405 6 AAB32119	Aae32119 Human cyt
66	62.5	12.9	439 6 ABU50419	Abu50419 Protein e
67	62	12.8	174 2 AAY34740	Aay34740 Chlamydia
68	62	12.8	409 8 ADT58047	Adt58047 Plant pol
69	62	12.8	435 4 ABG08894	Abg08894 Novel hum
70	62	12.8	533 2 AAR39705	Aar39705 Chicken p
71	62	12.8	646 3 AAY57307	Aay57307 P. aerugi
72	62	12.8	667 5 ABB93976	Abb93976 Herbicida
73	62	12.8	667 8 ADN73801	Adn73801 Thale cre
74	62	12.8	670 3 AAY57314	Aay57314 P. aerugi
75	62	12.8	686 7 ABO80650	ABO80650 Pseudomon

ALIGNMENTS

RESULT 1	
ABB78167	
ID	ABB78167 standard; protein; 90 AA.
AC	ABB78167;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	hydroxyl radical; DNA damage; YggX homologue.
OS	Xylella fastidiosa.
XX	
PH	Key
FT	Misc-difference 61 Location/Qualifiers

/note= "not specified"

FT (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
PN WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 90 AA;

Query Match 97.8%; Score 472.5; DB 5; Length 90;
Best Local Similarity 98.9%; Pred. No. 5.7e-50;
Matches 89; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MORIIFCEYEQRDTGLDFVPPYGGELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60
 |||||
Db 1 MORIIFCEYEQRDTGLDFVPPYGGELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60

QY 61 -SHRAFLBEEELNKFLFERRVAKPEGYIEPD 89
 |||||
Db 61 XSHRAFLBEEELNKFLFERRVAKPEGYIEPD 90

RESULT 2
ABB78153
ID ABB78153 standard; protein; 87 AA.
XX
AC ABB78153;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.
XX Downs D, Gralnick JA;
PI WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 50.9%; Score 246; DB 5; Length 87;
Best Local Similarity 51.2%; Pred. No. 4.1e-22;
Matches 44; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

QY 1 MORIIFCEYEQRDTGLDFVPPYGGELGQKIFACIGKVGWAAWLVHQTMLINENRLSPRNP 60
 ||::|||
Db 1 MARWVFCBYLKKBAEGLDLQLYPGELGKRIFNSISKQAWAEWIKKQTMLVNEKLNMMNP 60

QY 61 SHRAFLBEEELNKFLFERRVAKPEGYI 86
 |||
Db 61 EHRQLLEAEWVNFLEFGKDVHIDGYV 86

RESULT 3
ABO65445
ID ABO65445 standard; protein; 107 AA.
XX
AC ABO65445;
XX
DT 29-JUL-2004 (first entry)
XX
DE Klebsiella pneumoniae polypeptide seqid 11962.
XX
KW Recombinant expression vector; transcription regulatory element;
KW Klebsiella pneumoniae protein; antibacterial; Vaccine.
XX
OS Klebsiella pneumoniae.
XX
PN US6610836-B1.
XX
PD 26-AUG-2003.
XX
PF 27-JAN-2000; 2000US-00489039.
XX
PR 29-JAN-1999; 99US-0117747P.
XX
PA (GENO-) GENOME THERAPEUTICS CORP.
XX
PI Breton GL, Osborne M;
XX
DR WPI; 2003-895346/82.
DR N-PSDB; ACH98996.
XX
PT New nucleic acid encoding a Klebsiella pneumoniae polypeptide, useful for
PT preparing a vaccine composition against Klebsiella pneumoniae.
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:17:30 ; Search time 9.73121 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-22
Perfect score: 483
Sequence: 1 MGRIRFCYEQRTDTEGLDFV.....LNKFLFRRVAKPEGYIPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	483	100.0	105	2	C82624	conserved hypothe
2	243	50.3	90	2	C64013	hypothetical prote
3	232	48.0	91	2	AH0879	conserved hypothe
4	228	47.2	90	2	C82320	conserved hypothe
5	226	46.8	91	2	A85954	hypothetical prote
6	226	46.8	91	2	A65082	hypothetical prote
7	226	46.8	91	2	F91108	hypothetical prote
8	203	42.0	90	2	AI0116	conserved hypothe
9	201	41.6	88	2	H81014	conserved hypothe
10	198	41.0	90	2	H83003	conserved hypothe
11	185	38.3	93	2	B84994	hypothetical prote
12	67.5	14.0	272	2	H87075	probable conserved
13	67	13.9	302	2	B64584	GTP-binding protei
14	63.5	13.1	587	2	S23312	retrovirus-related
15	63.5	13.1	1131	2	T14517	hypothetical prote
16	63	13.0	105	2	E75442	conserved hypothe
17	63	13.0	415	2	S55617	hypothetical prote
18	62.5	12.9	219	2	C96510	hypothetical prote
19	62.5	12.9	439	2	AC0491	xylose isomerase (
20	62	12.8	188	2	C86508	hypothetical prote
21	62	12.8	188	2	H72114	transcription regu
22	62	12.8	305	1	OWPSAA	ornithine carbamoy
23	62	12.8	526	2	S26420	protein-tyrosine k
24	62	12.8	533	1	TVCHS	conserved hypothe
25	62	12.8	670	2	C83540	probable finger pr
26	61.5	12.7	863	2	S38140	hypothetical prote
27	61.5	12.7	359	2	C84983	hypothetical prote
28	61.5	12.7	445	2	T01591	hypothetical prote
29	61.5	12.7	494	2	S23315	hypothetical prote

30	61.5	12.7	729	2	G97169	protein containing
31	61.5	12.7	869	1	A47257	1-phosphatidylinos
32	61	12.6	143	2	I47053	relaxin B, C and A
33	61	12.6	301	2	G71929	GTP-binding protei
34	61	12.6	332	2	B47017	probable transcrip
35	61	12.6	332	2	AD2541	transcription init
36	61	12.6	379	2	A59180	Wnt inhibitory fac
37	60.5	12.5	440	2	AC0980	xylose isomerase (
38	60.5	12.5	1894	2	JC4980	3-keoacyl-acyl ca
39	60	12.4	243	2	AF1611	hypothetical prote
40	60	12.4	318	2	C83555	conserved hypothe
41	60	12.4	360	1	F64601	probable endopepti
42	60	12.4	878	2	G71371	alpha-actinin 3 -
43	60	12.4	901	1	FAHUA3	hypothetical prote
44	60	12.4	984	2	T48216	ribonucleoside-dip
45	59.5	12.3	761	2	AC0791	ribonucleoside-dip
46	59.5	12.3	761	2	S32629	glutamate receptor
47	59.5	12.3	997	2	S33754	hypothetical prote
48	59.5	12.3	1017	2	T08553	conserved hypothe
49	59	12.2	231	2	AE0725	hypothetical prote
50	59	12.2	231	2	AF3028	hypothetical prote
51	59	12.2	231	2	B98256	conserved hypothe
52	59	12.2	283	2	D72398	DNA polymerase, ba
53	59	12.2	290	2	AC3417	hypothetical prote
54	59	12.2	360	2	E71910	glutamate-tRNA lig
55	59	12.2	486	2	F98106	conserved hypothe
56	59	12.2	496	2	D83614	surfactin syntheta
57	59	12.2	3587	2	I40486	probable gastrin p
58	58.5	12.1	127	2	B72593	hypothetical prote
59	58.5	12.1	231	2	AF1838	hypothetical prote
60	58.5	12.1	323	2	H71481	cyclin-dependent k
61	58.5	12.1	496	2	JC5110	hypothetical prote
62	58.5	12.1	1327	2	T21268	hypothetical prote
63	58	12.0	194	2	I39526	hypothetical prote
64	58	12.0	247	2	T27205	hypothetical prote
65	58	12.0	251	2	B90428	hypothetical prote
66	58	12.0	457	2	F64095	argininosuccinate
67	58	12.0	526	1	TVFVR	protein-tyrosine k
68	58	12.0	526	2	S15582	protein-tyrosine k
69	58	12.0	632	2	H83106	chemotactic transd
70	58	12.0	1066	2	B95037	hyaluronidase limp
71	58	12.0	1078	2	F97907	hypothetical prote
72	58	12.0	1107	2	T21280	hypothetical prote
73	58	12.0	4450	2	JX0340	gramicidin S synth
74	58	12.0	4452	1	YGBSG2	gramicidin S synth
75	57.5	11.9	373	2	F70781	probable cita prot

ALIGNMENTS

RESULT 1
C82624
conserved hypothetical protein XF1908 [imported] - Xylella fastidiosa (strain 9a5c)
C/Species: Xylella fastidiosa
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82624
R/anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A/Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A/Reference number: A82515; MUID:20365717; PMID:10910347
A/Note: for a complete list of authors see reference number A59328 below
A/Accession: C82624
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-105 <SIM>
A/Cross-references: UNIPARC:UPI00000C288F; GB:AE004010; GB:AE003849; NID:g9106992; PIDN:
A/Experimental source: strain 9a5c
R/Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A/Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 19:14:27 ; Search time 65.6856 Seconds
(without alignments)
955.947 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MQRIFCFCEYQRDTGGLDFV.....LNKFLFERRVAKPEGYIEPD 89

Scoring table: BL0SUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	483	100.0	90	1	FETP_XYLFA Q9PC73 xylella fas
2	465	96.3	90	1	FETP_XYLFT Q87D06 xylella fas
3	380	78.7	92	1	FETP_XANCP Q8P829 xanthomonas
4	380	78.7	92	2	Q4UW14 XANCP Q4UW14 xanthomonas
5	367	76.0	91	1	FETP_XANAC Q8PJH7 xanthomonas
6	367	76.0	92	1	FETP_XANOR Q5GY22 xanthomonas
7	247	51.1	90	1	FETP_IDILO Q5GY58 idiomarina
8	246	50.9	94	1	FETP_HABDU Q7VKB6 haemophilus
9	244	50.5	90	1	FETP_PHOLU Q7N711 photohabdu
10	243	50.3	90	1	FETP_HAEIN P44048 haemophilus
11	243	50.3	90	1	FETP_PASMU Q9CLB9 pasteurella
12	243	50.3	90	2	Q4QMD9 HAB18 Q4QMD9 haemophilus
13	236	48.9	91	1	FETP_MANSM Q65VT7 manheimia
14	228	47.2	90	1	FETP_VIBCH Q9KUR4 vibrio chol
15	227	47.0	90	1	FETP_SALCH Q57K04 salmonella
16	227	47.0	90	1	FETP_SALPA Q5PMU1 salmonella
17	227	47.0	90	1	FETP_SALTI P67617 salmonella
18	227	47.0	90	1	FETP_SALTY P67617 salmonella
19	225	46.6	90	1	FETP_ERWCT Q6D8J9 erwina car
20	222	46.0	90	1	FETP_VIBPA Q87115 vibrio para
21	221	45.8	90	1	FETP_BCO57 P0A8P4 escherichia
22	221	45.8	90	1	FETP_BCO57 P0A8P4 escherichia
23	221	45.8	90	1	FETP_SHIFL P0A8P5 shigella fl
24	219	45.3	90	1	FETP_PHOPR Q6LMK7 photobacter
25	217	44.9	90	1	FETP_ECOL6 Q8FE19 escherichia
26	217	44.9	90	1	FETP_VIBVU Q8DCS5 vibrio vuln
27	217	44.9	90	1	FETP_VIBVU Q8DCS5 vibrio vuln
28	214	44.3	90	1	FETP_COXBU Q83D06 coxiella bu
29	212	43.9	91	1	FETP_RALSO Q8Y010 ralsconia s
30	211	43.7	90	1	FETP_BORBR Q7WH06 bordetella
31	211	43.7	90	1	FETP_BORPA Q7W9Q2 bordetella

32	211	43.7	90	1	FETP_BORPE	Q7WC4 bordetella
33	211	43.7	90	1	FETP_YERPS	Q66M3 yersinia ps
34	209	43.3	89	1	FETP_LEGPA	Q5X3X9 legioneila
35	209	43.3	89	1	FETP_LEGPH	Q5ZU80 legioneila
36	209	43.3	90	1	FETP_VIBF1	Q5E7C0 vibrio fisc
37	208	43.1	89	1	FETP_LEGPL	Q5WVC4 legioneila
38	207	42.9	90	1	FETP_METCA	Q60AJ7 methylococc
39	206	42.7	87	1	FETP_FRATT	Q5NHJ8 francisella
40	204.5	42.3	90	1	FETP_AC1AD	Q6FFB3 acinetobact
41	204	42.2	90	1	FETP_PSEPK	Q88R49 pseudomonas
42	203	42.0	90	1	FETP_YERPE	Q8ZHE7 yersinia pe
43	203	42.0	91	1	FETP_BURMA	Q62IU9 burkholderi
44	203	42.0	91	1	FETP_BURPS	Q63SJ4 burkholderi
45	203	42.0	91	2	Q4LS19_9BURK	Q4LS19 burkholderi
46	201	41.6	88	1	FETP_NEIGI	Q5F553 neisseria g
47	201	41.6	88	1	FETP_NEIMA	P67615 neisseria m
48	201	41.6	88	1	FETP_NEIMB	P67615 neisseria m
49	200	41.4	90	1	FETP_CHRVO	Q7NSR4 chromobacte
50	200	41.4	90	1	FETP_NITBU	Q82XF2 nitrosomona
51	200	41.4	90	1	FETP_PSESM	Q87UF5 pseudomonas
52	200	41.4	90	2	Q4ZLP3_PSESY	Q4ZLP3 pseudomonas
53	198	41.0	90	1	FETP_PSEAB	Q9HU36 pseudomonas
54	197	40.8	90	2	Q4J228_AZOVI	Q4J228 azotobacter
55	196	40.6	92	1	FETP_SHEON	Q4KJT2 pseudomonas
56	194	40.2	90	2	Q4KJT2_PSEF5	Q4KJT2 pseudomonas
57	191	39.5	90	1	FETP_BUCAP	Q8K925 buchnera ap
58	190	39.3	90	2	Q6T7F6_PSEPL	Q6T7F6 pseudomonas
59	185	38.3	77	1	FETP_BUCAI	P57618 buchnera ap
60	180	37.3	78	1	FETP_WIGBR	Q8D3C5 wigleswort
61	172	35.6	87	1	FETP_BUCBP	Q89A44 buchnera ap
62	168	34.8	92	2	Q4NWQ4_9DELT	Q4NWQ4 anaeromyxob
63	156	32.3	79	1	FETP_CANBF	Q7VRG9 candidatus
64	154	31.9	96	2	Q4FVJ7_9GAMM	Q4FVJ7 psychrobact
65	91.5	18.9	123	2	Q812Z1_BACCR	Q812Z1 bacillus ce
66	75.5	15.6	635	2	Q6YBY0_TOXGO	Q6YBY0 toxoplasma
67	74.5	15.4	402	2	Q7NVX6_CHRVO	Q7NVX6 chromobacte
68	73	15.1	174	2	Q68658_HELPY	Q68658 helicobacte
69	70.5	14.6	468	2	Q7UPU4_RHOBA	Q7UPU4 rhodopirell
70	70.5	14.6	764	2	Q81MT3_ORYSA	Q81MT3 oryza sativ
71	69.5	14.4	217	2	Q9DQB0_AHSV7	Q9DQB0 african hor
72	68.5	14.2	129	2	Q6BJ04_DEBHA	Q6BJ04 debaryomyce
73	68.5	14.2	1065	2	Q9FJL6_ARATH	Q9FJL6 arabidopsis
74	68	14.1	5141	2	Q7S6D3_NEUCR	Q7S6D3 neurospora
75	67.5	14.0	272	2	Q9ZBD7_MYCLE	Q9ZBD7 mycobacteri

ALIGNMENTS

RESULT 1
FETP_XYLFA
ID FETP_XYLFA STANDARD; PRT; 90 AA.
AC Q9PC73;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=Xf1908;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=9A5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Abreu F.A., Acencio M.,
RA Alvarenga R., Alves L.M.C., Araya J.E., Bata G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carer H.,
RA Colaudo N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Facincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,

RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.L., Hohnselt J.D., Junqueira M.L., Kemper B.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.B., Laigret F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
RA Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
RA de Rosa V.B. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tshako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
RT "The genome sequence of the plant pathogen *Xylella fastidiosa*,"
RL Nature 406:151-159(2000).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC removed.

DR EMBL; AE004010; AAF84714.1; ALT_INIT; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10555 MW; E9BEB3BCA6D104A3 CRC64;

Query Match 100.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-47;
Matches 89; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MORIIFCEYEQRDTGLDFVYPYGPGLGQKIFACIGKVGMAAWLVHQTMLINENRLSPNP 60
Db 1 MORIIFCEYEQRDTGLDFVYPYGPGLGQKIFACIGKVGMAAWLVHQTMLINENRLSPNP 60

QY 61 SHRAFLLEELINKFLFERRVAKPEGYIEPD 89
Db 61 SHRAFLLEELINKFLFERRVAKPEGYIEPD 89

RESULT 2
FETP_XYLFT STANDARD; PRT; 90 AA.
AC Q87D06;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=PD0883;
OS *Xylella fastidiosa* (strain Temecual / ATCC 700964).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=183190;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX MEDLINE=22421331; PubMed=12533478;
RX DOI=10.1128/JB.185.3.1018-1026.2003;
RA Van Sluys M.A., de Oliveira M.C., Monteiro-Vitorello C.B.,
RA Miyaki C.Y., Furlan L.R., Camargo L.E.A., da Silva A.C.R., Moon D.H.,

RA Takita M.A., Lemos E.G.M., Machado M.A., Ferro M.I.T., da Silva F.R.,
RA Goldman M.H.S., Goldman G.H., Lemos M.V.F., El-Dorry H., Tsai S.M.,
RA Carrer H., Carraro D.M., de Oliveira R.C., Nunes L.R., Siqueira W.J.,
RA Coutinho L.L., Kimura E.T., Ferro E.S., Haraoka R., Kuramae E.B.,
RA Marino C.L., Gigliotti E., Abreu I.L., Alves L.M.C., do Amaral A.M.,
RA Baia G.S., Blanco S.R., Brito M.S., Camnava F.S., Celestino A.V.,
RA da Cunha A.F., Fenille R.C., Ferro J.A., Formighieri E.F., Kishi L.T.,
RA Leoni S.G., Oliveira A.R., Rosa V.E. Jr., Sassaki F.T., Sena J.A.D.,
RA de Souza A.A., Truffi D., Teukumo F., Yanai G.M., Zaros L.G.,
RA Civerolo E.L., Simpson A.J.G., Almeida N.F. Jr., Setubal J.C.,
RA Kitajima J.P.;
RT "Comparative analyses of the complete genome sequences of *Pierce's*
RT disease and citrus variegated chlorosis strains of *Xylella*
RT *fastidiosa*,"
RL J. Bacteriol. 185:1018-1026(2003).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC removed.

DR EMBL; AE012556; AAO28748.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10430 MW; B5C6936496F4171D CRC64;

Query Match 96.3%; Score 465; DB 1; Length 90;
Best Local Similarity 95.5%; Pred. No. 1.9e-45;
Matches 85; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MORIIFCEYEQRDTGLDFVYPYGPGLGQKIFACIGKVGMAAWLVHQTMLINENRLSPNP 60
Db 1 MORIIFCEYEQRDTGLDFVYPYGPGLGQKIFACIGKVGMAAWLVHQTMLINENRLSPNP 60

QY 61 SHRAFLLEELINKFLFERRVAKPEGYIEPD 89
Db 61 SHRAFLLEELINKFLFERRVAKPEGYIEPD 89

RESULT 3
FETP_XANCP STANDARD; PRT; 92 AA.
AC Q8P829;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=XCC2419;
OS *Xanthomonas campestris* (pv. *campestris*).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A.,
RA Almeida N.F. Jr., Alves L.M.C., do Amaral A.M., Bertolini M.C.,
RA Camargo L.B.A., Camarotte G., Camnava F., Cardozo J., Chambergo F.,
RA Ciapina L.P., Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R.,
RA El-Dorry H., Faria J.B., Ferreira A.J.S., Ferreira R.C.C.,
RA Ferro M.I.T., Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:20:31 ; Search time 18.0433 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MQRIFCEYEQRDTEGIDFV.....LNKFLFRRVAKPEGYIEPD 89

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

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3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
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6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	238	49.3	107	2	US-09-489-039A-11962
2	227	47.0	93	2	US-09-543-681A-5443
3	203.5	42.1	92	2	US-09-328-352-5456
4	198	41.0	122	2	US-09-252-991A-23355
5	150	31.1	110	2	US-09-540-236-2859
6	62	12.8	174	2	US-09-198-452A-158
7	62	12.8	198	2	US-09-438-185A-141
8	62	12.8	645	2	US-09-328-501-1
9	62	12.8	646	2	US-09-777-710A-1
10	62	12.8	646	5	US-10-191-289A-1
11	62	12.8	670	2	US-09-328-501-15
12	62	12.8	670	2	US-09-777-710A-15
13	62	12.8	670	5	US-10-191-289A-15
14	62	12.8	686	2	US-09-252-991A-29396
15	61	12.6	333	2	US-09-107-532A-4544
16	61	12.6	461	2	US-09-107-433-2847
17	60.5	12.4	251	2	US-09-489-039A-7987
18	60	12.4	286	2	US-09-681A-5269
19	59.5	12.3	626	2	US-09-248-796A-27023
20	59.5	12.3	770	2	US-09-543-681A-4291
21	59	12.2	170	2	US-09-489-039A-7536
22	59	12.2	295	2	US-08-952-089A-1
23	59	12.2	295	2	US-09-690-885-1
24	59	12.2	320	2	US-09-248-796A-15469
25	59	12.2	348	1	US-08-844-153-2
26	59	12.2	480	1	US-08-962-203-2
27	59	12.2	480	2	US-09-282-125A-2

28	59	12.2	480	2	US-09-273-142-2	Sequence 2, Appli
29	58.5	12.1	185	2	US-09-270-767-36317	Sequence 36317, A
30	58.5	12.1	185	2	US-09-270-767-51534	Sequence 51534, A
31	58.5	12.1	496	2	US-09-695-795A-8	Sequence 8, Appli
32	58.5	12.1	771	1	US-08-742-753-2	Sequence 2, Appli
33	58	12.0	331	2	US-09-719-108-2	Sequence 2, Appli
34	58	12.0	640	2	US-09-252-991A-23252	Sequence 23252, A
35	58	12.0	776	2	US-09-284-180A-3	Sequence 3, Appli
36	58	12.0	2353	2	US-08-984-709A-50	Sequence 50, Appli
37	57.5	11.9	278	1	US-08-258-261B-20	Sequence 20, Appli
38	57.5	11.9	278	1	US-08-456-837-20	Sequence 20, Appli
39	57.5	11.9	278	1	US-08-457-342-20	Sequence 20, Appli
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43	57.5	11.9	278	1	US-08-729-214-20	Sequence 20, Appli
44	57.5	11.9	278	2	US-09-028-934-20	Sequence 20, Appli
45	57.5	11.9	647	2	US-09-252-991A-32816	Sequence 32816, A
46	57	11.8	184	2	US-09-270-767-46275	Sequence 46275, A
47	57	11.8	293	2	US-09-071-035-496	Sequence 496, App
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51	57	11.8	371	2	US-09-543-681A-6429	Sequence 6429, Ap
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53	57	11.8	379	2	US-09-905-125A-4	Sequence 4, Appli
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64	57	11.8	379	2	US-09-906-722A-4	Sequence 4, Appli
65	57	11.8	380	2	US-09-205-258-441	Sequence 441, App
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67	57	11.8	484	2	US-08-913-578-2	Sequence 2, Appli
68	57	11.8	484	2	US-08-785-427-2	Sequence 2, Appli
69	56.5	11.7	321	2	US-09-107-532A-4975	Sequence 4975, Ap
70	56.5	11.7	357	2	US-09-489-039A-13955	Sequence 13955, A
71	56.5	11.7	394	1	US-08-646-590B-40	Sequence 40, Appli
72	56.5	11.7	394	1	US-09-412-184-40	Sequence 40, Appli
73	56.5	11.7	527	1	US-08-365-486A-26	Sequence 26, Appli
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75	56.5	11.7	1206	2	US-09-252-991A-19632	Sequence 19632, A

ALIGNMENTS

RESULT 1

US-09-489-039A-11962

Sequence 11962, Application US/09489039A

Patent No. 6610836

GENERAL INFORMATION:

APPLICANT: Gary Breton et. al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

FILE REFERENCE: 2709.2004001

CURRENT APPLICATION NUMBER: US/09/489, 039A

CURRENT FILING DATE: 2000-01-27

PRIOR APPLICATION NUMBER: US 60/117, 747

PRIOR FILING DATE: 1999-01-29

NUMBER OF SEQ ID NOS: 14342

SEQ ID NO 11962

LENGTH: 107

TYPE: PRT

ORGANISM: Klebsiella pneumoniae

US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:24:18 ; Search time 56.1572 Seconds
(without alignments)
662.192 Million cell updates/sec

Title: US-09-955-502A-22

Perfect score: 483

Sequence: 1 MQRIFCEYEQRTGIDFV.....LNKFLFERRVAKPEGYIEPD 89

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications_AA_Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	246	50.9	87	3	US-09-955-502-8
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5	234	48.4	91	3	US-09-955-502-5
6	232	48.0	91	3	US-09-955-502-14
7	232	48.0	91	3	US-09-955-502-16
8	230	47.6	91	3	US-09-955-502-17
9	229	47.4	88	3	US-09-955-502-15
10	228	47.2	90	3	US-09-955-502-10
11	226	46.8	91	3	US-09-955-502-11
12	226	46.8	91	3	US-09-955-502-12
13	226	46.8	91	3	US-09-955-502-13
14	226	46.8	91	3	US-09-955-502-13
15	220	45.5	78	3	US-09-955-502-19
16	215	44.5	87	3	US-09-955-502-31
17	214	44.3	88	3	US-09-955-502-33
18	205	42.4	87	3	US-09-955-502-2
19	205	42.4	87	3	US-09-955-502-3
20	203	42.0	90	3	US-09-955-502-20
21	201	41.6	87	3	US-09-955-502-32
22	201	41.6	88	3	US-09-955-502-26
23	201	41.6	88	3	US-09-955-502-27
24	201	41.6	88	3	US-09-955-502-28
25	200	41.4	90	3	US-09-955-502-23
26	198	41.0	87	3	US-09-955-502-24
27	197	40.8	87	3	US-09-955-502-29

28	197	40.8	87	3	US-09-955-502-30	Sequence 30, Appl
29	196	40.6	88	3	US-09-955-502-9	Sequence 9, Appli
30	195	40.4	86	3	US-09-955-502-4	Sequence 4, Appli
31	192	39.8	87	3	US-09-955-502-25	Sequence 25, Appl
32	183	37.9	76	3	US-09-955-502-21	Sequence 21, Appl
33	71	14.7	580	4	US-10-425-115-224020	Sequence 224020,
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ALIGNMENTS

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; Sequence 22, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 89
; TYPE: PRT
; ORGANISM: Xylella fastidiosa

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	61	12.6	379	7	US-11-136-619-2 Sequence 2, Appl
6	58	12.0	351	7	US-11-136-619-14 Sequence 14, Appl
7	58	12.0	776	6	US-10-925-970-3 Sequence 3, Appl
8	57	11.8	378	7	US-11-129-143-49 Sequence 49, Appl
9	57	11.8	379	6	US-10-131-826A-308 Sequence 308, Appl
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12	56	11.6	536	6	US-10-821-231C-1 Sequence 1, Appl
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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwln99, version 1.04

GenCore version 5.1.7
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; Sequence 11, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: Oxygen-labile Proteins
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655

US-09-955-502-11

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RESULT 2

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; Sequence 12, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
;
; LENGTH: 91
;

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Query Match 100.0%; Score 486; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 7.2e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
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; LENGTH: 91
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; TYPE: PRT
;
; ORGANISM: Salmonella paratyphi
US-09-955-502-14

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[illegible]

RESULT 5

US-09-955-502-16
; Sequence 16, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella dublin
US-09-955-502-16

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Query Match	96.5%;	Score 469;	DB 3;	length 91;
Best Local Similarity	94.5%;	Pred. No. 5.9e-45;		
Matches 86;	Conservative 5;	Mismatches 0;	Indels 0;	Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 6.1975 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
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Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	43.8	88	6	US-10-467-657-968 Sequence 968, App
2	66	13.6	593	7	US-11-194-246-317 Sequence 317, App
3	65.5	13.5	395	7	US-11-009-658-46 Sequence 46, Appl
4	65	13.4	478	6	US-10-821-234-915 Sequence 915, App
5	62	12.8	1501	6	US-10-793-626-2850 Sequence 2850, App
6	61.5	12.7	179	6	US-10-467-657-6542 Sequence 6542, App
7	60.5	12.4	264	6	US-10-821-234-1555 Sequence 1555, App
8	60.5	12.4	404	7	US-11-009-658-48 Sequence 48, Appl
9	60.5	12.4	834	6	US-10-453-372-658 Sequence 658, App
10	60	12.3	448	6	US-10-618-320A-25 Sequence 25, Appl
11	60	12.3	480	6	US-10-510-386-12 Sequence 12, Appl
12	60	12.3	667	6	US-10-793-626-198 Sequence 198, App
13	59.5	12.2	177	6	US-10-467-657-1658 Sequence 1658, App
14	59	12.1	266	5	US-09-995-493-6 Sequence 6, Appl
15	59	12.1	604	6	US-10-942-072-4 Sequence 4, Appl
16	59	12.1	1142	7	US-11-109-156-22 Sequence 22, Appl
17	59	12.1	1167	6	US-10-942-072-6 Sequence 6, Appl
18	58.5	12.0	336	6	US-10-453-372-640 Sequence 640, App
19	58.5	12.0	349	6	US-10-821-234-1387 Sequence 1387, App
20	58.5	12.0	577	7	US-11-072-175-187 Sequence 187, App
21	58.5	12.0	695	6	US-10-453-372-648 Sequence 648, App
22	58.5	12.0	700	6	US-10-995-561-922 Sequence 922, App
23	58.5	12.0	700	6	US-10-995-561-924 Sequence 924, App
24	58.5	12.0	775	6	US-10-453-372-656 Sequence 656, App
25	58.5	12.0	793	6	US-10-995-561-925 Sequence 925, App

26	58.5	12.0	804	6	US-10-453-372-650	Sequence 650, App
27	58.5	12.0	847	6	US-10-453-372-654	Sequence 654, App
28	58.5	12.0	857	6	US-10-453-372-652	Sequence 652, App
29	58.5	12.0	905	6	US-10-453-372-638	Sequence 638, App
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32	58.5	12.0	963	6	US-10-995-561-923	Sequence 923, App
33	58.5	12.0	963	6	US-10-453-372-660	Sequence 660, App
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35	58.5	12.0	1299	6	US-10-821-234-1145	Sequence 1145, App
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38	58.5	12.0	5335	6	US-10-995-561-777	Sequence 777, App
39	58.5	12.0	5406	6	US-10-995-561-774	Sequence 774, App
40	58.5	12.0	5415	6	US-10-995-561-779	Sequence 779, App
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42	58.5	12.0	5935	6	US-10-995-561-776	Sequence 776, App
43	58	11.9	251	7	US-11-054-515-1496	Sequence 1496, App
44	58	11.9	1995	7	US-11-069-834-60	Sequence 60, Appl
45	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
46	57	11.7	194	7	US-11-072-512-2906	Sequence 2906, App
47	57	11.7	279	7	US-11-098-686-10812	Sequence 10812, App
48	57	11.7	504	7	US-11-072-512-3467	Sequence 3467, App
49	56	11.5	296	7	US-11-087-227-10	Sequence 10, Appl
50	56	11.5	372	7	US-11-143-986-5	Sequence 5, Appl
51	56	11.5	372	7	US-11-143-986-6	Sequence 6, Appl
52	56	11.5	386	7	US-11-143-986-2	Sequence 2, Appl
53	56	11.5	386	7	US-11-143-986-3	Sequence 3, Appl
54	56	11.5	397	7	US-11-022-562-223	Sequence 223, App
55	56	11.5	426	7	US-11-098-686-10340	Sequence 10340, App
56	56	11.5	427	7	US-11-186-284-91	Sequence 91, Appl
57	56	11.5	581	6	US-10-793-626-28	Sequence 28, Appl
58	56	11.5	697	6	US-10-485-517-202	Sequence 202, App
59	56	11.5	752	6	US-10-793-626-1036	Sequence 1036, App
60	56	11.5	1168	6	US-10-942-072-11	Sequence 11, Appl
61	56	11.5	1188	7	US-11-115-639-42	Sequence 42, Appl
62	56	11.5	1188	7	US-11-115-639-43	Sequence 43, Appl
63	56	11.5	1404	6	US-10-878-556A-169	Sequence 169, App
64	55.5	11.4	207	7	US-11-124-367A-438	Sequence 438, App
65	55.5	11.4	317	7	US-11-124-367A-437	Sequence 437, App
66	55.5	11.4	328	7	US-11-124-367A-436	Sequence 436, App
67	55.5	11.4	440	7	US-11-072-512-3856	Sequence 3856, App
68	55.5	11.4	623	7	US-11-072-512-2547	Sequence 2547, App
69	55.5	11.4	2101	6	US-10-857-780-23	Sequence 23, Appl
70	55	11.3	257	6	US-10-667-295-61	Sequence 61, Appl
71	55	11.3	257	7	US-11-054-515-1710	Sequence 1710, App
72	55	11.3	286	6	US-10-667-295-60	Sequence 60, Appl
73	55	11.3	327	6	US-10-667-295-59	Sequence 59, Appl
74	55	11.3	359	7	US-11-087-227-8	Sequence 8, Appl
75	55	11.3	359	7	US-11-192-450-6	Sequence 6, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-12
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Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	469	96.5	91	5	ABB78162	Abb78162 Amino aci
7	455	93.6	91	5	ABB78163	Abb78163 Amino aci
8	453	93.2	88	5	ABB78160	Abb78160 Amino aci
9	450	92.6	107	7	ABO65445	AbO65445 K1ebsteli
10	402	82.7	90	5	ABB78155	Abb78155 Amino aci
11	396	81.5	90	5	ABB78165	Abb78165 Amino aci
12	395	81.3	78	5	ABB78164	Abb78164 Amino aci
13	389	80.0	93	7	ADP05158	AdP05158 Bacterial
14	388	79.8	91	5	ABB78150	Abb78150 Amino aci
15	387	79.6	87	5	ABB78152	Abb78152 Amino aci
16	379	78.0	87	5	ABB78151	Abb78151 Amino aci
17	373	76.7	87	5	ABB78153	Abb78153 Amino aci
18	332	68.3	88	5	ABB78154	Abb78154 Amino aci
19	265	54.5	76	5	ABB78166	Abb78166 Amino aci
20	255	52.5	87	5	ABB78148	Abb78148 Amino aci
21	255	52.5	87	5	ABB78147	Abb78147 Amino aci
22	241	49.6	86	5	ABB78149	Abb78149 Amino aci
23	231.5	47.6	89	9	AEB41576	Aeb41576 L. pneumo
24	231.5	47.6	95	9	AEB38294	Aeb38294 L. pneumo

25	231	47.5	87	5	ABB78170	Abb78170 Amino aci
26	231	47.5	122	7	ABO74609	AbO74609 Pseudomon
27	227	46.7	88	5	ABB78178	Abb78178 Amino aci
28	227	46.7	90	5	ABB78168	Abb78168 Amino aci
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35	206	42.4	87	5	ABB78175	Abb78175 Amino aci
36	200	41.2	87	5	ABB78174	Abb78174 Amino aci
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43	81	16.7	507	6	AA774372	AaY74372 Neisseria
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46	78	16.0	548	4	ADN46828	Adn46828 Thermococ
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65	70.5	14.5	1206	5	ADe31497	AdE31497 Plant yie
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67	69.5	14.3	374	4	AA894458	AaB94458 Human lac
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ALIGNMENTS

RESULT 1	
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ID	ABB78158 standard; protein; 91 AA.
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AC	ABB78158;
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DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YggX homologue.
XX	
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX	
OS	hydroxyl radical; DNA damage; YggX homologue.
XX	
PN	Unidentified.
XX	
XX	US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
XX
PI Downs D, Gralnick JA;
XX
XX WPI, 2002-589476/63.
DR
XX
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match	100.0%;	Score 486;	DB 5;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 3.1e-48;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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Db 1 MSRTIFCTFLÖREAEAGÖDFÖLYPGBELGKRIYNEISKEAWAÖMÖHKÖTMLINEKLNMMNA 60

QY 61 EHRKLLÖEÖMVNFLFEGKEVHIßGYTPEDKK 91

Db 61 EHRKLLÖEÖMVNFLFEGKEVHIßGYTPEDKK 91

RESULT 2
ABB78157
ID ABB78157 standard: protein: 91 AA.

AC ABB78157;

DT 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium; hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

18-SEP-2001; 2001US-00955502.

22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

XX

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from *Salmonella enterica* serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues

Sequence 91 AA:

Query Match	100.0%;	Score 486;	DB 5;	Length 91;
Best Local Similarity	100.0%;	Pred. NO. 3.1e-48;		
Matches 91; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

QY	1	MSRT	FCTP	LQRE	AGQD	EQLY	PGEL	GKRI	YNEI	SKAW	AQWQ	HKQT	MLIN	EKLN	MNNA	600
Db	1	MSRT <td>FCTP <td>LQRE <td>AGQD <td>EQLY <td>PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td></td></td></td></td></td>	FCTP <td>LQRE <td>AGQD <td>EQLY <td>PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td></td></td></td></td>	LQRE <td>AGQD <td>EQLY <td>PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td></td></td></td>	AGQD <td>EQLY <td>PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td></td></td>	EQLY <td>PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td></td>	PGEL <td>GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td></td>	GKRI <td>YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td></td>	YNEI <td>SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td></td>	SKAW <td>AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td></td>	AQWQ <td>HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td></td>	HKQT <td>MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td></td>	MLIN <td>EKLN <td>MNNA</td> <td>600</td> </td>	EKLN <td>MNNA</td> <td>600</td>	MNNA	600

61 EHRKLEQEMVNFLEGEKVHIEGYTPEDKK 91

Db 61 EHRKLBQEMVNFLEGEKEVHIEGYTPEDKK 91

RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.

AC ABB78156;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a ygxX homologue.

Superoxide damage; cell; yggX; *Salmonella enterica* serovar typhimurium; KW

hydroxyl radical; DNA damage; yggx homologue..

Escherichia coli.

PN US2002072118-A1.

PD 13-JUN-2002.

18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

XX

native amount of YqjX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-12
Perfect score: 486
Sequence: 1 MSRTTCTPFLQREAGGQDFQ.....NFLPEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	486	100.0	91	2 A85954	hypothetical prote
2	486	100.0	91	2 A65082	hypothetical prote
3	486	100.0	91	2 F91108	hypothetical prote
4	469	96.5	91	2 AH0879	conserved hypothet
5	402	82.7	90	2 C82320	conserved hypothet
6	396	81.5	90	2 A10116	conserved hypothet
7	387	79.6	90	2 C64013	hypothetical prote
8	265	54.5	93	2 B84994	hypothetical prote
9	231	47.5	90	2 H83003	conserved hypothet
10	226	46.5	105	2 C82624	conserved hypothet
11	213	43.8	88	2 H81014	conserved hypothet
12	78	16.0	507	2 C81063	fumarate hydratase
13	78	16.0	546	2 A81807	fumarate hydratase
14	76	15.6	548	2 A54510	63K antigen - nema
15	75.5	15.5	1638	2 D87749	protein unc-73b [l
16	75.5	15.5	2488	2 T42739	guanine nucleotide
17	74.5	15.3	683	2 AC2256	hypothetical prote
18	72	14.8	265	2 T46013	hypothetical prote
19	72	14.8	447	2 T16527	hypothetical prote
20	72	14.8	507	2 A83105	probable fumarase
21	72	14.8	511	2 A99574	ABC transporter at
22	69	14.2	258	2 A97991	hypothetical prote
23	69	14.2	258	2 E95121	phosphoesterase, p
24	69	14.2	548	2 A28209	60K filarial antig
25	69	14.2	1119	2 T15842	hypothetical prote
26	68	14.0	2672	2 A48126	translation activa
27	67.5	13.9	209	2 I64172	hypothetical prote
28	67	13.8	235	2 G65212	hypothetical prote
29	67	13.8	324	2 T05429	hypothetical prote

30	67	13.8	433	2 A70465	probable GTP bindi
31	67	13.8	447	2 JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2 T40058	probable chromatin
33	66.5	13.7	1260	2 T04440	hypothetical prote
34	66	13.6	593	2 C64097	probable soluble 1
35	66	13.6	689	2 F83902	beta-galactosidase
36	65.5	13.5	173	2 H86869	hypothetical prote
37	65.5	13.5	305	2 A75211	asparaginase (EC 3
38	65.5	13.5	323	2 A90536	lipoprotein [impor
39	65.5	13.5	365	2 B54128	Fc-binding protein
40	65.5	13.5	821	2 A12417	hypothetical prote
41	65	13.4	251	2 B90428	hypothetical prote
42	65	13.4	330	2 S74456	regulatory protein
43	65	13.4	445	1 XDHUMB	alpha-1,3-mannosyl
44	65	13.4	456	2 G71152	hypothetical prote
45	65	13.4	1008	2 H85055	hypothetical prote
46	65	13.4	1141	2 T29185	probable transposo
47	65	13.4	1230	2 S56850	SMC1 protein homol
48	64.5	13.3	245	2 AG2300	hypothetical prote
49	64.5	13.3	305	2 A71247	probable L-asparag
50	64.5	13.3	495	2 AH0985	probable zinc-proc
51	64.5	13.3	859	2 T29630	hypothetical prote
52	64	13.2	220	2 S62410	hypothetical prote
53	64	13.2	438	2 T37786	probable RNA-bindi
54	64	13.2	447	1 A38561	hypothetical prote
55	64	13.2	583	2 T48365	hypothetical prote
56	64	13.2	604	2 S66993	hypothetical prote
57	64	13.2	990	2 T43445	hypothetical prote
58	64	13.2	1051	2 S27002	phospholipase C (E
59	64	13.2	1234	2 S52099	phospholipase C be
60	64	13.2	1234	2 I38994	phospholipase C-be
61	63.5	13.1	91	2 H90521	hypothetical prote
62	63.5	13.1	243	2 T29635	hypothetical prote
63	63.5	13.1	460	2 T00639	hypothetical prote
64	63.5	13.1	591	1 FOMVMM	gag polyprotein -
65	63	13.0	880	2 AB0179	probable ATPase ch
66	63	13.0	1251	2 A56677	neuronal cell cycl
67	63	13.0	1327	2 T14594	guanidine nucleoti
68	63	13.0	1611	1 WMTMPV	183K protein - pep
69	62.5	12.9	483	1 SYBSET	glutamate-tRNA lig
70	62.5	12.9	551	2 B84106	hypothetical prote
71	62.5	12.9	555	2 C96667	unknown protein, 7
72	62.5	12.9	617	2 B71071	probable prollyl en
73	62.5	12.9	964	2 T04325	probable ATP-depen
74	62.5	12.9	1417	2 T00661	hypothetical prote
75	62	12.8	169	2 PN0560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayner
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousts, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511; F
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yggx
C;Superfamily: fe(II) trafficking protein yggx
Query Match 100.0%; Score 486; DB 2; Length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 2
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)

C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997

A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-91 <BLAT>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein Y9gX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 3

F91108
hypothetical protein Ecs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1

C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796

A;Accession: F91108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <HA>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: Ecs3838
C;Superfamily: fe(II) trafficking protein Y9gX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 4

AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica

C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C;Accession: AH0879
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608

A;Accession: AH0879
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <PAR>
A;Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:gl6504189;
C;Genetics:
A;Gene: STY3266
C;Superfamily: fe(II) trafficking protein Y9gX

Query Match 96.5%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 7.9e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Oy 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKDAAWQHKTMLINEKLANMNA 60

Oy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKDVHIEGYTPEDKK 91

RESULT 5

C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr

C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82320
R;Hiddeberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.,
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301

A;Accession: C82320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN
A;Experimental source: serogroup O1, strain N16961, biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein Y9gX

Query Match 82.7%; Score 402; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 3.6e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Oy 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA 60
Db 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWQHKTMLINEKLANMDP 60

Oy 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-12
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEKGEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	481	99.0	90	1	FETP_ECOS7
2	481	99.0	90	1	FETP_ECOS7
3	481	99.0	90	1	FETP_SHIFL
4	477	98.1	90	1	FETP_ECOL6
5	464	95.5	90	1	FETP_SALCH
6	464	95.5	90	1	FETP_SALPA
7	464	95.5	90	1	FETP_SALTI
8	464	95.5	90	1	FETP_SALTY
9	411	84.6	90	1	FETP_ERWCT
10	404	83.1	90	1	FETP_YERPS
11	402	82.7	90	1	FETP_VIBCH
12	402	82.7	90	1	FETP_VIBVU
13	402	82.7	90	1	FETP_VIBVY
14	399	82.1	90	1	FETP_VIBPA
15	396	81.5	90	1	FETP_YERPE
16	389	80.0	90	1	FETP_MANSN
17	387	79.6	90	1	FETP_HABIN
18	387	79.6	90	2	Q4QMD9_HAB18
19	382	78.6	90	1	FETP_PHOPR
20	381	78.4	90	1	FETP_PASML
21	379	78.0	90	1	FETP_PASML
22	373	76.7	94	1	FETP_HABDU
23	366	75.3	90	1	FETP_VIBF1
24	335	68.9	90	1	FETP_IDILO
25	332	68.3	92	1	FETP_SHEON
26	265	54.5	77	1	FETP_BUCAL
27	255	52.5	90	1	FETP_BORBR
28	255	52.5	90	1	FETP_BORPA
29	255	52.5	90	1	FETP_BORPE
30	247	50.8	78	1	FETP_BUCAP
31	235	48.4	78	1	FETP_WIGBR

32	231.5	47.6	89	1	FETP_LEGPA	Q5x3x9 legionella
33	231.5	47.6	89	1	FETP_LEGPH	Q5zu80 legionella
34	231	47.5	90	1	FETP_PSEAE	Q9hu36 pseudomonas
35	231	47.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
36	228.5	47.0	89	1	FETP_LEGPL	Q5wvc4 legionella
37	227	46.7	90	1	FETP_COXBU	Q83d06 coxiella bu
38	227	46.7	90	1	FETP_PSESM	Q87uf5 pseudomonas
39	227	46.7	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
40	226	46.5	90	1	FETP_XYLPB	Q9pc73 xylella fas
41	225	46.3	90	1	FETP_PSEBK	Q88r49 pseudomonas
42	225	46.3	92	1	FETP_XANOR	Q5gy22 xanthomonas
43	223	45.9	90	2	Q4J228_AZCVI	Q4j228 azotobacter
44	222	45.7	90	1	FETP_XYLPF	Q87d06 xylella fas
45	222	45.7	92	1	FETP_XANCP	Q8p829 xanthomonas
46	222	45.7	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
47	220	45.3	90	1	FETP_NITEU	Q82xf2 nitrosomona
48	215	44.2	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
49	214	44.0	87	1	FETP_BUCBP	Q89a44 buchnera ap
50	213	43.8	88	1	FETP_NEIGI	Q5f553 neisseria g
51	213	43.8	88	1	FETP_NEIMA	Q5f553 neisseria m
52	213	43.8	88	1	FETP_NEIMB	Q5f553 neisseria m
53	212	43.6	79	1	FETP_CANBF	Q7vrg9 candidatus
54	212	43.6	90	2	Q4KJT2_PSEF5	Q4kjt2 pseudomonas
55	211	43.4	90	1	FETP_CHRYO	Q7n8r4 chromobacte
56	207	42.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
57	206	42.4	91	1	FETP_BURMA	Q62iur burkholderi
58	206	42.4	91	1	FETP_BURPS	Q63sj4 burkholderi
59	206	42.4	91	1	FETP_FALSO	Q8y010 ralstonia s
60	200	41.2	90	1	FETP_METCA	Q60ai7 methylococc
61	199	40.9	87	1	FETP_FRAFT	Q5nhj8 francisella
62	194.5	40.0	90	1	FETP_ACTAD	Q6fbf3 acinetobact
63	144	29.6	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	142	29.2	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	90.5	18.6	482	2	Q5NUV1_9BURK	Q5nuv1 ralstonia m
66	85.5	17.6	514	2	Q6AIZ9_DESPS	Q6aiz9 desulfofale
67	81	16.7	507	2	Q88PF3_PSEBK	Q88pf3 pseudomonas
68	81	16.7	508	2	Q7NSFO_CHRYO	Q7nsfo chromobacte
69	80	16.5	486	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
70	78.5	16.2	760	2	Q4YVR2_PLABE	Q4yvr2 plasmidium
71	78	16.0	507	2	Q9JYB3_NEIMB	Q9jyb3 neisseria m
72	78	16.0	546	2	Q9JTE3_NEIMA	Q9jte3 neisseria m
73	78	16.0	2248	2	Q4UB40_THEAN	Q4ub40 theileria a
74	77.5	15.9	337	2	Q8IAR8_BACCR	Q8iar8 bacillus ce
75	77.5	15.9	1123	2	Q7RJL0_PLAYO	Q7rjl0 plasmidium

ALIGNMENTS

RESULT 1
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ID FETP_ECOS7 STANDARD; PRT; 90 AA.
AC POA8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yg9X; Ordered locusNames=z4307, ECS3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
"Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


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RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Iida T., Takami H., Honda T., Saeakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE005174; AAG58093.1; -; Genomic DNA.
DR EMBL; BA000007; BAB37261.1; -; Genomic DNA.
DR PIR; A85954; A85954.
DR PIR; F91108; F91108.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgGX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YgGX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW INIT MET
FT SEQUENCE
SQ 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match          99.0%; Score 481; DB 1; Length 90;
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Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
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AC POA8F3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=ygGX; OrderedLocustNames=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
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RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).

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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphery-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12.";
RL FEMS Microbiol. Lett. 169:375-382(1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxypapillate chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the ygX gene of
RT Escherichia coli.";
RL J. Bacteriol. 185:6624-6632(2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein YgX
RT from Escherichia coli.";
RL Protein Sci. 14:1673-1678(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- INDUCTION: By oxidative stress and soxS.
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; U00096; AAC75999.1; -; Genomic DNA.
DR PIR; A65082; A65082.
DR PDB; 1YHD; NMR; A=1-90.
DR SWISS-2DPAGE; POA8F3; COLI.
DR Echobase; EB2809; -.
DR EcoGene; EG12984; YgGX.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YgGX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YgGX; 1.
DR ProDom; PD029191; DUF495; 1.
DR 3D-structure; Complete proteome; Direct protein sequencing; Iron.
FT INIT MET
FT SEQUENCE
SQ 90 AA; 10821 MW; D7C66C2A35E62402 CRC64;

Query Match          99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTPLQREAEAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLLNMNNAE 61

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
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407.805 Million cell updates/sec

Title: US-09-955-502A-12

Perfect score: 486

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Gapop 10.0 , Gapext 0.5

Searched: 572060 segs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	199.5	41.0	92	2	US-09-328-352-5456, Ap
5	131	27.0	110	2	US-09-540-236-2859, Ap
6	76	15.6	548	2	US-09-167-299-3, Appli
7	72	14.8	474	2	US-09-252-991A-24473, A
8	70.5	14.5	1214	2	US-10-164-595-24, Appl
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41	62.5	12.9	544	2	US-09-248-796A-18911, Sequence 18911, A
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46	62	12.8	1529	2	US-09-134-001C-3945, Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124, Sequence 124, App
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54	61	12.6	308	2	US-09-198-452A-1004, Sequence 1004, Ap
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56	61	12.6	480	2	US-09-438-185A-934, Sequence 934, App
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63	60.5	12.4	640	2	US-10-243-735-2, Sequence 2, Appli
64	60.5	12.4	1076	2	US-09-171-991-7, Sequence 7, Appli
65	60	12.3	98	2	US-09-270-767-41085, Sequence 41085, A
66	60	12.3	98	2	US-09-270-767-56301, Sequence 56301, A
67	60	12.3	184	2	US-09-270-767-61671, Sequence 61671, A
68	60	12.3	271	2	US-09-248-796A-19265, Sequence 19265, A
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70	60	12.3	279	2	US-09-438-185A-205, Sequence 205, App
71	60	12.3	331	2	US-09-328-352-6400, Sequence 6400, Ap
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ALIGNMENTS

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; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	455	93.6	91	3	US-09-955-502-18 Sequence 18, Appl
8	453	93.2	88	3	US-09-955-502-15 Sequence 15, Appl
9	402	82.7	90	3	US-09-955-502-10 Sequence 10, Appl
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12	388	79.8	91	3	US-09-955-502-5 Sequence 5, Appl
13	387	79.6	87	3	US-09-955-502-7 Sequence 7, Appl
14	379	78.0	87	3	US-09-955-502-6 Sequence 6, Appl
15	373	76.7	87	3	US-09-955-502-8 Sequence 8, Appl
16	332	68.3	88	3	US-09-955-502-9 Sequence 9, Appl
17	265	54.5	76	3	US-09-955-502-21 Sequence 21, Appl
18	255	52.5	87	3	US-09-955-502-2 Sequence 2, Appl
19	255	52.5	87	3	US-09-955-502-3 Sequence 3, Appl
20	241	49.6	86	3	US-09-955-502-4 Sequence 4, Appl
21	231	47.5	87	3	US-09-955-502-25 Sequence 25, Appl
22	227	46.7	88	3	US-09-955-502-33 Sequence 33, Appl
23	227	46.7	90	3	US-09-955-502-23 Sequence 23, Appl
24	226	46.5	89	3	US-09-955-502-22 Sequence 22, Appl
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56	67.5	13.9	184	4	US-10-732-923-9369	Sequence 9369, App
57	67.5	13.9	545	5	US-09-874-923-97	Sequence 97, Appl
58	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appl
59	67.5	13.9	546	3	US-10-098-732A-71	Sequence 71, Appl
60	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, App
61	67.5	13.9	955	3	US-09-991-496-127	Sequence 127, App
62	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
63	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
64	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
65	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
66	67.5	13.9	1641	3	US-09-874-923-96	Sequence 96, Appl
67	67.5	13.9	1641	3	US-10-425-114-44570	Sequence 44570, A
68	67.5	13.7	279	4	US-10-424-599-229257	Sequence 229257, A
69	66.5	13.7	675	4	US-10-437-963-195890	Sequence 195890, A
70	66.5	13.7	1026	4	US-10-437-963-189670	Sequence 189670, A
71	66.5	13.7	1374	4	US-10-437-963-189741	Sequence 189741, A
72	66.5	13.7	1588	4	US-10-282-122A-47787	Sequence 47787, A
73	66.5	13.7	507	4	US-10-282-122A-50464	Sequence 50464, A
74	66	13.6	511	4		
75	66	13.6	511	4		

ALIGNMENTS

RESULT 1
US-09-955-502-11
Sequence 11, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 11
LENGTH: 91
TYPE: PRT
ORGANISM: Escherichia coli K-12 MG1655

US-09-955-502-11

Query Match	100.0%;	Score 486;	DB 3;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 7.2e-47;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

[illegible]

RESULT 2

US-09-955-502-12
; Sequence 12, Application US/09955502
; Patent No. US20020072118A1

Query Match	100.0%;	Score 486;	DB 3;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 7.2e-47;		
Matches 91;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

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1 MSRTIFCTFLQREAGGDFQLYPGELGKRIYNEISKEAMVOMQKQTMLINEKCLNNMNA 600

Db 1 MSRTIFCTFLQREAGGDFQLYPGELGKRIYNEISKEAMVOMQKQTMLINEKCLNNMNA 600

QY 61 EHRKLLQEMVNFLEFGKEVHIIEGYTPEDKK 91
61 EHRKLLQEMVNFLEFGKEVHIIEGYTPEDKK 91

Db 61 EHRKLLQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 3

US-09-955-502-13
; Sequence 13, Application US/09955502
; Patent No. US20020072118A1

Query Match 100.0%; Score 486; DB 3; Length 91;

Best Local Similarity 100.0%; Pred. No. 7.2e-47;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

[illegible]

RESULT 4

US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1

Query Match	96.5%	Score 469;	DB 3;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 5.9e-45;		
Matches 86; Conservative		5; Mismatches 0;	Indels 0;	Gaps 0

```

QY      1 MSRTIFCTFLÖREAEQGDÖFÖLYPPELGKRIYNEISCSKAWAQÖHQÖTMLINЕКKLNNWNA      60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1 MSRTIFCTYLÖRDAEGDÖFÖLYPPELGKRIYNEISKDAMAQÖHQÖTMLINЕКKLNNWNA      60
QY      61 EHRKLLQEMVNFLEFGKSVHIEGYTPEDKK      91
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61 EHRKLLQEMVNFLEFGKSVHIEGYTPEDKK      91

```

RESULT 5
US-09-95

Sequence 16, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

Query Match	96.5%;	Score 469;	DB 3;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 5.9e-45;		
Matches 86; Conservative	5;	Mismatches 0;	Indels 0;	Gaps 0

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502A-12

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLPEGKEVHIIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications AA_New:*
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3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	213	43.8	88	6	US-10-467-657-968 Sequence 968, App
2	66	13.6	593	7	US-11-194-246-317 Sequence 317, App
3	65.5	13.5	395	7	US-11-009-658-46 Sequence 46, Appl
4	65	13.4	478	6	US-10-821-234-915 Sequence 915, App
5	62	12.8	1501	6	US-10-793-626-2850 Sequence 2850, App
6	61.5	12.7	179	6	US-10-467-657-6542 Sequence 6542, App
7	60.5	12.4	264	6	US-10-821-234-1555 Sequence 1555, App
8	60.5	12.4	404	7	US-11-009-658-48 Sequence 48, Appl
9	60.5	12.4	834	6	US-10-453-372-658 Sequence 658, App
10	60	12.3	448	6	US-10-618-320A-25 Sequence 25, Appl
11	60	12.3	480	6	US-10-510-386-12 Sequence 12, Appl
12	60	12.3	667	6	US-10-793-626-198 Sequence 198, Appl
13	59.5	12.2	177	6	US-10-467-657-1658 Sequence 1658, App
14	59	12.1	266	5	US-09-995-493-6 Sequence 6, Appli
15	59	12.1	604	6	US-10-942-072-4 Sequence 4, Appli
16	59	12.1	1142	7	US-11-109-156-22 Sequence 22, Appl
17	59	12.1	1167	6	US-10-942-072-6 Sequence 6, Appli
18	58.5	12.0	336	6	US-10-453-372-640 Sequence 640, App
19	58.5	12.0	349	6	US-10-821-234-1387 Sequence 1387, App
20	58.5	12.0	577	7	US-11-072-175-187 Sequence 187, App
21	58.5	12.0	695	6	US-10-453-372-648 Sequence 648, App
22	58.5	12.0	700	6	US-10-995-561-922 Sequence 922, App
23	58.5	12.0	700	6	US-10-995-561-924 Sequence 924, App
24	58.5	12.0	775	6	US-10-453-372-656 Sequence 656, App
25	58.5	12.0	793	6	US-10-995-561-925 Sequence 925, App

26	58.5	12.0	804	6	US-10-453-372-650 Sequence 650, App
27	58.5	12.0	847	6	US-10-453-372-654 Sequence 654, App
28	58.5	12.0	857	6	US-10-453-372-652 Sequence 652, App
29	58.5	12.0	905	6	US-10-453-372-638 Sequence 638, App
30	58.5	12.0	905	6	US-10-453-372-662 Sequence 662, App
31	58.5	12.0	905	6	US-10-453-372-664 Sequence 664, App
32	58.5	12.0	963	6	US-10-995-561-923 Sequence 923, App
33	58.5	12.0	963	6	US-10-453-372-660 Sequence 660, App
34	58.5	12.0	1012	6	US-10-453-372-646 Sequence 646, App
35	58.5	12.0	1299	6	US-10-821-234-1145 Sequence 1145, App
36	58.5	12.0	3960	6	US-10-995-561-773 Sequence 773, App
37	58.5	12.0	3960	6	US-10-995-561-771 Sequence 771, App
38	58.5	12.0	5335	6	US-10-995-561-777 Sequence 777, App
39	58.5	12.0	5406	6	US-10-995-561-774 Sequence 774, App
40	58.5	12.0	5415	6	US-10-995-561-779 Sequence 779, App
41	58.5	12.0	5464	6	US-10-995-561-775 Sequence 775, App
42	58.5	12.0	5935	6	US-10-995-561-776 Sequence 776, App
43	58	11.9	251	7	US-11-054-515-1496 Sequence 1496, App
44	58	11.9	1995	7	US-11-069-834-60 Sequence 60, Appl
45	57.5	11.8	752	7	US-11-072-512-3003 Sequence 3003, App
46	57	11.7	194	7	US-11-072-512-2906 Sequence 2906, App
47	57	11.7	279	7	US-11-098-686-10812 Sequence 10812, App
48	57	11.7	504	7	US-11-072-512-3467 Sequence 3467, App
49	56	11.5	296	7	US-11-087-227-10 Sequence 10, Appl
50	56	11.5	372	7	US-11-143-986-5 Sequence 5, Appli
51	56	11.5	372	7	US-11-143-986-6 Sequence 6, Appli
52	56	11.5	386	7	US-11-143-986-2 Sequence 2, Appli
53	56	11.5	386	7	US-11-143-986-3 Sequence 3, Appli
54	56	11.5	397	7	US-11-022-562-223 Sequence 223, App
55	56	11.5	426	7	US-11-098-686-10340 Sequence 10340, A
56	56	11.5	427	7	US-11-186-284-91 Sequence 91, Appl
57	56	11.5	581	6	US-10-793-626-28 Sequence 28, Appl
58	56	11.5	697	6	US-10-485-517-202 Sequence 202, App
59	56	11.5	752	6	US-10-793-626-1036 Sequence 1036, App
60	56	11.5	1168	6	US-10-942-072-11 Sequence 11, Appl
61	56	11.5	1188	7	US-11-115-639-42 Sequence 42, Appl
62	56	11.5	1188	7	US-11-115-639-43 Sequence 43, Appl
63	56	11.5	1404	6	US-10-878-556A-169 Sequence 169, App
64	55.5	11.4	207	7	US-11-124-367A-438 Sequence 438, App
65	55.5	11.4	317	7	US-11-124-367A-437 Sequence 437, App
66	55.5	11.4	328	7	US-11-124-367A-436 Sequence 436, App
67	55.5	11.4	440	7	US-11-072-512-3856 Sequence 3856, App
68	55.5	11.4	623	7	US-11-072-512-2547 Sequence 2547, App
69	55.5	11.4	2101	6	US-10-857-780-23 Sequence 23, Appl
70	55	11.3	257	6	US-10-667-295-61 Sequence 61, Appl
71	55	11.3	257	7	US-11-054-515-1710 Sequence 1710, App
72	55	11.3	286	6	US-10-667-295-60 Sequence 60, Appl
73	55	11.3	327	6	US-10-667-295-59 Sequence 59, Appl
74	55	11.3	359	7	US-11-087-227-8 Sequence 8, Appli
75	55	11.3	359	7	US-11-192-450-6 Sequence 6, Appli

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-13
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGGDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*
1: geneseqp1980s:*
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3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	486	100.0	91	5	ABB78158 Amino aci
2	486	100.0	91	5	ABB78157 Amino aci
3	486	100.0	91	5	ABB78156 Amino aci
4	469	96.5	91	5	ABB78161 Amino aci
5	469	96.5	91	5	ABB78159 Amino aci
6	469	96.5	91	5	ABB78162 Amino aci
7	455	93.6	91	5	ABB78163 Amino aci
8	453	93.2	88	5	ABB78160 Amino aci
9	450	92.6	107	7	ABO65445 Amino aci
10	402	82.7	90	5	ABB78155 Amino aci
11	396	81.5	90	5	ABB78165 Amino aci
12	395	81.3	78	5	ABB78164 Amino aci
13	389	80.0	93	7	ADFO5158 Bacterial
14	388	79.8	91	5	ABB78150 Amino aci
15	387	79.6	87	5	ABB78152 Amino aci
16	379	78.0	87	5	ABB78151 Amino aci
17	373	76.7	87	5	ABB78153 Amino aci
18	332	68.3	88	5	ABB78154 Amino aci
19	265	54.5	76	5	ABB78166 Amino aci
20	255	52.5	87	5	ABB78148 Amino aci
21	255	52.5	87	5	ABB78147 Amino aci
22	241	49.6	86	5	ABB78149 Amino aci
23	231.5	47.6	89	9	AEB41576 L. pneumo
24	231.5	47.6	95	9	AEB38294 L. pneumo

25	231	47.5	87	5	ABB78170 Amino aci
26	231	47.5	122	7	ABO74609 Pseudomon
27	227	46.7	88	5	ABB78178 Amino aci
28	227	46.7	90	5	ABB78168 Amino aci
29	225	46.3	87	5	ABB78169 Amino aci
30	216.5	44.5	90	5	ABB78167 Amino aci
31	213	43.8	88	5	ABB78171 Amino aci
32	213	43.8	88	5	ABB78172 Amino aci
33	213	43.8	88	5	ABB78173 Amino aci
34	213	43.8	88	6	ABP77219 N. gonorr
35	206	42.4	87	5	ABB78175 Amino aci
36	200	41.2	87	5	ABB78177 Amino aci
37	200	41.2	87	5	ABB78174 Amino aci
38	200	41.2	87	5	ABB78176 Amino aci
39	199.5	41.0	92	6	ADA34169 Acinetoba
40	131	27.0	110	8	ADL05173 M. catarr
41	83	17.1	506	3	AAV74371 Neisseria
42	83	17.1	1647	4	ABG10750 Novel hum
43	81	16.7	507	6	ABU40210 Protein e
44	78	16.0	507	3	AAV74372 Neisseria
45	78	16.0	507	3	AAV74373 Neisseria
46	78	16.0	546	6	ABU38097 Protein e
47	76	15.6	548	4	AAE04737 Brugia ma
48	75	15.4	309	8	ADN46828 Thermococ
49	74.5	15.3	632	8	ADS29711 Bacterial
50	72	14.8	474	7	ABO75727 Pseudomon
51	71.5	14.7	679	9	ADZ85056 Partial F
52	71	14.6	311	7	ADM26256 Hyperther
53	70.5	14.5	285	4	AAAB92683 Human pro
54	70.5	14.5	414	6	ABU11747 Human MDD
55	70.5	14.5	614	9	ADY16108 PRO polyP
56	70.5	14.5	614	9	ADY16108 PRO polyP
57	70.5	14.5	764	5	ABB77432 Human tum
58	70.5	14.5	764	7	ADC99062 Human KRP
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61	70.5	14.5	1135	8	ADS10706 Human the
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64	70.5	14.5	1188	8	ADH45460 Human mol
65	70.5	14.5	1206	5	ADH48860 NOV61 pro
66	70.5	14.5	1214	7	ADK65785 Angiogene
67	69.5	14.3	374	4	AAAM39682 Human pol
68	69.5	14.3	389	4	AAAM41468 Human pol
69	69.5	14.3	481	5	AAU93169 Arabidops
70	69.5	14.3	481	7	ADD30148 Plant yie
71	69.5	14.3	481	7	ADZ31497 Plant yie
72	69.5	14.3	481	8	ADL41933 Plant tra
73	69.5	14.3	485	5	ABB08477 Human lat
74	69.5	14.3	488	4	AAAB94458 Human pro
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ALIGNMENTS

RESULT 1	ABB78158	standard; protein; 91 AA.
ID	ABB78158;	
AC	ABB78158;	
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DT	05-NOV-2002	(first entry)
DE	Amino acid sequence of a YggX homologue.	
XX		
KW	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
XX	hydroxyl radical; DNA damage; YggX homologue.	
OS	Unidentified.	
XX		
PN	US2002072118-A1.	
XX		

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60
|||
1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60

Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||
61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX
AC ABB78157;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||
1 MSRTIFCTFLQREAGQDFOLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLNMMNA 60

Db 61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91
|||
61 EHRKLEQEMVNFLEFGKEVHIEGYTPEDKK 91

RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.

AC ABB78156;

DT 05-NOV-2002 (first entry)

DE Amino acid sequence of a YggX homologue.

KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Escherichia coli.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

PD WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-13
Perfect score: 486
Sequence: 1 MSRTFCTFLQREABGDFQ.....NFLPEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	486	100.0	91	2 A85954	hypothetical prote
2	486	100.0	91	2 A65082	hypothetical prote
3	486	100.0	91	2 F91108	hypothetical prote
4	469	96.5	91	2 AH0879	conserved hypothet
5	402	82.7	90	2 C82320	conserved hypothet
6	396	81.5	90	2 A10116	conserved hypothet
7	387	79.6	90	2 C64013	hypothetical prote
8	265	54.5	93	2 E84994	hypothetical prote
9	231	47.5	90	2 H83003	conserved hypothet
10	226	46.5	105	2 C82624	conserved hypothet
11	213	43.8	88	2 H81014	conserved hypothet
12	78	16.0	507	2 C81063	fumarate hydratase
13	78	16.0	546	2 A81807	fumarate hydratase
14	76	15.6	548	2 A54510	63k antigen - nema
15	75.5	15.5	1638	2 D87749	protein unc-73b [l
16	75.5	15.5	2488	2 T42739	guanine nucleotide
17	74.5	15.3	683	2 AC2256	hypothetical prote
18	72	14.8	265	2 T46013	hypothetical prote
19	72	14.8	447	2 T16527	hypothetical prote
20	72	14.8	507	2 A83105	probable fumarase
21	72	14.8	511	2 A99574	ABC transporter at
22	69	14.2	258	2 A97991	hypothetical prote
23	69	14.2	258	2 E95121	phosphoesterase, p
24	69	14.2	548	2 A28209	60k filarial antig
25	69	14.2	1119	2 T15842	hypothetical prote
26	68	14.0	2672	2 A48126	translation activa
27	67.5	13.9	209	2 I64172	hypothetical prote
28	67	13.8	235	2 G65212	hypothetical prote
29	67	13.8	324	2 T05429	hypothetical prote

30	67	13.8	433	2 A70465	probable GTP bindi
31	67	13.8	447	2 JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2 T40058	probable chromatin
33	66.5	13.7	1260	2 T04440	hypothetical prote
34	66	13.6	593	2 C64097	probable soluble 1
35	66	13.6	689	2 F83902	beta-galactosidase
36	65.5	13.5	173	2 H86869	hypothetical prote
37	65.5	13.5	305	2 A75211	asparaginase (EC 3
38	65.5	13.5	323	2 A90536	lipoprotein (limpor
39	65.5	13.5	365	2 B54128	Fe-binding protein
40	65.5	13.5	821	2 A12417	hypothetical prote
41	65	13.4	251	2 E90428	hypothetical prote
42	65	13.4	330	2 S74456	regulatory protein
43	65	13.4	445	1 XUHUMB	alpha-1,3-mannosyl
44	65	13.4	456	2 G71152	hypothetical prote
45	65	13.4	1008	2 H85055	probable transposo
46	65	13.4	1141	2 T29185	hypothetical prote
47	65	13.4	1230	2 S56850	SMC1 protein homol
48	64.5	13.3	245	2 AG2300	hypothetical prote
49	64.5	13.3	305	2 A71247	probable L-asparag
50	64.5	13.3	495	2 AH0985	probable zinc-prot
51	64.5	13.3	859	2 T29630	hypothetical prote
52	64	13.2	220	2 S62410	hypothetical prote
53	64	13.2	438	2 T37786	probable RNA-bind
54	64	13.2	447	1 A38561	alpha-1,3-mannosyl
55	64	13.2	583	2 T48365	hypothetical prote
56	64	13.2	604	2 S66993	hypothetical prote
57	64	13.2	990	2 T43445	phospholipase C (E
58	64	13.2	1051	2 S27002	phospholipase C (E
59	64	13.2	1234	2 S52099	phospholipase C be
60	64	13.2	1234	2 I38994	phospholipase C-be
61	63.5	13.1	91	2 H90521	hypothetical prote
62	63.5	13.1	243	2 T29635	hypothetical prote
63	63.5	13.1	460	2 T00639	hypothetical prote
64	63.5	13.1	591	1 FOMVMM	gag polyprotein -
65	63	13.0	880	2 AB0179	probable ATPase ch
66	63	13.0	1251	2 A56677	neuronal cell cycl
67	63	13.0	1327	2 T14594	guanidine nucleoti
68	63	13.0	1611	1 WMTMPV	183k protein - pep
69	62.5	12.9	483	1 SYBSET	glutamate-tRNA lig
70	62.5	12.9	551	2 E84106	hypothetical prote
71	62.5	12.9	555	2 C96667	unknown protein, 7
72	62.5	12.9	617	2 B71071	probable prollyl en
73	62.5	12.9	964	2 T04325	probable ATP-depen
74	62.5	12.9	1417	2 T00661	hypothetical prote
75	62	12.8	169	2 PNO560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL9:
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamouisis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:G12517511;
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yggx
C:Superfamily: fe(II) trafficking protein Yggx
Query Match 100.0%; Score 486; DB 2; length 91;

Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60
Db 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 2

A65082 hypothetical protein b2962 - Escherichia coli (strain K-12)

C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C.
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BIAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB000378; GB:U00096; NID:9
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60
Db 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 3

F91108

hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RI
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 486; DB 2; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60
Db 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 4

AH0879

conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0879
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:gl6504189;
C/Genetics:
A/Gene: STY3266
C/Superfamily: fe(II) trafficking protein YggX

Query Match 96.5%; Score 469; DB 2; Length 91;
Best Local Similarity 94.5%; Pred. No. 7.9e-40;
Matches 86; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60
Db 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60

QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91
Db 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDKK 91

RESULT 5

C82320

conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serog
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heidelberg, J.F.; Eissen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.,
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, J
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein YggX

Query Match 82.7%; Score 402; DB 2; Length 90;
Best Local Similarity 83.3%; Pred. No. 3.6e-33;
Matches 75; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MSRTTCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKNMNA 60
Db 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKAEAWAQWQHKTMLINEKKNMMDP 60

QY 61 EHRKLEQEMVNFLEFGKEVHIIEGYTPEDK 90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-13
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGGDFQ.....NFLFEKKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	481	99.0	90 1 FETP_ECO57	P0a8p4 escherichia
2	481	99.0	90 1 FETP_ECOLI	P0a8p3 escherichia
3	481	99.0	90 1 FETP_SHIFL	P0a8p5 shigella fl
4	477	98.1	90 1 FETP_ECOL6	Q8fe19 escherichia
5	464	95.5	90 1 FETP_SALCH	Q57k04 salmonella
6	464	95.5	90 1 FETP_SALPA	Q5pmn1 salmonella
7	464	95.5	90 1 FETP_SALTI	P67618 salmonella
8	464	95.5	90 1 FETP_SALTY	P67617 salmonella
9	411	84.6	90 1 FETP_ERWCT	Q6d8j9 erwinia car
10	404	83.1	90 1 FETP_YERPS	Q66m3 yersinia ps
11	402	82.7	90 1 FETP_VIBCH	Q9kura4 vibrio chol
12	402	82.7	90 1 FETP_VIBVU	Q8dc5 vibrio vuln
13	402	82.7	90 1 FETP_VIBVY	Q7mb14 vibrio vuln
14	399	82.1	90 1 FETP_VIBPA	Q87115 vibrio para
15	396	81.5	90 1 FETP_YERPE	Q8zhe7 yersinia pe
16	389	80.0	90 1 FETP_MANSN	Q65vt7 mannheimia
17	387	79.6	90 1 FETP_HABIN	P44048 haemophilus
18	387	79.6	90 2 Q4QMD9_HAB18	Q4qmd9 haemophilus
19	382	78.6	90 1 FETP_PHOPR	Q6lmk7 photobacter
20	381	78.4	90 1 FETP_PHOLL	Q7n711 photorhabdu
21	379	78.0	90 1 FETP_PASMU	Q9c1b9 pasteurella
22	373	76.7	90 1 FETP_HABDU	Q9vkb6 haemophilus
23	366	75.3	90 1 FETP_VIBF1	Q5e7c0 vibrio fisc
24	335	68.9	90 1 FETP_IDILO	Q5gy58 idiomarina
25	332	68.3	92 1 FETP_SHON	Q8ebx6 shewanella
26	265	54.5	77 1 FETP_BUCAI	P57618 buchnera ap
27	255	52.5	90 1 FETP_BORBR	Q7wh06 bordetella
28	255	52.5	90 1 FETP_BORPA	Q7w9q2 bordetella
29	255	52.5	90 1 FETP_BORPE	Q7wvc4 bordetella
30	247	50.8	78 1 FETP_BUCAP	Q8k925 buchnera ap
31	235	48.4	78 1 FETP_WIGBR	Q8d3c5 wigglewort

32	231.5	47.6	89 1	FETP_LEGPA	Q5x3x9 legionella
33	231.5	47.6	89 1	FETP_LEGPH	Q5zu80 legionella
34	231	47.5	90 1	FETP_PSEAE	Q9hu36 pseudomonas
35	231	47.5	91 1	FETP_XANAC	Q8pjh7 xanthomonas
36	228.5	47.0	89 1	FETP_LEGPI	Q5wvc4 legionella
37	227	46.7	90 1	FETP_COXBU	Q83d06 coxiella bu
38	227	46.7	90 1	FETP_PSESM	Q87uf5 pseudomonas
39	227	46.7	90 2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
40	226	46.5	90 1	FETP_XYLFA	Q9pc73 xylella fas
41	225	46.3	90 1	FETP_PSEBK	Q88r49 pseudomonas
42	225	46.3	92 1	FETP_XANOR	Q5gy22 xanthomonas
43	223	45.9	90 2	Q4J228_AZOV1	Q4j228 azotobacter
44	222	45.7	90 1	FETP_XYLFT	Q87d06 xylella fas
45	222	45.7	92 1	FETP_XANCP	Q8p829 xanthomonas
46	222	45.7	92 2	Q4UW14_XANCP	Q4uw14 xanthomonas
47	220	45.3	90 1	FETP_NITEU	Q82xf2 nitrosomona
48	215	44.2	90 2	Q6TTF6_PSEFL	Q82xf6 pseudomonas
49	214	44.0	87 1	FETP_BUCBP	Q89a44 buchnera ap
50	213	43.8	88 1	FETP_NEIG1	Q5f553 neisseria m
51	213	43.8	88 1	FETP_NEIMA	P67615 neisseria m
52	213	43.8	88 1	FETP_NEIMB	P67616 neisseria m
53	212	43.6	79 1	FETP_CANBF	Q7vr99 candidatus
54	212	43.6	90 2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
55	211	43.4	90 1	FETP_CHRVO	Q7nsr4 chromobacte
56	207	42.6	91 2	Q4LS19_9BURK	Q4ls19 burkholderi
57	206	42.4	91 1	FETP_BURMA	Q62ius burkholderi
58	206	42.4	91 1	FETP_BURPS	Q63s14 burkholderi
59	206	42.4	91 1	FETP_RALSO	Q8y010 ralstonia s
60	200	41.2	90 1	FETP_METCA	Q60a17 methylococc
61	199	40.9	87 1	FETP_FRAAT	Q5nhj8 francisella
62	194.5	40.0	90 1	FETP_ACIAD	Q6fjb3 acinetobact
63	144	29.6	96 2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	142	29.2	92 2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	90.5	18.6	482 2	Q5NUV1_9BURK	Q5nuv1 ralstonia m
66	85.5	17.6	514 2	Q6AIZ9_DESPS	Q6aiz9 desulfotale
67	81	16.7	507 2	Q8BPF3_PSEPK	Q8bpf3 pseudomonas
68	81	16.7	508 2	Q7NSFO_CHRVO	Q7nsf0 chromobacte
69	80	16.5	486 2	Q7WXS1_ALCEU	Q7wx51 alcaligenes
70	78.5	16.2	760 2	Q4YVR2_PLABE	Q4yvr2 plasmidium
71	78	16.0	507 2	Q9JYB3_NEIMB	Q9jye3 neisseria m
72	78	16.0	546 2	Q9JYB3_NEIMA	Q9jye3 neisseria m
73	78	16.0	2248 2	Q4UB40_THEAN	Q4ub40 theileria a
74	77.5	15.9	337 2	Q81AR6_BACCR	Q81ar6 bacillus ce
75	77.5	15.9	1123 2	Q7RJ10_PLAYO	Q7rj10 plasmidium

ALIGNMENTS

RESULT 1
FETP_ECO57
ID FETP_ECO57 STANDARD; PRT; 90 AA.
AC P0A8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; Ordered locus names=z4307, Ecs3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Postai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoukis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


```
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tohe T.,
RA Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AE005174; AAG58093.1; -; Genomic_DNA.
DR EMBL; BA000007; BAB37261.1; -; Genomic_DNA.
DR PIR; A85954; A85954.
DR PIR; F91108; F91108.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
KW INIT MET
FT INIT MET
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match          99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREABGQDFOLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNAE 61
Db 1 SRTIFCTFLQREABGQDFOLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNAE 60

QY 62 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 91
Db 61 HRKLLQEMVNFLEFGKEVHIEGYTPEDKK 90

RESULT 2
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AC P0A8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, last sequence update)
DT 13-SEP-2005 (Rel. 48, last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; Ordered locus names=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12.";
RL FEBS Microbiol. Lett. 169:375-382(1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the yggX gene of
RT Escherichia coli.";
RL J. Bacteriol. 185:6624-6632(2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/ps.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein YggX
RT from Escherichia coli.";
RL Protein Sci. 14:1673-1678(2005).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -1- SUBUNIT: Monomer (Probable).
CC -1- INDUCTION: By oxidative stress and soxS.
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; U28377; AAA69129.1; -; Genomic_DNA.
DR EMBL; U00096; AAC75999.1; -; Genomic_DNA.
DR PIR; A65082; A65082.
DR PDB; 1YHD; NMR; A=1-90.
DR SWISS-2DPAGE; P0A8P3; COLI.
DR Echobase; EB2809; -.
DR Ecogene; EG12984; yggX.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR 3D-structure; Complete proteome; Direct protein sequencing; Iron.
KW INIT MET
FT INIT MET
SQ SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match          99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTFLQREABGQDFOLYPGLGKRIYNEISKEAWAQWQHQTMLINEKKNMNAE 61
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-13

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEKRVHIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-2859
6	76	15.6	548	2	US-09-167-299-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	2	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
13	67.5	13.9	546	2	US-09-551-974A-2
14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
16	67.5	13.9	546	2	US-09-874-923-2
17	67.5	13.9	546	2	US-08-798-841-2
18	67.5	13.9	982	2	US-09-551-974A-95
19	67.5	13.9	982	2	US-09-565-501A-95
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22	67.5	13.9	1427	2	US-09-551-974A-97
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25	67.5	13.9	1427	2	US-09-874-923-97
26	67.5	13.9	1641	2	US-09-551-974A-96
27	67.5	13.9	1641	2	US-09-565-501A-96

28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	395	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5836	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998E-37	Sequence 37, Appl
35	64	13.2	448	2	US-09-270-767-42959	Sequence 42959, A
36	64	13.2	534	2	US-09-312-762A-5	Sequence 5, Appli
37	63.5	13.1	591	2	US-09-370-368-8	Sequence 8, Appli
38	63	13.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
39	63	13.0	569	2	US-09-107-532A-6689	Sequence 6689, Ap
40	62.5	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-18911	Sequence 18911, A
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
43	62	12.8	959	2	US-09-543-681A-6879	Sequence 6879, Ap
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45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 124, App
48	61.5	12.7	116	2	US-09-562-737-125	Sequence 125, App
49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 26397, A
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 7295, Ap
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 4, Appli
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1, Appli
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 1004, Ap
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 16, Appl
55	61	12.6	444	2	US-09-861-451A-16	Sequence 934, App
56	61	12.6	480	2	US-09-438-185A-934	Sequence 4802, Ap
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 6012, Ap
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 4800, Ap
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 11703, A
60	60.5	12.4	276	2	US-09-949-016-11703	Sequence 48, Appl
61	60.5	12.4	404	2	US-09-914-098-48	Sequence 2, Appli
62	60.5	12.4	640	2	US-09-873-404-2	Sequence 7, Appli
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64	60.5	12.4	1076	2	US-09-171-991-7	Sequence 56301, A
65	60	12.3	98	2	US-09-270-767-41085	Sequence 61671, A
66	60	12.3	98	2	US-09-270-767-56301	Sequence 19265, A
67	60	12.3	184	2	US-09-270-767-61671	Sequence 221, App
68	60	12.3	271	2	US-09-248-796A-19265	Sequence 205, App
69	60	12.3	279	2	US-09-198-452A-221	Sequence 6400, Ap
70	60	12.3	279	2	US-09-438-185A-205	Sequence 41746, A
71	60	12.3	331	2	US-09-328-352-6400	Sequence 8705, Ap
72	60	12.3	337	2	US-09-270-767-41746	Sequence 32, Appl
73	60	12.3	389	2	US-09-270-767-46116	
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75	60	12.3	411	2	US-09-886-319A-32	

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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RESULT 2
US-09-543-681A-5443

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; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
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; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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RESULT 3
US-09-25

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; Sequence 23355, Application US/09252991A
; Patent NO. 6551795
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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
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; LENGTH: 122
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; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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QY 61 EHRKLLBQEMVNFLEEGKEVHIIGYTP 87

Db 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352

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; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
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; TYPE: PR
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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RESULT 5
US-09-540-236-2859

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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
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; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
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US-09-540-236-2859

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QY 65 LLEQEMVNFLEFGKEVHIIEGYTP 87
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Db 85 YINEQREKFLDNGDYEKPAGYKP 107

RESULT 6
US-09-167-299-3

Sequence 3, Application US/09167299

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-13

Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	486	100.0	91	3	US-09-955-502-13 Sequence 13, Appl
4	469	96.5	91	3	US-09-955-502-14 Sequence 14, Appl
5	469	96.5	91	3	US-09-955-502-16 Sequence 16, Appl
6	469	96.5	91	3	US-09-955-502-17 Sequence 17, Appl
7	455	93.6	91	3	US-09-955-502-18 Sequence 18, Appl
8	453	93.2	88	3	US-09-955-502-15 Sequence 15, Appl
9	402	82.7	90	3	US-09-955-502-20 Sequence 20, Appl
10	396	81.5	90	3	US-09-955-502-20 Sequence 20, Appl
11	395	81.3	78	3	US-09-955-502-19 Sequence 19, Appl
12	388	79.8	91	3	US-09-955-502-5 Sequence 5, Appl
13	387	79.6	87	3	US-09-955-502-7 Sequence 7, Appl
14	379	78.0	87	3	US-09-955-502-6 Sequence 6, Appl
15	373	76.7	87	3	US-09-955-502-8 Sequence 8, Appl
16	332	68.3	88	3	US-09-955-502-9 Sequence 9, Appl
17	265	54.5	76	3	US-09-955-502-21 Sequence 21, Appl
18	255	52.5	87	3	US-09-955-502-2 Sequence 2, Appl
19	255	52.5	87	3	US-09-955-502-3 Sequence 3, Appl
20	241	49.6	86	3	US-09-955-502-4 Sequence 4, Appl
21	231	47.5	87	3	US-09-955-502-25 Sequence 25, Appl
22	227	46.7	88	3	US-09-955-502-33 Sequence 33, Appl
23	227	46.7	90	3	US-09-955-502-23 Sequence 23, Appl
24	226	46.5	89	3	US-09-955-502-22 Sequence 22, Appl
25	225	46.3	87	3	US-09-955-502-24 Sequence 24, Appl
26	213	43.8	88	3	US-09-955-502-26 Sequence 26, Appl
27	213	43.8	88	3	US-09-955-502-27 Sequence 27, Appl

28	213	43.8	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.4	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.4	87	3	US-09-955-502-30	Sequence 30, Appl
31	200	41.2	87	3	US-09-955-502-31	Sequence 31, Appl
32	200	41.2	87	3	US-09-955-502-32	Sequence 32, Appl
33	83	17.1	1647	5	US-10-450-763-41109	Sequence 41109, A
34	81	16.7	507	4	US-10-282-122A-68134	Sequence 68134, A
35	78	16.0	546	4	US-10-282-122A-66021	Sequence 66021, A
36	74.5	15.3	632	4	US-10-369-493-18744	Sequence 18744, A
37	71.5	14.7	679	5	US-10-805-684-105	Sequence 105, App
38	70.5	14.5	764	4	US-10-416-330-37	Sequence 37, Appl
39	70.5	14.5	764	5	US-10-491-467-15	Sequence 15, Appl
40	70.5	14.5	786	5	US-10-732-923-4885	Sequence 4885, Ap
41	70.5	14.5	1206	4	US-10-085-198-144	Sequence 144, App
42	70.5	14.5	1214	5	US-10-717-665-24	Sequence 24, Appl
43	69.5	14.3	481	3	US-09-934-455-466	Sequence 466, App
44	69.5	14.3	481	4	US-10-225-066A-180	Sequence 180, App
45	69.5	14.3	481	4	US-10-225-067-64	Sequence 64, Appl
46	69.5	14.3	481	4	US-10-374-780A-396	Sequence 396, App
47	69.5	14.3	481	5	US-10-225-066A-180	Sequence 180, App
48	69.5	14.3	561	4	US-10-437-963-169643	Sequence 169643, A
49	69.5	14.3	660	6	US-11-097-143-24705	Sequence 24705, A
50	69.5	14.3	1261	4	US-10-437-963-189166	Sequence 189166, A
51	69	14.2	258	4	US-10-415-478A-36	Sequence 36, Appl
52	69	14.2	258	5	US-10-472-928-2088	Sequence 2088, Ap
53	68.5	14.1	184	4	US-10-393-840-52	Sequence 52, Appl
54	68	14.0	102	3	US-09-864-408A-768	Sequence 768, App
55	67.5	13.9	184	4	US-10-219-220-66	Sequence 66, Appl
56	67.5	13.9	184	4	US-10-393-840-118	Sequence 118, App
57	67.5	13.9	545	5	US-10-732-923-9369	Sequence 9369, Ap
58	67.5	13.9	546	3	US-09-874-923-2	Sequence 2, Appl
59	67.5	13.9	546	3	US-09-991-496-2	Sequence 2, Appl
60	67.5	13.9	546	4	US-10-098-732A-71	Sequence 71, Appl
61	67.5	13.9	926	3	US-09-991-496-128	Sequence 128, App
62	67.5	13.9	955	3	US-09-991-496-127	Sequence 127, App
63	67.5	13.9	982	3	US-09-874-923-95	Sequence 95, Appl
64	67.5	13.9	982	3	US-09-991-496-95	Sequence 95, Appl
65	67.5	13.9	1427	3	US-09-874-923-97	Sequence 97, Appl
66	67.5	13.9	1427	3	US-09-991-496-97	Sequence 97, Appl
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68	67.5	13.9	1641	3	US-09-991-496-96	Sequence 96, Appl
69	66.5	13.7	279	4	US-10-425-114-44570	Sequence 44570, A
70	66.5	13.7	675	4	US-10-424-599-229257	Sequence 229257, A
71	66.5	13.7	1026	4	US-10-437-963-195890	Sequence 195890, A
72	66.5	13.7	1374	4	US-10-437-963-189670	Sequence 189670, A
73	66.5	13.7	1588	4	US-10-437-963-189741	Sequence 189741, A
74	66	13.6	507	4	US-10-282-122A-47787	Sequence 47787, A
75	66	13.6	511	4	US-10-282-122A-50464	Sequence 50464, A

ALIGNMENTS

RESULT 1
US-09-955-502-11
; Sequence 11, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Down, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 11
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Escherichia coli K-12 MG1655

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502A-13
Perfect score: 486
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA_New:*
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5: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB.pep:*
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7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	213	43.8	88	US-10-467-657-968	Sequence 968, App
2	66	13.6	593	US-11-194-246-317	Sequence 317, App
3	65.5	13.5	395	US-11-009-658-46	Sequence 46, Appl
4	65	13.4	478	US-10-821-234-915	Sequence 915, App
5	62	12.8	1501	US-10-793-626-2850	Sequence 2850, App
6	61.5	12.7	179	US-10-467-657-6542	Sequence 6542, App
7	60.5	12.4	264	US-10-821-234-1555	Sequence 1555, App
8	60.5	12.4	404	US-11-009-658-48	Sequence 48, Appl
9	60.5	12.4	834	US-10-453-372-658	Sequence 658, App
10	60	12.3	448	US-10-618-320A-25	Sequence 25, Appl
11	60	12.3	480	US-10-510-386-12	Sequence 12, Appl
12	60	12.3	667	US-10-793-626-198	Sequence 198, App
13	59.5	12.2	177	US-10-467-657-1658	Sequence 1658, App
14	59	12.1	266	US-09-995-493-6	Sequence 6, Appl1
15	59	12.1	604	US-10-942-072-4	Sequence 4, Appl1
16	59	12.1	1142	US-11-109-156-22	Sequence 22, Appl
17	59	12.1	1167	US-10-942-072-6	Sequence 6, Appl1
18	58.5	12.0	336	US-10-453-372-640	Sequence 640, App
19	58.5	12.0	349	US-10-821-234-1387	Sequence 1387, App
20	58.5	12.0	577	US-11-072-175-187	Sequence 648, App
21	58.5	12.0	695	US-10-453-372-648	Sequence 922, App
22	58.5	12.0	700	US-10-995-561-922	Sequence 924, App
23	58.5	12.0	700	US-10-995-561-924	Sequence 924, App
24	58.5	12.0	775	US-10-453-372-656	Sequence 656, App
25	58.5	12.0	793	US-10-995-561-925	Sequence 925, App

26	58.5	12.0	804	6	US-10-453-372-650	Sequence 650, App
27	58.5	12.0	847	6	US-10-453-372-654	Sequence 654, App
28	58.5	12.0	857	6	US-10-453-372-652	Sequence 652, App
29	58.5	12.0	905	6	US-10-453-372-638	Sequence 638, App
30	58.5	12.0	905	6	US-10-453-372-662	Sequence 662, App
31	58.5	12.0	905	6	US-10-453-372-664	Sequence 664, App
32	58.5	12.0	963	6	US-10-995-561-923	Sequence 923, App
33	58.5	12.0	963	6	US-10-453-372-660	Sequence 660, App
34	58.5	12.0	1012	6	US-10-453-372-646	Sequence 646, App
35	58.5	12.0	1299	6	US-10-821-234-1145	Sequence 1145, App
36	58.5	12.0	3960	6	US-10-995-561-773	Sequence 773, App
37	58.5	12.0	3960	6	US-10-995-561-771	Sequence 771, App
38	58.5	12.0	5335	6	US-10-995-561-777	Sequence 777, App
39	58.5	12.0	5406	6	US-10-995-561-774	Sequence 774, App
40	58.5	12.0	5415	6	US-10-995-561-779	Sequence 779, App
41	58.5	12.0	5464	6	US-10-995-561-775	Sequence 775, App
42	58.5	12.0	5935	6	US-10-995-561-776	Sequence 776, App
43	58	11.9	251	7	US-11-054-515-1496	Sequence 1496, App
44	58	11.9	1995	7	US-11-069-834-60	Sequence 60, Appl
45	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
46	57	11.7	194	7	US-11-072-512-2906	Sequence 2906, App
47	57	11.7	279	7	US-11-098-686-10812	Sequence 10812, A
48	57	11.7	504	7	US-11-072-512-3467	Sequence 3467, App
49	56	11.5	296	7	US-11-087-227-10	Sequence 10, Appl
50	56	11.5	372	7	US-11-143-986-5	Sequence 5, Appl1
51	56	11.5	372	7	US-11-143-986-6	Sequence 6, Appl1
52	56	11.5	386	7	US-11-143-986-2	Sequence 2, Appl1
53	56	11.5	386	7	US-11-143-986-3	Sequence 3, Appl1
54	56	11.5	397	7	US-11-022-562-223	Sequence 223, App
55	56	11.5	426	7	US-11-098-686-10340	Sequence 10340, A
56	56	11.5	427	7	US-11-186-284-91	Sequence 91, Appl
57	56	11.5	581	6	US-10-793-626-28	Sequence 28, Appl
58	56	11.5	697	6	US-10-485-517-202	Sequence 202, App
59	56	11.5	752	6	US-10-793-626-1036	Sequence 1036, App
60	56	11.5	1168	6	US-10-942-072-11	Sequence 11, Appl
61	56	11.5	1188	7	US-11-115-639-42	Sequence 42, Appl
62	56	11.5	1188	7	US-11-115-639-43	Sequence 43, Appl
63	56	11.5	1404	6	US-10-878-556A-169	Sequence 169, App
64	55.5	11.4	207	7	US-11-124-367A-438	Sequence 438, App
65	55.5	11.4	317	7	US-11-124-367A-437	Sequence 437, App
66	55.5	11.4	328	7	US-11-124-367A-436	Sequence 436, App
67	55.5	11.4	440	7	US-11-072-512-3856	Sequence 3856, App
68	55.5	11.4	623	7	US-11-072-512-2547	Sequence 2547, App
69	55.5	11.4	2101	6	US-10-857-780-23	Sequence 23, Appl
70	55	11.3	257	6	US-10-667-295-61	Sequence 61, Appl
71	55	11.3	257	7	US-11-054-515-1710	Sequence 1710, App
72	55	11.3	286	6	US-10-667-295-60	Sequence 60, Appl
73	55	11.3	327	6	US-10-667-295-59	Sequence 59, Appl
74	55	11.3	359	7	US-11-087-227-8	Sequence 8, Appl1
75	55	11.3	359	7	US-11-192-450-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWln99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

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535.055 Million cell updates/sec

Title: US-09-955-502a-14
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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6:	Geneseqp2003as:*
7:	Geneseqp2003bs:*
8:	Geneseqp2004s:*
9:	Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	488	100.0	91	5	ABB78161 Amino aci
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4	474	97.1	91	5	ABB78163 Amino aci
5	472	96.7	88	5	ABB78160 Amino aci
6	469	96.1	91	5	ABB78158 Amino aci
7	469	96.1	91	5	ABB78157 Amino aci
8	469	96.1	91	5	ABB78156 Amino aci
9	445	91.2	107	7	ABO65445 KLebsie11
10	393	80.5	90	5	ABB78165 Amino aci
11	389	79.7	90	5	ABB78155 Amino aci
12	386	79.1	78	5	ABB78164 Amino aci
13	385	78.9	87	5	ABB78152 Amino aci
14	383	78.5	91	5	ABB78150 Amino aci
15	383	78.5	93	7	ADP05158 Bacterial
16	377	77.3	87	5	ABB78151 Amino aci
17	371	76.0	87	5	ABB78153 Amino aci
18	336	68.9	88	5	ABB78154 Amino aci
19	259	53.1	76	5	ABB78166 Amino aci
20	249	51.0	87	5	ABB78148 Amino aci
21	249	51.0	87	5	ABB78147 Amino aci
22	235	48.2	86	5	ABB78149 Amino aci
23	228	46.7	87	5	ABB78170 Amino aci
24	228	46.7	122	7	ABO74609 Pseudomon

25	224.5	46.0	89	9	AEB41576 L. pneumo
26	224.5	46.0	95	9	AEB38294 L. pneumo
27	222.5	45.6	90	5	ABB78167 Amino aci
28	222	45.5	90	5	ABB78168 Amino aci
29	218	44.7	87	5	ABB78169 Amino aci
30	218	44.7	88	5	ABB78178 Amino aci
31	211	43.2	88	5	ABB78171 Amino aci
32	211	43.2	88	5	ABB78172 Amino aci
33	211	43.2	88	5	ABB78173 Amino aci
34	211	43.2	88	6	ABP77219 N. gonorr
35	206	42.2	87	5	ABB78175 Amino aci
36	200	41.0	87	5	ABB78174 Amino aci
37	197	40.4	87	5	ABB78176 Amino aci
38	195.5	40.1	92	6	ADA34169 Acinetoba
39	195	40.0	87	5	ABB78177 Amino aci
40	130	26.6	110	8	ADL05173 M. catarr
41	77	15.8	1647	4	ABG10750 Novel hum
42	72	14.8	309	8	ADN46828 Thermococ
43	72	14.8	506	3	AAY74371 Neisseria
44	72	14.8	507	6	ABU40210 Protein e
45	71.5	14.7	184	3	AAB16290 Pinus rad
46	71	14.5	447	2	AAR52657 Rat N-ace
47	71	14.5	447	7	ADRS5944 Rat Prote
48	71	14.5	507	3	AAY74372 Neisseria
49	71	14.5	507	3	AAY74373 Neisseria
50	71	14.5	546	6	ABU38097 Proteine
51	71	14.5	548	4	AAE04737 Brugia ma
52	70.5	14.4	184	3	AAB16325 Pinus rad
53	70.5	14.4	184	4	AAB65734 Annexin-1
54	70.5	14.4	184	7	ADB94702 Programme
55	70.5	14.4	593	4	ABG19947 Novel hum
56	70	14.3	257	3	AAG31203 Arabidops
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59	70	14.3	758	9	ADW71760 Salomonell
60	69.5	14.2	227	3	AAG38052 Arabidops
61	69.5	14.2	1377	8	ADV81847 Streptoco
62	69.5	14.2	1387	8	ADV88434 Streptoco
63	69.5	14.2	1387	8	ADV79687 Streptoco
64	69	14.1	503	4	ABG16577 Novel hum
65	69	14.1	679	9	ADZ85056 Partial F
66	68.5	14.0	608	5	ABP73745 Candida a
67	68.5	14.0	632	8	ADS29711 Bacterial
68	68	13.9	239	3	ADT07537 Human col
69	68	13.9	280	3	AAY54294 Amino aci
70	68	13.9	280	5	ABG93905 Lactuca s
71	68	13.9	280	8	ADJ50292 Oil-assoc
72	68	13.9	285	4	AAH92683 Human pro
73	68	13.9	302	4	AAH88379 Human mem
74	68	13.9	302	9	ADY63123 Human c10
75	68	13.9	414	6	ABU11747 Human MDD

ALIGNMENTS

RESULT 1	ABB78161	standard; protein; 91 AA.
ID	ABB78161;	
XX	05-NOV-2002	(first entry)
XX	Amino acid sequence of a YggX homologue.	
DE	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX	Unidentified.	
OS	US2002072118-A1.	
XX		
PN		
XX		

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
PS
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQRDABGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLANMNA 60
Db 1 MSRTIFCTYLQRDABGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLANMNA 60

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 2
ABB78159
ID ABB78159 standard; protein; 91 AA.

XX AC ABB78159;

XX DT 05-NOV-2002 (first entry)

XX DE Amino acid sequence of a YggX homologue.

XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

XX OS Unidentified.

XX PN US2002072118-A1.

XX PD 13-JUN-2002.

XX PF 18-SEP-2001; 2001US-00955502.

XX PR 22-SEP-2000; 2000US-0234588P.

XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.

XX PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.

XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQRDABGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLANMNA 60
Db 1 MSRTIFCTYLQRDABGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLANMNA 60

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3
ABB78162
ID ABB78162 standard; protein; 91 AA.

XX AC ABB78162;

XX DT 05-NOV-2002 (first entry)

XX DE Amino acid sequence of a YggX homologue.

XX KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.

XX OS Salmonella typhi.

XX PN US2002072118-A1.

XX PD 13-JUN-2002.

XX PF 18-SEP-2001; 2001US-00955502.

XX PR 22-SEP-2000; 2000US-0234588P.

XX PA (DOWN/) DOWNS D.
XX PA (GRAL/) GRALNICK J A.

XX PI Downs D, Gralnick JA;

XX DR WPI; 2002-589476/63.

XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-14

Perfect score: 488
Sequence: 1 MSRTIFCTYIQDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR, 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	488	100.0	91	2 AH0879	conserved hypothet
2	469	96.1	91	2 A85954	hypothetical prote
3	469	96.1	91	2 A65082	hypothetical prote
4	469	96.1	91	2 F91108	hypothetical prote
5	393	80.5	90	2 AI0116	conserved hypothet
6	389	79.7	90	2 C82320	conserved hypothet
7	385	78.9	90	2 C64013	hypothetical prote
8	259	53.1	93	2 B84994	hypothetical prote
9	232	47.5	105	2 C82624	conserved hypothet
10	228	46.7	90	2 H83003	conserved hypothet
11	211	43.2	88	2 H81014	conserved hypothet
12	79.5	16.3	1638	2 D87749	protein unc-73b [i
13	79.5	16.3	2488	2 T42739	guanine nucleotide
14	78	16.0	1260	2 T04440	hypothetical prote
15	73.5	15.1	495	2 AH0985	hypothetical prote
16	71.5	14.7	209	2 I64172	probable zinc-prot
17	71	14.5	447	2 JC2076	hypothetical prote
18	71	14.5	507	2 C81063	alpha-1,3-mannosyl
19	71	14.5	546	2 A81807	fumarate hydratase
20	71	14.5	548	2 A54510	fumarate hydratase
21	70	14.3	324	2 T05429	63K antigen - nema
22	70	14.3	758	2 AD0763	hypothetical prote
23	70	14.3	758	2 A57143	thiosulfate reduct
24	69.5	14.2	859	2 T29630	thiosulfate-dithio
25	69	14.1	265	2 T46013	hypothetical prote
26	69	14.1	447	2 T16527	hypothetical prote
27	68.5	14.0	683	2 AC2256	hypothetical prote
28	68	13.9	445	2 XUHUMB	alpha-1,3-mannosyl
29	68	13.9	689	2 F83902	beta-galactosidase

30	67.5	13.8	166	2 F70562	hypothetical prote
31	67	13.7	447	1 A38561	alpha-1,3-mannosyl
32	67	13.7	1111	2 T23047	hypothetical prote
33	66.5	13.6	410	1 KHMSD	cathepsin D (EC 3.
34	66	13.5	447	1 A42500	alpha-1,3-mannosyl
35	66	13.5	703	2 B82148	ATP-dependent heli
36	66	13.5	1085	2 S62516	hypothetical coile
37	65.5	13.4	287	2 F82265	conserved hypothet
38	65.5	13.4	365	2 B54128	Fc-binding protein
39	65	13.3	433	2 A70465	probable GTP bindi
40	65	13.3	507	2 A83105	probable fumarase
41	65	13.3	511	2 A99574	ABC transporter at
42	65	13.3	593	2 C64097	probable soluble 1
43	65	13.3	1230	2 S56850	SMC1 protein homol
44	64.5	13.2	327	2 AD2129	transcription regu
45	64.5	13.2	385	2 D87723	protein R06A10.2 [
46	64.5	13.2	401	2 AE1978	hypothetical prote
47	64.5	13.2	544	2 T40058	probable chromatin
48	64.5	13.2	1197	2 S26947	DNA-directed DNA p
49	64	13.1	251	2 B90428	hypothetical prote
50	64	13.1	548	2 A28209	60K filarial antig
51	64	13.1	643	2 A43647	parasporeal crys
52	63.5	13.0	379	2 S70709	type II site-speci
53	63.5	13.0	438	2 T37786	probable RNA-bindi
54	63.5	13.0	2672	2 A48126	translation activa
55	63	12.9	205	2 C26135	keratin, 50K type
56	63	12.9	235	2 G65212	hypothetical 26.7K
57	63	12.9	258	2 A97991	hypothetical prote
58	63	12.9	258	2 B95121	phosphoesterase, p
59	63	12.9	483	2 G64799	ybeV protein - Esc
60	63	12.9	543	2 T16015	hypothetical prote
61	63	12.9	549	2 T16016	hypothetical prote
62	63	12.9	1119	2 T15842	hypothetical prote
63	63	12.9	1166	2 H71609	hypothetical prote
64	63	12.9	1209	2 T46027	guanine nucleoti
65	63	12.9	1327	2 T14594	SNF2alpha protein
66	63	12.9	1572	2 S45251	HBM protein - hum
67	63	12.9	1586	2 S39580	salikimate kinase (
68	62.5	12.8	165	2 A81382	conserved hypothet
69	62.5	12.8	259	2 G83203	asparaginase (EC 3
70	62.5	12.8	305	2 A75211	GTP-binding regula
71	62.5	12.8	375	2 T37245	hypothetical prote
72	62.5	12.8	498	2 G91179	hypothetical prote
73	62.5	12.8	498	2 H86025	53.1K protein prec
74	62.5	12.8	498	2 S47748	chemotactic transd
75	62.5	12.8	629	2 B83107	

ALIGNMENTS

RESULT 1
AH0879
Conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C:Species: Salmonella enterica subsp. enterica serovar Typh
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C:Accession: AH0879
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A:Reference number: AB0502; MUID:21534947; PMID:11677608
A:Accession: AH0879
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <PAR>
A:Cross-references: UNIPARC:UPI000005A4C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
C:Genetics:
A:Gene: STY3266
C:Superfamily: fe(II) trafficking protein YgX

	Query Match	100.0%;	Score 488;	DB 2;	Length 91;	
	Best Local Similarity	100.0%;	Pred. No. 2.1e-42;			
	Matches	91;	Conservative	0;	Mismatches	0; Indels 0; Gaps 0;
QY	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
DB	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
QY	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDKK 91					
DB	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDKK 91					
RESULT 2						
A85954	hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93					
C/Species:	Escherichia coli					
C/Date:	16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004					
C/Accession:	A85954					
R/Perna, N.T.;	Plunkett III, G.;	Burland, V.;	Mau, B.;	Glasner, J.D.;	Rose, D.J.;	Mayhew
iller, L.;	Grotbeck, E.J.;	Davis, N.W.;	Lim, A.;	Dimalanta, E.;	Potamouets, K.;	Apodaca,
Nature	409, 529-533, 2001					
A/Title:	Genome sequence of enterohemorrhagic Escherichia coli O157:H7.					
A/Reference number:	A85480; MUID:21074935; PMID:11206551					
A/Accession:	A85954					
A/Status:	preliminary					
A/Molecule type:	DNA					
A/Residues:	1-91 <STO>					
A/Cross-references:	UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:gl2517511; F					
A/Experimental source:	strain O157:H7, substrain EDL933					
C/Genetics:						
A/Gene:	yggX					
C/Superfamily:	fe(ii) trafficking protein yggX					
Query Match	96.1%;	Score 469;	DB 2;	Length 91;		
Best Local Similarity	94.5%;	Pred. No. 1.8e-40;				
Matches	86;	Conservative	5;	Mismatches	0; Indels 0; Gaps 0;	
QY	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
DB	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA	60				
QY	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDKK 91					
DB	61 EHRKLLSEQEMVNFLLFEGKEVHIEGYTPEDKK 91					
RESULT 3						
A65082	hypothetical protein b2962 - Escherichia coli (strain K-12)					
C/Species:	Escherichia coli					
C/Date:	12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004					
C/Accession:	A65082					
R/Blattner, F.R.;	Plunkett III, G.;	Bloch, C.A.;	Perna, N.T.;	Burland, V.;	Riley, M.;	Cd
A.;	Rose, D.J.;	Mau, B.;	Shao, Y.			
Science	277, 1453-1462, 1997					
A/Title:	The complete genome sequence of Escherichia coli K-12.					
A/Reference number:	A64720; MUID:97426617; PMID:9278503					
A/Accession:	A65082					
A/Status:	preliminary; nucleic acid sequence not shown; translation not shown					
A/Molecule type:	DNA					
A/Residues:	1-91 <BLAT>					
A/Cross-references:	UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9					
A/Experimental source:	strain K-12, substrain MG1655					
C/Superfamily:	fe(ii) trafficking protein YggX					
Query Match	96.1%;	Score 469;	DB 2;	Length 91;		
Best Local Similarity	94.5%;	Pred. No. 1.8e-40;				
Matches	86;	Conservative	5;	Mismatches	0; Indels 0; Gaps 0;	
QY	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
DB	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				

DB	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA	60				
QY	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDKK 91					
DB	61 EHRKLLSEQEMVNFLLFEGKEVHIEGYTPEDKK 91					
RESULT 4						
F91108	hypothetical protein ECS3838 [imported] - Escherichia coli (strain O157:H7, substrain RI					
C/Species:	Escherichia coli					
C/Date:	18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004					
C/Accession:	F91108					
R/Hayashi, T.;	Makino, K.;	Ohnishi, M.;	Kurokawa, K.;	Ishii, K.;	Yokoyama, K.;	Han, C.G
gasawara, N.;	Yasunaga, T.;	Kuhara, S.;	Shiba, T.;	Hattori, M.;	Shinagawa, H.	
DNA Res.	8, 11-22, 2001					
A/Title:	Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc					
A/Reference number:	A99629; MUID:21156231; PMID:11258796					
A/Accession:	F91108					
A/Status:	preliminary					
A/Molecule type:	DNA					
A/Residues:	1-91 <HAY>					
A/Cross-references:	UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1,					
A/Experimental source:	strain O157:H7, substrain RIMD 0509952					
C/Genetics:						
A/Gene:	ECS3838					
C/Superfamily:	fe(ii) trafficking protein YggX					
Query Match	96.1%;	Score 469;	DB 2;	Length 91;		
Best Local Similarity	94.5%;	Pred. No. 1.8e-40;				
Matches	86;	Conservative	5;	Mismatches	0; Indels 0; Gaps 0;	
QY	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
DB	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLANMNA	60				
QY	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDKK 91					
DB	61 EHRKLLSEQEMVNFLLFEGKEVHIEGYTPEDKK 91					
RESULT 5						
A10116	conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)					
C/Species:	Yersinia pestis					
C/Date:	02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004					
C/Accession:	A10116					
R/Parkhill, J.;	Wren, B.W.;	Thomson, N.R.;	Titball, R.W.;	Holden, M.T.G.;	Prentice, M.B.	
deno-Tarraga, A.M.;	Chillingworth, T.;	Cronin, A.;	Davies, R.M.;	Davis, P.;	Dougan, G.;	
ll, M.;	Rutherford, K.;	Simmonds, M.;	Skelton, J.;	Stevens, K.;	Whitehead, S.;	Barrell,
Nature	413, 523-527, 2001					
A/Title:	Genome sequence of Yersinia pestis, the causative agent of plague.					
A/Reference number:	AB0001; MUID:21470413; PMID:11586360					
A/Accession:	A10116					
A/Status:	preliminary					
A/Molecule type:	DNA					
A/Residues:	1-90 <KUR>					
A/Cross-references:	UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:gl5979022;					
C/Genetics:						
A/Gene:	YPO0953					
C/Superfamily:	fe(ii) trafficking protein YggX					
Query Match	80.5%;	Score 393;	DB 2;	Length 90;		
Best Local Similarity	81.1%;	Pred. No. 8.1e-33;				
Matches	73;	Conservative	9;	Mismatches	8; Indels 0; Gaps 0;	
QY	1 MSRTIFCTYIQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKLANMNA	60				
DB	1 MSRTIFCTFLKDAERQDFQLYPGELGKRIYNEISKEAWSQWITKQTMLINEKLSMNI	60				
QY	61 EHRKLLSEQEMVSFLFEGKDVHIEGYTPEDK 90					
DB	61 EDRKLLSEQEMVNFLLFEGQDVHIAGYTPPSK 90					

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-14
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	483	99.0	90	1 FETP_SALCH	O57K04 salmonella
2	483	99.0	90	1 FETP_SALPA	O5pmn1 salmonella
3	483	99.0	90	1 FETP_SALTY	P67618 salmonella
4	483	99.0	90	1 FETP_SALTY	P67617 salmonella
5	464	95.1	90	1 FETP_ECOS7	POa8p4 escherichia
6	464	95.1	90	1 FETP_ECOS7	POa8p3 escherichia
7	464	95.1	90	1 FETP_SCOLI	POa8p5 shigella fl
8	460	94.3	90	1 FETP_SCOL6	O8fe19 escherichia
9	416	85.2	90	1 FETP_ERWCT	O6d8j9 erwinia car
10	401	82.2	90	1 FETP_YERPS	O666m3 yersinia ps
11	393	80.5	90	1 FETP_VIBPA	O871i5 vibrio para
12	393	80.5	90	1 FETP_YERPS	O8zhe7 yersinia pe
13	389	79.7	90	1 FETP_VIBCH	O9kuc4 vibrio chol
14	389	79.7	90	1 FETP_VIBVU	O8dcs5 vibrio vuln
15	389	79.7	90	1 FETP_VIBVY	O7mbi4 vibrio vuln
16	387	79.3	91	1 FETP_MANSN	O65vt7 manheimia
17	385	78.9	90	1 FETP_HAEIN	P44048 haemophilus
18	385	78.9	90	2 O4QMD9_HAEI8	O4qmd9 haemophilus
19	383	78.5	90	1 FETP_PHOBR	O6lmk7 photobacter
20	377	77.3	90	1 FETP_PASNU	O9clb9 pasteurilla
21	376	77.0	90	1 FETP_PASNU	O7n7i1 photorhabdu
22	371	76.0	94	1 FETP_HABDU	O7vkb6 haemophilus
23	365	74.8	90	1 FETP_VIBF1	O5e7t0 vibrio fisc
24	341	69.9	90	1 FETP_IDILO	O5gy58 idiomarina
25	336	68.9	92	1 FETP_SHEON	O8ebx6 shewanella
26	259	53.1	77	1 FETP_BUCAI	P57618 bucheneria ap
27	249	51.0	90	1 FETP_BORBR	O7wh06 bordetella
28	249	51.0	90	1 FETP_BORPA	O7w9q2 bordetella
29	249	51.0	90	1 FETP_BORPE	O7wvc4 bordetella
30	243	49.8	78	1 FETP_XNACP	O8pjh7 xanthomonas
31	239	49.0	91	1 FETP_XNAC	O8pjh7 xanthomonas

32	232	47.5	90	1 FETP_XYLEFA	O9pc73 xylella fas
33	232	47.5	92	1 FETP_XANOR	O5gy22 xanthomonas
34	228.5	46.8	89	1 FETP_LEGPR	O5huc3 legionella
35	228	46.7	90	1 FETP_PSEAB	O9hu36 pseudomonas
36	228	46.7	90	1 FETP_XYLEFT	O87d06 xylella fas
37	228	46.7	92	1 FETP_XANCP	O8p829 xanthomonas
38	228	46.7	92	2 O4UWI4_XANCP	O4uw14 xanthomonas
39	225	46.1	78	1 FETP_WIGBR	O8d3c5 wigleswort
40	224.5	46.0	89	1 FETP_LEGPA	O5x3x9 legionella
41	224.5	46.0	89	1 FETP_LEGPH	O5zu80 legionella
42	222	45.5	90	1 FETP_NITEU	O82xf2 nitrosomona
43	222	45.5	90	1 FETP_PSESM	O87uf5 pseudomonas
44	222	45.5	90	2 O4ZLP3_PSESY	O42lp3 pseudomonas
45	222	45.5	90	1 FETP_COXBU	O83d06 coxiella bu
46	218	44.7	90	1 FETP_PSEPK	O88r49 pseudomonas
47	218	44.7	90	2 O4J228_AZOVY	O4j228 azotobacter
48	215	44.1	90	2 O6T7F6_PSEFL	O6t7f6 pseudomonas
49	213	43.6	90	1 FETP_CHRVO	O7n8r4 chromobacte
50	212	43.4	79	1 FETP_CANBF	O7vrg9 candidatus
51	211	43.2	88	1 FETP_NEIGI	O5f553 neisseria g
52	211	43.2	88	1 FETP_NEIMA	P67615 neisseria m
53	211	43.2	88	1 FETP_NEIMA	P67616 neisseria m
54	207	42.4	87	1 FETP_BUCBP	O89a44 bucheneria ap
55	206	42.2	91	1 FETP_BURMA	O62iuv burkholderi
56	206	42.2	91	1 FETP_BURPS	O63sf4 burkholderi
57	205	42.0	90	2 O4KUJ2_PSEF5	O4kjt2 pseudomonas
58	205	42.0	91	1 FETP_RALSO	O8y010 ralstonia s
59	203	41.6	91	2 O4LSI9_9BURK	O4ls19 burkholderi
60	195	40.0	90	1 FETP_METCA	O60aj7 methylococc
61	192	39.3	87	1 FETP_PRAAT	O5mhj8 francisella
62	190.5	39.0	90	1 FETP_ACTAD	O6ffj7 psychrobact
63	146	29.9	96	2 O4FVJ7_9GAMM	O4fwj7 psychrobact
64	145	29.7	92	2 O4NWQ4_DDELT	O4nwq4 anaeromyxob
65	82.5	16.9	482	2 O5NUY1_9BURK	O5nyu1 ralstonia m
66	82.5	16.9	514	2 O6AIZ9_DESPS	O6aiz9 desulfotale
67	79.5	16.3	1638	2 O7KPP4_CABEL	O7kpp4 caenorhabdi
68	79.5	16.3	2140	2 O6BEW2_CABEL	O6bew2 caenorhabdi
69	79.5	16.3	2488	2 O61528_CABEL	O61528 caenorhabdi
70	78.5	16.1	337	2 O81AR8_BACCR	O81ar8 bacillus ce
71	78	16.0	1260	2 O49677_ARATH	O49677 arabidopsis
72	77.5	15.9	1047	2 O5CJ53_CRYHO	O5cj53 cryptospori
73	76.5	15.7	486	2 O7WX51_ALCEU	O7wx51 alcaligenes
74	75.5	15.5	1278	2 O5CYM7_CRYPV	O5cym7 cryptospori
75	75	15.4	385	2 O734A2_BACCI	O734a2 bacillus ce

ALIGNMENTS

RESULT 1
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC O57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y9GX; OrderedLocustNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or


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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE017220; AAX66958.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;

Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKLANMNAE 60

QY 62 HRKLEQEMVVSFLFEGKDVHIEGYTPEDKK 91
   |||
Db 61 HRKLEQEMVVSFLFEGKDVHIEGYTPEDKK 90

RESULT 2
FETP_SALPA STANDARD; PRT; 90 AA.
ID FETP_SALPA STANDARD; PRT; 90 AA.
AC QSPMML;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocusNames=SPA2974;
OS Salmonella paratyphi-a.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=54388;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 9150 / SARB42;
RX PubMed=15531882; DOI=10.1038/ng1470;
RA McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLeelllan M.,
RA Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA Delehauntz K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA Spieth J., Wilson R.K.;
RT "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT restricted serovars of Salmonella enterica that cause typhoid.";
RL Nat. Genet. 36:1268-1274(2004).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR SMR; QSPMML; 1-91.
DR HAMAP; MF_00686; -; 1.
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DR InterPro; IPR007457; YggX.
DR ProDom; PD029191; DUF495; 1.
KM Complete proteome; Iron.
FT INIT MET 0 0 By similarity.
SQ SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;

Query Match 99.0%; Score 483; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 2.5e-42;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKLANMNAE 61
   |||
Db 1 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAMAQWQHKTMLINEKLANMNAE 60

QY 62 HRKLEQEMVVSFLFEGKDVHIEGYTPEDKK 91
   |||
Db 61 HRKLEQEMVVSFLFEGKDVHIEGYTPEDKK 90

RESULT 3
FETP_SALTI STANDARD; PRT; 90 AA.
ID FETP_SALTI STANDARD; PRT; 90 AA.
AC P67618; Q8XFFV6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocusNames=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrett B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18.";
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18.";
RL J. Bacteriol. 185:2330-2337(2003).
CC -I- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -I- SUBUNIT: Monomer (By similarity).
CC -I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR EMBL; AE016844; AA070576.1; -; Genomic_DNA.
DR SMR; P67618; 1-90.
DR HAMAP; MF_00686; -; 1.
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-14

Perfect score: 488
Sequence: 1 MSRTICTYTLQRDAEGQDFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	91.2	107	2	US-09-489-039A-11962 Sequence 11962, A
2	383	78.5	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	228	46.7	122	2	US-09-252-991A-23355 Sequence 23355, A
4	195.5	40.1	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	130	26.6	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	14.5	548	2	US-09-167-299-3 Sequence 3, Appli
7	70.5	14.4	184	2	US-09-325-932A-66 Sequence 66, Appli
8	68.5	14.0	544	2	US-09-248-796A-18911 Sequence 18911, A
9	68	13.9	280	2	US-09-323-998E-37 Sequence 37, Appli
10	68	13.9	337	2	US-09-270-767-41746 Sequence 41746, A
11	68	13.9	1214	2	US-10-164-595-24 Sequence 24, Appli
12	66.5	13.6	325	2	US-09-134-000C-4346 Sequence 4346, Ap
13	66	13.5	292	2	US-09-328-352-5836 Sequence 5836, Ap
14	65.5	13.4	546	1	US-08-533-669A-2 Sequence 2, Appli
15	65.5	13.4	546	2	US-09-183-861-2 Sequence 2, Appli
16	65.5	13.4	546	2	US-09-022-765-2 Sequence 2, Appli
17	65.5	13.4	546	2	US-09-551-974A-2 Sequence 2, Appli
18	65.5	13.4	546	2	US-09-565-501A-2 Sequence 2, Appli
19	65.5	13.4	546	2	US-09-639-206A-2 Sequence 2, Appli
20	65.5	13.4	546	2	US-09-874-923-2 Sequence 2, Appli
21	65.5	13.4	546	2	US-08-798-841-2 Sequence 2, Appli
22	65.5	13.4	982	2	US-09-551-974A-95 Sequence 95, Appli
23	65.5	13.4	982	2	US-09-565-501A-95 Sequence 95, Appli
24	65.5	13.4	982	2	US-09-639-206A-95 Sequence 95, Appli
25	65.5	13.4	982	2	US-09-874-923-95 Sequence 95, Appli
26	65.5	13.4	1427	2	US-09-551-974A-97 Sequence 97, Appli
27	65.5	13.4	1427	2	US-09-565-501A-97 Sequence 97, Appli

28	65.5	13.4	1427	2	US-09-639-206A-97	Sequence 97, Appli
29	65.5	13.4	1427	2	US-09-874-923-97	Sequence 97, Appli
30	65.5	13.4	1641	2	US-09-551-974A-96	Sequence 96, Appli
31	65.5	13.4	1641	2	US-09-565-501A-96	Sequence 96, Appli
32	65.5	13.4	1641	2	US-09-639-206A-96	Sequence 96, Appli
33	65.5	13.4	1641	2	US-09-874-923-96	Sequence 96, Appli
34	65	13.3	474	2	US-09-252-991A-24473	Sequence 24473, A
35	64	13.1	98	2	US-09-270-767-41085	Sequence 41085, A
36	64	13.1	98	2	US-09-270-767-56301	Sequence 56301, A
37	64	13.1	569	2	US-09-107-532A-6689	Sequence 6689, Ap
38	64	13.1	644	2	US-08-793-331-7	Sequence 7, Appli
39	64	13.1	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
40	63.5	13.0	921	2	US-09-248-796A-14950	Sequence 14950, A
41	63	12.9	1586	2	US-09-538-092-1171	Sequence 1171, Ap
42	62.5	12.8	260	2	US-09-252-991A-17498	Sequence 17498, A
43	62.5	12.8	419	2	US-09-543-681A-7295	Sequence 7295, Ap
44	62.5	12.8	662	2	US-09-583-110-5119	Sequence 5119, Ap
45	62.5	12.8	664	2	US-09-107-433-2775	Sequence 2775, Ap
46	62.5	12.8	701	2	US-09-252-991A-23288	Sequence 23288, A
47	62	12.7	227	2	US-09-270-767-58283	Sequence 58283, A
48	62	12.7	238	2	US-09-323-998E-41	Sequence 41, Appli
49	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
50	62	12.7	604	2	US-09-008-097-4	Sequence 4, Appli
51	62	12.7	604	2	US-09-472-667-4	Sequence 4, Appli
52	62	12.7	898	2	US-09-583-110-3750	Sequence 3750, Ap
53	62	12.7	899	2	US-09-107-433-3196	Sequence 3196, Ap
54	62	12.7	1167	2	US-09-008-097-6	Sequence 6, Appli
55	62	12.7	1167	2	US-09-472-667-6	Sequence 6, Appli
56	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appli
57	61	12.5	143	2	US-09-270-767-45872	Sequence 45872, A
58	61	12.5	184	2	US-09-270-767-61671	Sequence 61671, A
59	61	12.5	271	2	US-09-248-796A-19265	Sequence 19265, A
60	61	12.5	389	2	US-09-270-767-46116	Sequence 46116, A
61	61	12.5	1394	2	US-09-248-796A-19555	Sequence 19555, A
62	60.5	12.4	223	2	US-09-543-681A-5667	Sequence 5667, Ap
63	60.5	12.4	504	2	US-10-104-047-3467	Sequence 3467, Ap
64	60.5	12.4	525	2	US-09-540-236-2250	Sequence 2250, Ap
65	60.5	12.4	527	2	US-09-489-039A-10883	Sequence 10883, A
66	60	12.3	232	2	US-09-201-641-8	Sequence 8, Appli
67	60	12.3	232	2	US-09-323-998E-36	Sequence 36, Appli
68	60	12.3	421	2	US-09-489-039A-7512	Sequence 7512, Ap
69	60	12.3	734	2	US-10-008-355-5	Sequence 5, Appli
70	59.5	12.2	139	2	US-09-513-999C-4802	Sequence 4802, Ap
71	59.5	12.2	209	2	US-09-252-991A-20905	Sequence 20905, A
72	59.5	12.2	258	2	US-09-513-999C-4800	Sequence 4800, Ap
73	59.5	12.2	264	2	US-09-949-016-6012	Sequence 6012, Ap
74	59.5	12.2	276	2	US-09-949-016-11703	Sequence 11703, A
75	59.5	12.2	434	2	US-09-303-518D-334	Sequence 334, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Best Local Similarity	89.0%;	Pred. No. 3.5e-49;		
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Qy 61 EHRKLLQEMVSFLFEGKDVHIEGTPBEDKK 91
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Db 77 EHRKLLQEMVQFLFEGKDVHIEGTPPEKQ 107
|||

RESULT 2
US-09-543-681A-5443

APPLICANT: GARY BRETON
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS

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; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Query Match	78.5%;	Score 383;	DB 2;	Length 93;
Best Local Similarity	77.8%;	Pred. No. 2.5e-41;		
Matches 70; Conservative	9;	Mismatches 11;	Indels 0;	Gaps 0;

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RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795

APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

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1 CURRENT APPLICATION NUMBER: US/09/252,991A
2 CURRENT FILING DATE: 1999-02-18
3 PRIOR APPLICATION NUMBER: US 60/074,788
4 PRIOR FILING DATE: 1998-02-18
5 PRIOR APPLICATION NUMBER: US 60/094,190
6 PRIOR FILING DATE: 1998-07-27
7 NUMBER OF SEQ ID NOS: 33142
8 SEQ ID NO 12355
9
10 LENGTH: 122
11
12 TYPE: PRT
13 ORGANISM: Pseudomonas aeruginosa
14
15 US-09-252-991A-23355

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Query Match	46.7%;	Score 228;	DB 2;	Length 122;
Best Local Similarity	52.3%;	Pred. No. 2.4e-21;		
Matches 46;	Conservative 11;	Mismatches 29;	Indels 2;	Gaps 2;

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Db 33 MSRTVMCRKYHEELPGIDRPPYPGAKGEDIYNNVSRKAWDEWQKHQTMLINBRLLNMNNA 92

Qy 61 EHRKLLQEMWVSFLFEKGD-VHIEGYTP 87

Db 93 EDRKFLQEMDKFL-SGEDYAKADGYTP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352

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RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Query Match	40.1%;	Score 195.5;	DB 2;	Length 92;
Best Local Similarity	41.6%;	Pred. No. 2.4e-17;		
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RESULT 5
US-09-54

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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
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; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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Query Match	26.6%	Score 130;	DB 2;	Length 110;
Best Local Similarity	34.9%	Pred. No. 7.4e-09;		
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Db     25 VFCKRYQQNLPKLPNPFPNAGGOEIQDTISAKANNAWLBLQTMLINEKHLSMTDQAKK   84
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QY 65 LLEQEMVSFLFECKDVHIEGYTP 87
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DB 85 YLNEQREKFLDNGDYEKDPAGYKP 107

RESULT 6
US-09-167-299-3
; Sequence 3, Application US/09167299

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-14
Perfect score: 488
Sequence: 1 MSRTICTYLQDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA Main:*
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5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	488	100.0	91	3	US-09-955-502-16
3	488	100.0	91	3	US-09-955-502-17
4	474	97.1	91	3	US-09-955-502-18
5	472	96.7	88	3	US-09-955-502-15
6	469	96.1	91	3	US-09-955-502-11
7	469	96.1	91	3	US-09-955-502-12
8	469	96.1	91	3	US-09-955-502-13
9	393	80.5	90	3	US-09-955-502-20
10	389	79.7	90	3	US-09-955-502-10
11	386	79.1	78	3	US-09-955-502-19
12	385	78.9	87	3	US-09-955-502-7
13	383	78.5	91	3	US-09-955-502-5
14	377	77.3	87	3	US-09-955-502-6
15	371	76.0	87	3	US-09-955-502-8
16	336	68.9	88	3	US-09-955-502-9
17	259	51.0	76	3	US-09-955-502-21
18	249	51.0	87	3	US-09-955-502-2
19	249	51.0	87	3	US-09-955-502-3
20	235	48.2	86	3	US-09-955-502-4
21	232	47.5	89	3	US-09-955-502-22
22	228	46.7	87	3	US-09-955-502-25
23	222	45.5	90	3	US-09-955-502-23
24	218	44.7	87	3	US-09-955-502-24
25	218	44.7	88	3	US-09-955-502-33
26	211	43.2	88	3	US-09-955-502-26
27	211	43.2	88	3	US-09-955-502-27

28	211	43.2	88	3	US-09-955-502-28	Sequence 28, Appl
29	206	42.2	87	3	US-09-955-502-29	Sequence 29, Appl
30	206	42.2	87	3	US-09-955-502-30	Sequence 30, Appl
31	197	40.4	87	3	US-09-955-502-31	Sequence 31, Appl
32	195	40.0	87	3	US-09-955-502-32	Sequence 32, Appl
33	77	15.8	1647	5	US-10-450-763-41109	Sequence 41109, A
34	72.5	14.9	786	5	US-10-732-923-4885	Sequence 4885, Ap
35	72	14.8	507	4	US-10-282-122A-68134	Sequence 68134, A
36	72	14.8	1261	4	US-10-437-963-189166	Sequence 189166,
37	71.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
38	71	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
39	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
40	70.5	14.4	184	4	US-10-393-840-118	Sequence 118, App
41	70.5	14.4	593	5	US-10-450-763-50306	Sequence 50306, A
42	69	14.1	503	5	US-10-450-763-46936	Sequence 46936, A
43	69	14.1	679	5	US-10-805-684-105	Sequence 105, App
44	68.5	14.0	449	4	US-10-424-599-279212	Sequence 279212,
45	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, Ap
46	68.5	14.0	632	4	US-10-369-493-18744	Sequence 18744, A
47	68	13.9	280	3	US-09-323-998D-37	Sequence 37, Appl
48	68	13.9	280	4	US-10-389-566-2296	Sequence 2296, Ap
49	68	13.9	445	4	US-10-844-874-14	Sequence 14, Appl
50	68	13.9	445	5	US-10-713-970-13	Sequence 13, Appl
51	68	13.9	478	4	US-10-087-192-378	Sequence 378, App
52	68	13.9	689	4	US-10-369-493-17280	Sequence 17280, A
53	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
54	68	13.9	1206	5	US-10-491-467-15	Sequence 15, Appl
55	68	13.9	1206	4	US-10-085-198-144	Sequence 144, App
56	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
57	67.5	13.8	166	5	US-10-482-706-269	Sequence 269, App
58	67	13.7	119	4	US-10-389-566-1126	Sequence 1126, Ap
59	67	13.7	167	4	US-10-437-963-158697	Sequence 158697,
60	67	13.7	306	4	US-10-424-599-241560	Sequence 241560,
61	66.5	13.6	315	4	US-10-282-122A-57222	Sequence 57222, A
62	66.5	13.6	315	5	US-10-958-216-464	Sequence 464, App
63	66.5	13.6	315	5	US-10-958-216-466	Sequence 466, App
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65	66.5	13.6	638	5	US-10-831-070-272	Sequence 272, App
66	66.5	13.6	2910	5	US-10-732-923-3342	Sequence 3342, Ap
67	66	13.5	120	4	US-10-389-566-1079	Sequence 1079, Ap
68	66	13.5	120	4	US-10-389-566-1125	Sequence 1125, Ap
69	66	13.5	459	4	US-10-087-192-375	Sequence 375, App
70	65.5	13.4	221	4	US-10-767-701-41912	Sequence 41912, A
71	65.5	13.4	481	5	US-10-732-923-982	Sequence 982, App
72	65.5	13.4	545	5	US-10-732-923-9369	Sequence 9369, Ap
73	65.5	13.4	546	3	US-09-874-923-2	Sequence 2, Appl
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ALIGNMENTS

RESULT 1
US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi

US-09-955-502-14

Query Match	100.0%;	Score 488;	DB 3;	Length 91;
Best Local Similarity	100.0%;	Pred. No. 6.8e-49;		
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RESULT 2

US-09-955-502-16

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; Sequence 16, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
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; LENGTH: 91

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Best Local Similarity	100.0%;	Pred. No. 6.8e-49;		
Matches 91; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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RESULT 3

US-09-955-502-17

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; Sequence 17, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 91

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Best Local Similarity 100.0%; Pred. No. 6.8e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 4

US-09-955-502-18

; Sequence 18, Application US/09955502
; Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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; SEQ ID NO 18
; LENGTH: 91
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; ORGANISM: Salmonella typhimurium
US-09-955-502-18

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Oy 61 EHRKLLQEWVSFLPEGKDVIHIEGYTPEDKK 91
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RESULT 5
US-09-955-502-15

03-03-302-13
Sequence 15, A

Patent No. US20020072118A1

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PR1
; ORGANISM: Salmonella enteritidis
US-09-955-502-15

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Best Local Similarity	100.0%	Pred. No. 4.8e-47;		
Matches 88; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:15:00 ; Search time 5.07859 Seconds
(without alignments)
266.755 Million cell updates/sec

Title: US-09-955-502A-14
Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SFLPEGRDVHIEGYTPEDKK 91

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. NO. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	68	13.9	478	6	US-10-821-234-915 Sequence 915, App
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4	64.5	13.2	177	6	US-10-467-657-1658 Sequence 1658, App
5	63.5	13.0	1432	6	US-10-510-386-218 Sequence 218, App
6	62	12.7	251	7	US-11-054-515-1496 Sequence 1496, App
7	62	12.7	604	6	US-10-942-072-4 Sequence 4, Appli
8	62	12.7	1167	6	US-10-942-072-6 Sequence 6, Appli
9	60.5	12.4	504	7	US-11-072-512-3467 Sequence 3467, App
10	59.5	12.2	264	6	US-10-821-234-1555 Sequence 1555, App
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12	59.5	12.2	285	6	US-10-467-657-8230 Sequence 8230, App
13	59.5	12.2	650	6	US-10-467-657-1948 Sequence 1948, App
14	59.5	12.2	834	6	US-10-453-372-658 Sequence 658, App
15	59.5	12.2	1995	7	US-11-069-834-60 Sequence 60, Appli
16	59	12.1	257	7	US-11-054-515-1710 Sequence 1710, App
17	59	12.1	697	6	US-10-485-517-202 Sequence 202, App
18	59	12.1	1168	6	US-10-942-072-11 Sequence 11, Appli
19	59	12.1	1450	6	US-10-485-517-152 Sequence 152, App
20	58.5	12.0	695	6	US-10-453-372-648 Sequence 648, App
21	58.5	12.0	700	6	US-10-995-561-922 Sequence 922, App
22	58.5	12.0	700	6	US-10-995-561-924 Sequence 924, App
23	58.5	12.0	749	7	US-11-098-686-10505 Sequence 10505, A
24	58.5	12.0	782	6	US-10-793-626-2352 Sequence 2352, App
25	58	11.9	448	6	US-10-618-320A-25 Sequence 25, Appli

26	58	11.9	480	6	US-10-510-386-12	Sequence 12, Appli
27	58	11.9	1501	6	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	6	US-10-453-372-640	Sequence 640, App
30	57.5	11.8	577	7	US-11-072-175-187	Sequence 187, App
31	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	6	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	6	US-10-995-561-925	Sequence 925, App
34	57.5	11.8	804	6	US-10-453-372-650	Sequence 650, App
35	57.5	11.8	847	6	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	6	US-10-453-372-652	Sequence 652, App
37	57.5	11.8	905	6	US-10-453-372-638	Sequence 638, App
38	57.5	11.8	905	6	US-10-453-372-662	Sequence 662, App
39	57.5	11.8	905	6	US-10-453-372-664	Sequence 664, App
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42	57.5	11.8	1012	6	US-10-453-372-646	Sequence 646, App
43	57.5	11.8	3803	6	US-10-995-561-773	Sequence 773, App
44	57.5	11.8	3960	6	US-10-995-561-771	Sequence 771, App
45	57.5	11.8	5335	6	US-10-995-561-777	Sequence 777, App
46	57.5	11.8	5406	6	US-10-995-561-774	Sequence 774, App
47	57.5	11.8	5415	6	US-10-995-561-779	Sequence 779, App
48	57.5	11.8	5464	6	US-10-995-561-775	Sequence 775, App
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51	57	11.7	234	6	US-10-524-972-108	Sequence 108, App
52	57	11.7	432	6	US-10-821-234-1463	Sequence 1463, App
53	57	11.7	440	7	US-11-072-512-3856	Sequence 3856, App
54	56.5	11.6	647	7	US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254	6	US-10-528-031-47	Sequence 47, Appli
56	56.5	11.6	1897	6	US-10-821-234-1635	Sequence 1635, App
57	56.5	11.6	1907	7	US-11-000-463-250	Sequence 250, App
58	56.5	11.6	3433	6	US-10-714-781A-67	Sequence 67, Appli
59	56	11.5	206	7	US-11-124-367A-316	Sequence 316, App
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61	55.5	11.4	279	7	US-11-098-686-10812	Sequence 10812, A
62	55.5	11.4	1188	7	US-11-115-639-42	Sequence 42, Appli
63	55.5	11.4	1188	7	US-11-115-639-43	Sequence 43, Appli
64	55	11.3	189	7	US-11-071-262-1	Sequence 1, Appli
65	55	11.3	667	7	US-10-793-626-198	Sequence 198, App
66	55	11.3	692	7	US-11-038-284-33	Sequence 33, Appli
67	55	11.3	783	7	US-11-037-243-67	Sequence 67, Appli
68	55	11.3	873	7	US-11-038-284-35	Sequence 35, Appli
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70	55	11.3	1142	7	US-11-109-156-22	Sequence 22, Appli
71	55	11.3	2665	7	US-11-124-368A-214	Sequence 214, App
72	55	11.3	2668	7	US-11-124-368A-215	Sequence 215, App
73	54.5	11.2	317	6	US-10-523-503-74	Sequence 74, Appli
74	54.5	11.2	450	6	US-10-618-320A-26	Sequence 26, Appli
75	54.5	11.2	496	7	US-11-069-642-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467, 657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 72.2642 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-15
Perfect score: 474
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Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	98.1	88	5	ABB78160 Amino aci
2	465	98.1	91	5	ABB78161 Amino aci
3	465	98.1	91	5	ABB78159 Amino aci
4	465	98.1	91	5	ABB78162 Amino aci
5	451	95.1	91	5	ABB78163 Amino aci
6	446	94.1	91	5	ABB78158 Amino aci
7	446	94.1	91	5	ABB78157 Amino aci
8	446	94.1	91	5	ABB78156 Amino aci
9	431	90.9	107	7	ABO65445 KLebsiell
10	382	80.6	90	5	ABB78165 Amino aci
11	380	80.2	90	5	ABB78155 Amino aci
12	379	80.0	78	5	ABB78164 Amino aci
13	378	79.7	87	5	ABB78152 Amino aci
14	371	78.3	91	5	ABB78150 Amino aci
15	370	78.1	87	5	ABB78151 Amino aci
16	370	78.1	93	7	ADFO5158 Bacterial
17	364	76.8	87	5	ABB78153 Amino aci
18	329	69.4	88	5	ABB78154 Amino aci
19	252	53.2	76	5	ABB78166 Amino aci
20	242	51.1	87	5	ABB78148 Amino aci
21	242	51.1	87	5	ABB78147 Amino aci
22	228	48.1	86	5	ABB78149 Amino aci
23	221	46.6	87	5	ABB78170 Amino aci
24	221	46.6	122	7	ABO74609 Pseudomon

25	217.5	45.9	89	9	AEB41576	Aeb41576 L. pneumo
26	217.5	45.9	95	9	AEB38294	Aeb38294 L. pneumo
27	212.5	44.8	90	5	ABB78167	Abb78167 Amino aci
28	211	44.5	87	5	ABB78169	Abb78169 Amino aci
29	211	44.5	88	5	ABB78178	Abb78178 Amino aci
30	209	44.1	90	5	ABB78168	Abb78168 Amino aci
31	204	43.0	88	5	ABB78171	Abb78171 Amino aci
32	204	43.0	88	5	ABB78172	Abb78172 Amino aci
33	204	43.0	88	5	ABB78173	Abb78173 Amino aci
34	204	43.0	88	6	ABP77219	Abp77219 N. gonorr
35	199	42.0	87	5	ABB78175	Abb78175 Amino aci
36	193	40.7	87	5	ABB78174	Abb78174 Amino aci
37	190	40.1	87	5	ABB78176	Abb78176 Amino aci
38	188.5	39.8	92	6	ADA34169	Ada34169 Acinetoba
39	188	39.7	87	5	ABB78177	Abb78177 Amino aci
40	130	27.4	110	8	ADL05173	Adl05173 M. catarr
41	72	15.2	309	8	ADN46828	Adn46828 Thermococ
42	72	15.2	506	3	AAV74371	Aay74371 Neisseria
43	72	15.2	507	6	ABU40210	Abu40210 Protein e
44	71	15.0	447	2	AAR52657	Aar52657 Rat N-ace
45	71	15.0	447	7	ADE55944	Ade55944 Rat Prote
46	71	15.0	507	3	AAV74372	Aay74372 Neisseria
47	71	15.0	507	3	AAV74373	Aay74373 Neisseria
48	71	15.0	546	6	ABU38097	Abu38097 Protein e
49	70	14.8	758	9	ADW71760	Adw71760 Salmonell
50	69.5	14.7	184	3	AAB16290	Aab16290 Pinus rad
51	69.5	14.7	1377	8	ADV81847	Adv81847 Streptoco
52	69.5	14.7	1387	8	ADV88434	Adv88434 Streptoco
53	69.5	14.7	1387	8	ADV79687	Adv79687 Streptoco
54	69	14.6	503	4	ABG16577	Abg16577 Novel hum
55	69	14.6	679	9	ADZ85056	Adz85056 Partial F
56	68.5	14.5	184	3	AAB16325	Aab16325 Pinus rad
57	68.5	14.5	184	4	AAB65734	Aab65734 Annexin-1
58	68.5	14.5	184	7	ADB394702	Adb394702 Programme
59	68.5	14.5	608	5	ABP73745	Abp73745 Candida a
60	68	14.3	239	8	ADT07537	Adt07537 Human col
61	68	14.3	257	3	AAG31203	Aag31203 Arabidops
62	68	14.3	280	3	AAV54294	Aay54294 Amino aci
63	68	14.3	280	5	ABG39305	Abg39305 Lactuca s
64	68	14.3	280	8	ADJ50292	Adj50292 Oil-asso
65	68	14.3	285	4	AAB92683	Aab92683 Human pro
66	68	14.3	297	3	AAG31202	Aag31202 Arabidops
67	68	14.3	302	4	AAB88379	Aab88379 Human mem
68	68	14.3	302	9	ADY63123	Ady63123 Human c1o
69	68	14.3	324	3	AAG31201	Aag31201 Arabidops
70	68	14.3	414	6	ABU11747	Abu11747 Human MDD
71	68	14.3	445	2	AAR24781	Aar24781 Human Gnt
72	68	14.3	445	4	AAG67094	Aag67094 Human bet
73	68	14.3	445	7	ADE55946	Ade55946 Human pro
74	68	14.3	445	7	ADI63026	Adi63026 Human apo
75	68	14.3	445	7	ADI63046	Adi63046 Human apo

ALIGNMENTS

RESULT 1	
ABB78160	standard; protein; 88 AA.
ID	ABB78160
XX	
AC	ABB78160;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a YgX homologue.
XX	
KW	Superoxide damage; cell; YgX; Salmonella enterica serovar typhimurium;
XX	
OS	hydroxyl radical; DNA damage; YgX homologue.
XX	
PN	Unidentified.
XX	
XX	US2002072118-A1.

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
DR
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

Query Match 98.1%; Score 465; DB 5; Length 88;
Best Local Similarity 98.9%; Pred. No. 5.4e-47;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKCLNMNNA 60
|||
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKCLNMNNA 60

Qy 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 2
ABB78161
ID ABB78161 standard; protein; 91 AA.

XX ABB78161;
AC
XX 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.
OS
XX US2002072118-A1.
PN
XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homologue, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues

XX Sequence 91 AA;

Query Match 98.1%; Score 465; DB 5; Length 91;
Best Local Similarity 98.9%; Pred. No. 5.6e-47;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSPTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKCLNMNNA 60
|||
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKCLNMNNA 60

Qy 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
|||||
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 3
ABB78159
ID ABB78159 standard; protein; 91 AA.

XX ABB78159;

XX 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.

XX US2002072118-A1.
PN
XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

XX Downs D, Gralnick JA;

XX WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.62187 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-15

Perfect score: 474
Sequence: 1 MSPTIFCTYLQDAEGQDFQ.....EMVSEFLFEKGKDVHIEGYTPS 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	465	98.1	91	2 AH0879	conserved hypotnet
2	446	94.1	91	2 A85954	hypothetical prote
3	446	94.1	91	2 A65082	hypothetical prote
4	446	94.1	91	2 F91108	hypothetical prote
5	382	80.6	90	2 A10116	conserved hypotnet
6	380	80.2	90	2 C82320	conserved hypotnet
7	378	79.7	90	2 C64013	hypothetical prote
8	252	53.2	93	2 E84994	hypothetical prote
9	222	46.8	105	2 C82624	conserved hypotnet
10	221	46.6	90	2 H83003	conserved hypotnet
11	204	43.0	88	2 H81014	conserved hypotnet
12	79.5	16.8	1638	2 D87749	protein unc-73b li
13	79.5	16.8	2488	2 T42739	guanine nucleotide
14	74	15.6	1260	2 T04440	hypothetical prote
15	73.5	15.5	495	2 AH0985	probable zinc-prot
16	71.5	15.1	209	2 I64172	hypothetical prote
17	71	15.0	447	2 JC2076	alpha-1,3-mannosyl
18	71	15.0	507	2 C81063	fumarate hydratase
19	71	15.0	546	2 A81807	fumarate hydratase
20	70	14.8	758	2 AD0763	thiosulfate reduct
21	70	14.8	758	2 A57143	thiosulfate-dithio
22	69.5	14.7	859	2 T29630	hypothetical prote
23	69	14.6	265	2 T46013	hypothetical prote
24	68	14.3	324	2 T05429	hypothetical prote
25	68	14.3	445	1 XUHUMB	alpha-1,3-mannosyl
26	68	14.3	689	2 F83902	beta-galactosidase
27	67.5	14.2	166	2 F70562	hypothetical prote
28	67	14.1	447	1 A38561	alpha-1,3-mannosyl
29	67	14.1	1111	2 T23047	hypothetical prote

30	66.5	14.0	548	2 A54510	63K antigen - nema
31	66.5	14.0	618	2 A71364	probable phosphoen
32	66	13.9	447	1 A42500	alpha-1,3-mannosyl
33	66	13.9	1085	2 S62516	hypothetical coile
34	65.5	13.8	365	2 B54128	Fc-binding protein
35	65	13.7	251	2 E90428	hypothetical prote
36	65	13.7	507	2 A83105	probable fummarase
37	65	13.7	593	2 C64097	probable soluble 1
38	65	13.7	628	2 AF2393	hypothetical prote
39	65	13.7	1230	2 S56850	SMC1 protein homol
40	64.5	13.6	401	2 AE1978	hypothetical prote
41	64.5	13.6	511	2 A99574	ABC transporter at
42	64.5	13.6	544	2 T40058	probable chromatin
43	63.5	13.4	327	2 AD2129	transcription regu
44	63.5	13.4	379	2 S70709	type II site-speci
45	63.5	13.4	410	1 KHM5D	cathepsin D (EC 3.
46	63.5	13.4	1119	2 T15842	hypothetical prote
47	63.5	13.4	2672	2 A48126	translation activa
48	63	13.3	235	2 G65212	hypothetical prote
49	63	13.3	258	2 A97991	phosphoesterase, p
50	63	13.3	258	2 E95121	hypothetical prote
51	63	13.3	447	2 T16527	ybeV protein - Esc
52	63	13.3	483	2 G64799	hypothetical prote
53	63	13.3	543	2 T16015	hypothetical prote
54	63	13.3	549	2 T16016	ATP-dependent heli
55	63	13.3	703	2 B82148	hypothetical prote
56	63	13.3	1209	2 T46027	guandine nucleoti
57	63	13.3	1327	2 T14594	SNF2alpha protein
58	63	13.3	1572	2 S45251	HBRM protein - hum
59	63	13.3	1586	2 S39580	shikimate kinase (
60	62.5	13.2	165	2 A81382	conserved hypotnet
61	62.5	13.2	259	2 G83203	conserved hypotnet
62	62.5	13.2	287	2 F82265	asparaginase (EC 3
63	62.5	13.2	305	2 A75211	hypothetical prote
64	62.5	13.2	498	2 G91179	hypothetical prote
65	62.5	13.2	498	2 H86025	53.1K protein prec
66	62.5	13.2	498	2 S47748	alanyl-tRNA synthe
67	62.5	13.2	906	2 G69531	hypothetical prote
68	62.5	13.2	1141	2 T29185	conserved hypotnet
69	62	13.1	156	2 F70382	paraasporal crystal
70	62	13.1	643	2 A43647	phosphoenolpyruvat
71	62	13.1	898	2 D95123	phosphoenolpyruvat
72	62	13.1	898	2 F97993	genome polyprotein
73	62	13.1	3388	1 GNMVDP	probable L-asparag
74	61.5	13.0	305	2 A71247	hypothetical prote
75	61.5	13.0	414	2 T49916	

ALIGNMENTS

RESULT 1
AH0879
conserved hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_rev1sion 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0879
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
C/Genetic8:
A/Gene: STY3266
C/Superfamily: fe(II) trafficking protein YggX

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Query Match      98.1%; Score 465; DB 2; Length 91;
Best Local Similarity 98.9%; Pred. No. 7.2e-41;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 MSPTFCTYLORDAEGODFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNA 60
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DB      1 MSRTIFCTYLORDAEGODFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMNNA 60

QY      61 EHRKLLEQEMWSFLFEGKDVIHIEGYTPR 88
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB      61 EHRKLLEQEMWSFLFEGKDVIHIEGYTPR 88

RESULT 2
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UP10000163A04; GB:AE005174; NID:g12517511; F
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
C/Superfamily: fe(II) trafficking protein YggX

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Query Match          94.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 6.4e-39;
Matches 82; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSPTICTYLQDAEGDQFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNA 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MSRTIFCTFLQREAEGDQFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNA 60

OY 61 EHRKLEQEMVSLFEGKDVHIEGYTPE 88
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EHRKLEQEMVNFLEGEKDVHIEGYTPE 88

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:G
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein YggX

Query Match          94.1%; Score 446; DB 2; Length 91;
Best Local Similarity 93.2%; Pred. No. 6.4e-39;
Matches 82; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSPTICTYLQDAEGDQFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKLNMMNA 60
    |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db          1 MSRTIFCTPLQREABGQDFQLYPGLGKRIYNEISKEAMAOHQKQTMLINEKLNMMNNA 60
OY          61 EHRKLEQEMVSYFLFEGKDVHIEGYTPE 88
            |||||||:|||||:|||||
Db          61 EHRKLEQEMVNYFLFEGKEVHIEGYTPE 88

RESULT 4
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain RIMD
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629, MUID:21156231, PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065, UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein yggX

```

[illegible]

RESULT 5
AI0116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
C/Accession: AI0116
R/Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
Il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AI0116
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <KUR>
A/Cross-references: UNIPARC:UPI0000DDCC4; GB:AL590842; PIDN:CAC89796.1; PID:G15979022;
C/Genetics:
A/Gene: YPO0953
C/Superfamily: fe(II) trafficking protein YggX

	Query Match	80.6%;	Score 382;	DB 2;	length 90;	
	Best Local Similarity	81.6%;	Pred. No. 2.4e-32;			
Matches	71; Conservative	9;	Mismatches 7;	Indels 0;	Gaps 0	
QY	1 MSPITFCTYLQRDAEGQDFOLYPGELGKRIYNEISKDAAWQHOKOTMLINEKGLNMNNA 60 ::: : ::: :					
Dd	1 MSRTIFCTFLKKDAERQDFQLYPGEIGKRIYNEISKEAWSQWTTKQTMLINEKSLSPNNI 60					
QY	61 EHRKLLEQEMWSFLPEGKDVIHIEGYTP 87 ::: : :					
Dd	61 EDRLLEQEMWNFLPEGDVHIAGYTP 87					

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 64.8474 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-15
Perfect score: 474
Sequence: 1 MSPTFCTYLQRDAGQDFQ.....EMVSFLFEKDVHIEGYTPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	460	97.0	90	1	FETP_SALCH Q57K04 salmonella
2	460	97.0	90	1	FETP_SALPA Q5pmn1 salmonella
3	460	97.0	90	1	FETP_SALTI P67618 salmonella
4	460	97.0	90	1	FETP_SALTY P67617 salmonella
5	441	93.0	90	1	FETP_ECOS7 P0a8p4 escherichia
6	441	93.0	90	1	FETP_ECOLI P0a8p3 escherichia
7	441	93.0	90	1	FETP_SHIFL P0a8p5 shigella fl
8	437	92.2	90	1	FETP_ECOL6 Q8fe19 escherichia
9	409	86.3	90	1	FETP_ERWCT Q6d8j9 erwinia car
10	390	82.3	90	1	FETP_YERPS Q666m3 yersinia ps
11	386	81.4	90	1	FETP_VIBPA Q871i5 vibrio para
12	382	80.6	90	1	FETP_YERPE Q8zhe7 yersinia pe
13	380	80.2	90	1	FETP_VIBCH Q9kura4 vibrio chol
14	380	80.2	91	1	FETP_MANSN Q65vt7 manheimia
15	378	79.7	90	1	FETP_HAEIN P44048 haemophilus
16	378	79.7	90	1	FETP_VIBVU Q8dcs5 vibrio vuln
17	378	79.7	90	1	FETP_VIBVY Q7mh14 vibrio vuln
18	378	79.7	90	2	Q4QMD9_HAEI8 Q4qmd9 haemophilus
19	372	78.5	90	1	FETP_PHOPR Q6lmk7 photobacter
20	370	78.1	90	1	FETP_PASMU Q9c1b9 pasteurilla
21	364	76.8	94	1	FETP_HAEDU Q7vkb6 haemophilus
22	363	76.6	90	1	FETP_PHOHL Q7n711 photorhabdu
23	358	75.5	90	1	FETP_VIBF1 Q5e7c0 vibrio fisc
24	333	70.3	90	1	FETP_IDILO Q5qy58 idiomarina
25	329	69.4	92	1	FETP_SHEON Q8ebx6 shewanella
26	252	53.2	77	1	FETP_BUCAI P57618 buchenera ap
27	242	51.1	90	1	FETP_BORBR Q7wh06 bordetella
28	242	51.1	90	1	FETP_BORPA Q7w9q2 bordetella
29	242	51.1	90	1	FETP_BORPE Q7wvc4 bordetella
30	236	49.8	78	1	FETP_BUCAP Q8k925 buchenera ap
31	232	48.9	91	1	FETP_XANAC Q8pjh7 xanthomonas

32	225	47.5	92	1	FETP_XANOR	Q5gy22 xanthomonas
33	222	46.8	90	1	FETP_XYLFA	Q9pc73 xylella fas
34	221.5	46.7	89	1	FETP_LEGPL	Q5wvc4 legionella
35	221	46.6	90	1	FETP_PSEAB	Q9hu36 pseudomonas
36	221	46.6	92	1	FETP_XANCP	Q8p829 xanthomonas
37	221	46.6	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
38	218	46.0	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
39	218	46.0	90	1	FETP_XYLFT	Q87d06 xylella fas
40	217.5	45.9	89	1	FETP_LEGPA	Q5x3x9 legionella
41	217.5	45.9	89	1	FETP_LEGPH	Q5zu80 legionella
42	211	44.5	90	1	FETP_PSEBK	Q83d06 coxiella bu
43	211	44.5	90	2	Q4J228_AZOVI	Q88r49 pseudomonas
44	209	44.1	79	1	FETP_CANBF	Q4j228 azotobacter
45	209	44.1	90	1	FETP_PSEBSM	Q7vrg9 candidatus
46	209	44.1	90	1	Q4ZLP3_PSESY	Q87uf5 pseudomonas
47	209	44.1	90	2	Q6T7F6_PSEFL	Q4zlp3 pseudomonas
48	208	43.9	90	2	FETP_CHRVO	Q6t7f6 pseudomonas
49	206	43.5	90	1	FETP_NITEU	Q7nsr4 chromobacte
50	205	43.2	90	1	FETP_NEIGI	Q82xf2 nitrosomona
51	204	43.0	88	1	FETP_NEIMA	Q5f553 neisseria g
52	204	43.0	88	1	FETP_NEIMB	P67615 neisseria m
53	204	43.0	88	1	FETP_BURMA	Q89a44 buchenera ap
54	201	42.4	87	1	FETP_BURPS	Q62iur burkholderi
55	199	42.0	91	1	Q4KJT2_PSEFS	Q63ej4 burkholderi
56	199	42.0	90	2	FETP_RALSO	Q4kjt2 pseudomonas
57	198	41.8	91	2	Q4LSI9_9BURK	Q8y010 ralstonia s
58	196	41.4	91	2	FETP_FRATT	Q4ls19 burkholderi
59	192	40.5	87	1	FETP_METCA	Q5nhj8 francisella
60	188	39.7	90	1	FETP_AC1AD	Q60aj7 methylococc
61	183.5	38.7	90	1	Q4FWJ7_9GAMM	Q4fvj7 psychrobact
62	145	30.6	96	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
63	135	28.5	92	2	Q5NUY1_9BURK	Q5nuyl1 ralstonia m
64	82.5	17.4	482	2	Q6AIZ9_DESPS	Q6aiz9 desulfotale
65	82.5	17.4	514	2	Q7KXP4_CABEL	Q7kxp4 caenorhabdi
66	79.5	16.8	1638	2	Q6BHW2_CABEL	Q6bew2 caenorhabdi
67	79.5	16.8	2140	2	O61528_CABEL	O61528 caenorhabdi
68	79.5	16.8	2488	2	O5CJ53_CRYHO	O5cj53 cryptospori
69	77	16.2	1047	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
70	76.5	16.1	486	2	Q5CYM7_CRYPV	Q5cym7 cryptospori
71	75	15.8	508	2	Q49677_ARATH	Q49677 arabidopsis
72	75	15.8	1278	2	YHUJ_SALTI	Q8z286 salmonella
73	74	15.6	1260	2		
74	74	15.6	495	1		
75	73.5	15.5				

ALIGNMENTS

RESULT 1
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=YsgX; OrderedLocNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
RT Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-requiring processes, such as synthesis and/or


```
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AB017220; AAX66958.1; -; Genomic_DNA.
DR      HAMAP; MF_00686; -; 1.
DR      InterPro; IPR007457; YggX.
DR      ProDom; PD029191; DUF495; 1.
KM      Complete proteome; Iron.
FT      INIT MET 0
SQ      SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;

Query Match          97.0%; Score 460; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.7e-41;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 SPTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNAE 61
        |||
        1 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNAE 60

QY      62 HRKLLQEMVSFLFEGKDVHIEGYTPE 88
        |||
        61 HRKLLQEMVSFLFEGKDVHIEGYTPE 87

Db

RESULT 2
FETP_SALPA
ID      FETP_SALPA          STANDARD;          PRT;          90 AA.
AC      Q5PMM1;
RC      STRAIN=ATCC 9150 / SARB42;
RX      PubMed=15531882; DOI=10.1038/ng1470;
RA      McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA      Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., McLellan M.,
RA      Harkins C.R., Wang C., Nguyen C., Berghoff A., Elliott G.,
RA      Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA      Leonard S., Sun H., Fulton L., Nash W., Miner T., Minx P.,
RA      Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA      Spieth J., Wilson R.K.;
RT      "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT      restricted serovars of Salmonella enterica that cause typhoid.";
RL      Nat. Genet. 36:1268-1274(2004).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-requiring processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
DR      SMR; Q5PMM1; 1-91.
DR      HAMAP; MF_00686; -; 1.
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DR      InterPro; IPR007457; YggX.
DR      ProDom; PD029191; DUF495; 1.
KM      Complete proteome; Iron.
FT      INIT MET 0
SQ      SEQUENCE 90 AA; 10768 MW; B3B6A1EE22555E3C CRC64;

Query Match          97.0%; Score 460; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 2.7e-41;
Matches 86; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 SPTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNAE 61
        |||
        1 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNAE 60

Db

QY      62 HRKLLQEMVSFLFEGKDVHIEGYTPE 88
        |||
        61 HRKLLQEMVSFLFEGKDVHIEGYTPE 87

Db

RESULT 3
FETP_SALTI
ID      FETP_SALTI          STANDARD;          PRT;          90 AA.
AC      P67618; Q8XFV6;
DT      10-OCT-2003 (Rel. 42, Created)
DT      10-OCT-2003 (Rel. 42, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Probable Fe(2+) trafficking protein.
GN      Name=YggX; OrderedLocustNames=STRY3266, t3024;
OS      Salmonella typhi.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmonella.
OX      NCBI_TaxID=601;
RN      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=CT18;
RX      MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA      Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA      Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA      Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA      Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA      Felwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA      Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA      Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA      Whitehead S., Barrett B.G.;
RT      "Complete genome sequence of a multiple drug resistant Salmonella
RT      enterica serovar Typhi CT18.";
RL      Nature 413:848-852(2001).
RN      [2]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=Ty2 / ATCC 700931;
RX      MEDLINE=22531367; PubMed=12644504;
RX      DOI=10.1128/JB.185.7.2330-2337.2003;
RA      Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA      Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT      "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT      and CT18.";
RL      J. Bacteriol. 185:2330-2337(2003).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-requiring processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
DR      EMBL; AL627277; CAD02936.1; -; Genomic_DNA.
DR      EMBL; AB016844; AAO70576.1; -; Genomic_DNA.
DR      SMR; P67618; 1-90.
DR      HAMAP; MF_00686; -; 1.
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 17.8405 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-15

Perfect score: 474
Sequence: 1 MSPFTICTYLQRDAGGDFQ.....EMVSLFEGKDVHIEGYTP 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	431	90.9	107	2	US-09-489-039A-11962 Sequence 11962, A
2	370	78.1	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	221	46.6	122	2	US-09-252-991A-23355 Sequence 23355, A
4	188.5	39.8	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	130	27.4	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	68.5	14.5	184	2	US-09-325-932A-66 Sequence 66, Appl
7	68.5	14.5	544	2	US-09-248-796A-18911 Sequence 18911, A
8	68	14.3	280	2	US-09-323-998E-37 Sequence 37, Appl
9	68	14.3	1214	2	US-10-164-595-24 Sequence 24, Appl
10	66.5	14.0	548	2	US-09-167-299-3 Sequence 3, Appli
11	66	13.9	292	2	US-09-328-352-5836 Sequence 5836, Ap
12	65	13.7	474	2	US-09-252-991A-24473 Sequence 24473, A
13	64	13.5	337	2	US-09-270-767-41746 Sequence 41746, A
14	64	13.5	1176	2	US-09-489-039A-8879 Sequence 8879, Ap
15	63	13.3	1586	2	US-09-538-092-1171 Sequence 1171, Ap
16	62.5	13.2	260	2	US-09-252-991A-17498 Sequence 17498, A
17	62.5	13.2	419	2	US-09-543-681A-7295 Sequence 7295, Ap
18	62.5	13.2	662	2	US-09-513-999C-4800 Sequence 4800, Ap
19	62.5	13.2	664	2	US-09-107-433-2775 Sequence 2775, Ap
20	62	13.1	227	2	US-09-270-767-58283 Sequence 58283, A
21	62	13.1	238	2	US-09-323-998E-41 Sequence 41, Appl
22	62	13.1	448	2	US-09-270-767-42959 Sequence 42959, A
23	62	13.1	604	2	US-09-008-097-4 Sequence 4, Appli
24	62	13.1	604	2	US-09-472-667-4 Sequence 4, Appli
25	62	13.1	644	2	US-08-793-331-7 Sequence 7, Appli
26	62	13.1	898	2	US-09-583-110-3750 Sequence 3750, Ap
27	62	13.1	899	2	US-09-107-433-3196 Sequence 3196, Ap

28	62	13.1	1167	2	US-09-008-097-6	Sequence 6, Appli
29	62	13.1	1167	2	US-09-472-667-6	Sequence 6, Appli
30	61.5	13.0	591	2	US-09-370-368-8	Sequence 8, Appli
31	61	12.9	143	2	US-09-270-767-45872	Sequence 45872, A
32	61	12.9	184	2	US-09-270-767-61671	Sequence 61671, A
33	61	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
34	61	12.9	389	2	US-09-270-767-46116	Sequence 46116, A
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36	60.5	12.8	525	2	US-09-540-236-2250	Sequence 2250, Ap
37	60.5	12.8	527	2	US-09-489-039A-10883	Sequence 10883, A
38	60.5	12.8	701	2	US-09-252-991A-23288	Sequence 23288, A
39	60	12.7	232	2	US-09-201-641-8	Sequence 8, Appli
40	60	12.7	232	2	US-09-323-998E-36	Sequence 36, Appli
41	60	12.7	421	2	US-09-489-039A-7512	Sequence 7512, Ap
42	59.5	12.6	139	2	US-09-513-999C-4802	Sequence 4802, Ap
43	59.5	12.6	258	2	US-09-513-999C-4800	Sequence 4800, Ap
44	59.5	12.6	264	2	US-09-949-016-6012	Sequence 6012, Ap
45	59.5	12.6	276	2	US-09-949-016-11703	Sequence 11703, A
46	59.5	12.6	434	2	US-09-303-518D-334	Sequence 334, App
47	59.5	12.6	680	2	US-09-298-924-4	Sequence 4, Appli
48	59.5	12.6	687	2	US-09-538-092-539	Sequence 539, App
49	59.5	12.6	720	1	US-08-840-236-1	Sequence 1, Appli
50	59.5	12.6	720	1	US-08-505-448A-1	Sequence 1, Appli
51	59.5	12.6	921	2	US-09-248-796A-14950	Sequence 14950, A
52	59	12.4	98	2	US-09-270-767-41085	Sequence 41085, A
53	59	12.4	98	2	US-09-270-767-56301	Sequence 56301, A
54	59	12.4	113	2	US-08-894-173-93	Sequence 93, Appl
55	59	12.4	113	2	US-09-398-193-93	Sequence 93, Appl
56	59	12.4	119	2	US-09-328-352-7391	Sequence 7391, Ap
57	59	12.4	234	2	US-09-296-754-2	Sequence 2, Appli
58	59	12.4	284	1	US-08-624-125-16	Sequence 16, Appl
59	59	12.4	284	2	US-08-937-155-16	Sequence 16, Appl
60	59	12.4	284	2	US-09-323-998E-16	Sequence 16, Appl
61	59	12.4	331	2	US-09-328-352-6400	Sequence 6400, Ap
62	59	12.4	444	2	US-09-861-451A-16	Sequence 16, Appl
63	59	12.4	697	2	US-08-816-177-2	Sequence 2, Appli
64	59	12.4	1094	2	US-09-949-016-8755	Sequence 8755, Ap
65	59	12.4	1094	2	US-09-949-016-8756	Sequence 8756, Ap
66	59	12.4	1147	2	US-09-949-016-8861	Sequence 8861, Ap
67	59	12.4	1147	2	US-09-949-016-8862	Sequence 8862, Ap
68	59	12.4	1165	1	US-08-240-357-2	Sequence 2, Appli
69	59	12.4	1168	2	US-09-474-076-2	Sequence 2, Appli
70	59	12.4	1168	2	US-09-472-667-11	Sequence 11, Appl
71	59	12.4	1168	2	US-10-201-000-2	Sequence 2, Appli
72	58.5	12.3	57	2	US-09-562-737-124	Sequence 124, App
73	58.5	12.3	116	2	US-09-562-737-125	Sequence 125, App
74	58.5	12.3	233	1	US-08-557-309B-40	Sequence 40, Appl
75	58.5	12.3	233	2	US-08-834-306-40	Sequence 40, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 55.7267 Seconds
(without alignments)
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Title: US-09-955-502A-15

Perfect score: 474

Sequence: 1 MSPRTFCTYLQDAEGQDFQ.....EMVSFLPEKDVHIEGYTP 88

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Published Applications AA Main:*

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- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	465	98.1	91	3	US-09-955-502-17
5	451	95.1	91	3	US-09-955-502-18
6	446	94.1	91	3	US-09-955-502-11
7	446	94.1	91	3	US-09-955-502-12
8	446	94.1	91	3	US-09-955-502-13
9	382	80.6	90	3	US-09-955-502-20
10	380	80.2	90	3	US-09-955-502-10
11	379	80.0	78	3	US-09-955-502-19
12	378	79.7	87	3	US-09-955-502-7
13	371	78.3	91	3	US-09-955-502-5
14	370	78.1	87	3	US-09-955-502-6
15	364	76.8	87	3	US-09-955-502-8
16	329	69.4	88	3	US-09-955-502-9
17	252	53.2	76	3	US-09-955-502-21
18	242	51.1	87	3	US-09-955-502-2
19	242	51.1	87	3	US-09-955-502-3
20	228	48.1	86	3	US-09-955-502-4
21	222	46.8	89	3	US-09-955-502-22
22	221	46.6	87	3	US-09-955-502-25
23	211	44.5	87	3	US-09-955-502-24
24	211	44.5	88	3	US-09-955-502-33
25	209	44.1	90	3	US-09-955-502-23
26	204	43.0	88	3	US-09-955-502-26
27	204	43.0	88	3	US-09-955-502-27

28	204	43.0	88	3	US-09-955-502-28	Sequence 28, Appl
29	199	42.0	87	3	US-09-955-502-29	Sequence 29, Appl
30	199	42.0	87	3	US-09-955-502-30	Sequence 30, Appl
31	190	40.1	87	3	US-09-955-502-31	Sequence 31, Appl
32	188	39.7	87	3	US-09-955-502-32	Sequence 32, Appl
33	72	15.2	507	4	US-10-282-122A-68134	Sequence 68134, A
34	72	15.2	1261	4	US-10-437-963-189166	Sequence 189166, A
35	71	15.0	546	4	US-10-282-122A-66021	Sequence 66021, A
36	69.5	14.7	184	4	US-10-393-840-52	Sequence 52, Appl
37	69	14.6	503	5	US-10-450-763-46936	Sequence 46936, A
38	69	14.6	679	5	US-10-805-684-105	Sequence 105, Appl
39	68.5	14.5	184	4	US-10-219-220-66	Sequence 66, Appl
40	68.5	14.5	184	4	US-10-393-840-118	Sequence 118, Appl
41	68.5	14.5	449	4	US-10-424-599-279212	Sequence 279212, A
42	68.5	14.5	608	4	US-10-032-585-7582	Sequence 7582, Ap
43	68	14.3	280	3	US-09-323-998D-37	Sequence 37, Appl
44	68	14.3	280	4	US-10-389-566-2296	Sequence 2296, Ap
45	68	14.3	445	4	US-10-844-874-14	Sequence 14, Appl
46	68	14.3	445	5	US-10-713-970-13	Sequence 13, Appl
47	68	14.3	478	4	US-10-087-192-378	Sequence 378, Appl
48	68	14.3	689	4	US-10-369-493-17280	Sequence 17280, A
49	68	14.3	764	4	US-10-416-330-37	Sequence 37, Appl
50	68	14.3	764	5	US-10-491-467-15	Sequence 15, Appl
51	68	14.3	1206	4	US-10-085-198-144	Sequence 144, Appl
52	68	14.3	1214	5	US-10-717-665-24	Sequence 24, Appl
53	67.5	14.2	166	5	US-10-482-706-269	Sequence 269, Appl
54	67.5	14.2	835	4	US-10-282-122A-53271	Sequence 53271, A
55	67	14.1	119	4	US-10-389-566-1126	Sequence 1126, Ap
56	67	14.1	167	4	US-10-437-963-158697	Sequence 158697, A
57	67	14.1	561	4	US-10-437-963-158697	Sequence 158697, A
58	66.5	14.0	786	5	US-10-732-923-4885	Sequence 4885, Ap
59	66	13.9	120	4	US-10-389-566-1079	Sequence 1079, Ap
60	66	13.9	120	4	US-10-389-566-1125	Sequence 1125, Ap
61	66	13.9	459	4	US-10-087-192-375	Sequence 375, Appl
62	65.5	13.8	306	4	US-10-424-599-241560	Sequence 241560, A
63	65.5	13.8	2910	5	US-10-732-923-3342	Sequence 3342, Ap
64	65	13.7	290	4	US-10-389-566-2247	Sequence 2247, Ap
65	65	13.7	1230	4	US-10-369-493-22160	Sequence 22160, A
66	64.5	13.6	239	6	US-11-097-143-6306	Sequence 6306, Ap
67	64	13.5	325	4	US-10-369-493-19793	Sequence 19793, A
68	63.5	13.4	102	3	US-09-864-408A-768	Sequence 768, Appl
69	63.5	13.4	172	5	US-10-450-763-34132	Sequence 34132, A
70	63.5	13.4	176	4	US-10-425-115-346175	Sequence 346175, A
71	63.5	13.4	242	4	US-10-393-840-55	Sequence 55, Appl
72	63.5	13.4	1588	4	US-10-437-963-189741	Sequence 189741, A
73	63	13.3	246	4	US-10-424-599-156020	Sequence 156020, A
74	63	13.3	251	3	US-09-880-748-1496	Sequence 1496, Ap
75	63	13.3	251	4	US-10-293-418-1496	Sequence 1496, Ap

ALIGNMENTS

RESULT 1
US-09-955-502-15
; Sequence 15, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnicks, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmonella enteritidis

US-09-955-502-15

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Best Local Similarity 98.9%; Pred. No. 1e-46;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
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Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 2

US-09-955-502-14

; Sequence 14, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 14

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella paratyphi

US-09-955-502-14

Query Match 98.1%; Score 465; DB 3; Length 91;
Best Local Similarity 98.9%; Pred. No. 1e-46;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
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Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 3

US-09-955-502-16

; Sequence 16, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 16

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella dublin

US-09-955-502-16

Query Match 98.1%; Score 465; DB 3; Length 91;

Best Local Similarity 98.9%; Pred. No. 1e-46;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
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Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 4

US-09-955-502-17

; Sequence 17, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 17

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhi CT18

US-09-955-502-17

Query Match 98.1%; Score 465; DB 3; Length 91;
Best Local Similarity 98.9%; Pred. No. 1e-46;
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QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88
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Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPE 88

RESULT 5

US-09-955-502-18

; Sequence 18, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; PRIOR FILING DATE: 2000-09-22

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 18

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Salmonella typhimurium

US-09-955-502-18

Query Match 95.1%; Score 451; DB 3; Length 91;
Best Local Similarity 96.6%; Pred. No. 4.6e-45;
Matches 85; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

GenCore version 5.1.7
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Title: US-09-955-502A-15

Perfect score: 474
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- 4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	68	14.3	478	6	US-10-821-234-915 Sequence 915, App
3	65	13.7	593	7	US-11-194-246-317 Sequence 317, App
4	63	13.3	251	7	US-11-054-515-1496 Sequence 1496, App
5	62	13.1	604	6	US-10-942-072-6 Sequence 4, Appl1
6	62	13.1	1167	6	US-10-942-072-6 Sequence 6, Appl1
7	60.5	12.8	1177	6	US-10-467-657-1658 Sequence 1658, App
8	60.5	12.8	1432	6	US-10-510-386-218 Sequence 218, App
9	59.5	12.6	264	6	US-10-821-234-1555 Sequence 1555, App
10	59.5	12.6	650	6	US-10-467-657-1948 Sequence 1948, App
11	59.5	12.6	834	6	US-10-453-372-658 Sequence 658, App
12	59.5	12.6	1995	7	US-11-069-834-60 Sequence 60, Appl1
13	59	12.4	697	6	US-10-485-517-202 Sequence 202, App
14	59	12.4	1168	6	US-10-942-072-11 Sequence 11, Appl1
15	59	12.4	1450	6	US-10-485-517-152 Sequence 152, App
16	58.5	12.3	285	6	US-10-467-657-222 Sequence 222, App
17	58.5	12.3	285	6	US-10-467-657-8230 Sequence 8230, App
18	58.5	12.3	695	6	US-10-453-372-648 Sequence 648, App
19	58.5	12.3	700	6	US-10-995-561-922 Sequence 922, App
20	58.5	12.3	700	6	US-10-995-561-924 Sequence 924, App
21	58.5	12.3	749	7	US-11-098-686-10505 Sequence 10505, App
22	58.5	12.3	782	6	US-10-793-626-2352 Sequence 2352, App
23	58	12.2	257	7	US-11-054-515-1710 Sequence 1710, App
24	58	12.2	480	6	US-10-510-386-12 Sequence 12, Appl1
25	57.5	12.1	336	6	US-10-453-372-640 Sequence 640, App

26	57.5	12.1	752	7	US-11-072-512-3003	Sequence 3003, App
27	57.5	12.1	775	6	US-10-453-372-656	Sequence 656, App
28	57.5	12.1	793	6	US-10-995-561-925	Sequence 925, App
29	57.5	12.1	804	6	US-10-453-372-650	Sequence 650, App
30	57.5	12.1	847	6	US-10-453-372-654	Sequence 654, App
31	57.5	12.1	857	6	US-10-453-372-652	Sequence 652, App
32	57.5	12.1	905	6	US-10-453-372-638	Sequence 638, App
33	57.5	12.1	905	6	US-10-453-372-662	Sequence 662, App
34	57.5	12.1	905	6	US-10-453-372-664	Sequence 664, App
35	57.5	12.1	963	6	US-10-995-561-923	Sequence 923, App
36	57.5	12.1	963	6	US-10-453-372-660	Sequence 660, App
37	57.5	12.1	1012	6	US-10-453-372-646	Sequence 646, App
38	57	12.0	234	6	US-10-524-647-120	Sequence 120, App
39	57	12.0	234	6	US-10-524-972-108	Sequence 108, App
40	57	12.0	432	6	US-10-821-234-1463	Sequence 1463, App
41	57	12.0	504	7	US-11-072-512-3467	Sequence 3467, App
42	56.5	11.9	242	7	US-11-022-562-220	Sequence 220, App
43	56.5	11.9	647	7	US-11-000-463-722	Sequence 722, App
44	56.5	11.9	692	7	US-11-038-284-33	Sequence 33, Appl1
45	56.5	11.9	873	7	US-11-038-284-35	Sequence 35, Appl1
46	56.5	11.9	889	7	US-11-038-284-15	Sequence 15, Appl1
47	56.5	11.9	1254	6	US-10-528-031-47	Sequence 47, Appl1
48	56.5	11.9	1897	6	US-10-821-234-1635	Sequence 1635, App
49	56.5	11.9	1907	7	US-11-000-463-250	Sequence 250, App
50	56	11.8	206	7	US-11-124-367A-316	Sequence 316, App
51	56	11.8	1011	7	US-11-098-686-10257	Sequence 10257, App
52	56	11.8	3433	7	US-10-714-781A-67	Sequence 67, Appl1
53	55.5	11.7	279	7	US-11-098-686-10812	Sequence 10812, App
54	55	11.6	189	7	US-11-071-262-1	Sequence 1, Appl1
55	55	11.6	667	6	US-10-793-626-198	Sequence 198, App
56	55	11.6	1142	7	US-11-109-156-22	Sequence 22, Appl1
57	55	11.6	1501	6	US-10-793-626-2850	Sequence 2850, App
58	54.5	11.5	317	6	US-10-523-503-74	Sequence 74, Appl1
59	54.5	11.5	496	7	US-11-069-642-20	Sequence 20, Appl1
60	54	11.4	111	6	US-10-771-257-34	Sequence 34, Appl1
61	54	11.4	111	7	US-11-127-677-34	Sequence 34, Appl1
62	54	11.4	426	7	US-11-098-686-10340	Sequence 10340, App
63	54	11.4	783	7	US-11-037-243-67	Sequence 67, Appl1
64	53.5	11.3	179	6	US-10-467-657-6542	Sequence 6542, App
65	53.5	11.3	313	6	US-10-995-561-972	Sequence 972, App
66	53.5	11.3	335	6	US-10-995-561-970	Sequence 970, App
67	53.5	11.3	345	6	US-10-995-561-971	Sequence 971, App
68	53.5	11.3	384	6	US-10-467-657-2024	Sequence 2024, App
69	53.5	11.3	774	7	US-11-070-627-7	Sequence 7, Appl1
70	53.5	11.3	3803	6	US-10-995-561-773	Sequence 773, App
71	53.5	11.3	3960	6	US-10-995-561-771	Sequence 771, App
72	53.5	11.3	5335	6	US-10-995-561-777	Sequence 777, App
73	53.5	11.3	5406	6	US-10-995-561-774	Sequence 774, App
74	53.5	11.3	5415	6	US-10-995-561-779	Sequence 779, App
75	53.5	11.3	5464	6	US-10-995-561-775	Sequence 775, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-16
Perfect score: 490
Sequence: 1 MSPTIFCTYIQRDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	481	98.2	91	5	ABB78161	Abb78161 Amino aci
2	481	98.2	91	5	ABB78159	Abb78159 Amino aci
3	481	98.2	91	5	ABB78162	Abb78162 Amino aci
4	467	95.3	91	5	ABB78163	Abb78163 Amino aci
5	465	94.9	88	5	ABB78160	Abb78160 Amino aci
6	462	94.3	91	5	ABB78158	Abb78158 Amino aci
7	462	94.3	91	5	ABB78157	Abb78157 Amino aci
8	462	94.3	91	5	ABB78156	Abb78156 Amino aci
9	438	89.4	107	7	ABO65445	AbO65445 K1ebsiell
10	386	78.8	90	5	ABB78165	Abb78165 Amino aci
11	382	78.0	90	5	ABB78155	Abb78155 Amino aci
12	379	77.3	78	5	ABB78164	Abb78164 Amino aci
13	378	77.1	87	5	ABB78152	Abb78152 Amino aci
14	376	76.7	91	5	ABB78150	Abb78150 Amino aci
15	376	76.7	93	7	ADF05158	Adf05158 Bacterial
16	370	75.5	87	5	ABB78151	Abb78151 Amino aci
17	364	74.3	87	5	ABB78153	Abb78153 Amino aci
18	329	67.1	88	5	ABB78154	Abb78154 Amino aci
19	252	51.4	76	5	ABB78166	Abb78166 Amino aci
20	242	49.4	87	5	ABB78148	Abb78148 Amino aci
21	242	49.4	87	5	ABB78147	Abb78147 Amino aci
22	228	46.5	86	5	ABB78149	Abb78149 Amino aci
23	221	45.1	87	5	ABB78170	Abb78170 Amino aci
24	221	45.1	122	7	ABO74609	AbO74609 Pseudomon

25	217.5	44.4	89	9	AEB41576	Aeb41576 L. pneumo
26	217.5	44.4	95	9	AEB38294	Aeb38294 L. pneumo
27	215.5	44.0	90	5	ABB78167	Abb78167 Amino aci
28	215	43.9	90	5	ABB78168	Abb78168 Amino aci
29	211	43.1	87	5	ABB78169	Abb78169 Amino aci
30	211	43.1	88	5	ABB78178	Abb78178 Amino aci
31	204	41.6	88	5	ABB78171	Abb78171 Amino aci
32	204	41.6	88	5	ABB78172	Abb78172 Amino aci
33	204	41.6	88	5	ABB78173	Abb78173 Amino aci
34	204	41.6	88	6	ABP77219	Abp77219 N. gonorr
35	199	40.6	87	5	ABB78175	Abb78175 Amino aci
36	193	39.4	87	5	ABB78174	Abb78174 Amino aci
37	190	38.8	87	5	ABB78176	Abb78176 Amino aci
38	188.5	38.5	92	6	ADA34169	Ada34169 Acinetoba
39	188	38.4	87	5	ABB78177	Abb78177 Amino aci
40	130	26.5	110	8	ADL05173	Adl05173 M. catarr
41	77	15.7	1647	4	ABG10750	Abg10750 Novel hum
42	72	14.7	309	8	ADN46828	Adn46828 Thermococ
43	72	14.7	506	3	AAV74371	Aay74371 Neisseria
44	72	14.7	507	6	ABU40210	Abu40210 Protein e
45	71.5	14.6	184	3	AAB16290	Aab16290 Pinus rad
46	71	14.5	447	2	AAR52657	Aae52657 Rat N-ace
47	71	14.5	447	7	ADE55944	Ades55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aay74372 Neisseria
49	71	14.5	507	3	AAV74373	Aay74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 Protein e
51	70.5	14.4	184	3	AAB16325	Aab16325 Pinus rad
52	70.5	14.4	184	4	AAB65734	Aab65734 Annexin-1
53	70.5	14.4	184	7	ADB94702	Adb94702 Programme
54	70	14.3	758	9	ADW71760	Adw71760 Salmonell
55	69.5	14.2	1377	8	ADV81847	Adv81847 Streptoco
56	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
57	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
58	69	14.1	503	4	ABG16577	Abg16577 Novel hum
59	69	14.1	679	9	ADZ85056	Adz85056 Partial F
60	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
61	68.5	14.0	632	8	ADS29711	Ads29711 Bacterial
62	68	13.9	239	8	ADT07537	Adt07537 Human col
63	68	13.9	257	3	AAG31203	Aag31203 Arabidops
64	68	13.9	280	3	AAV54294	Aay54294 Amino aci
65	68	13.9	280	5	ABG93905	Abg93905 Lactuca s
66	68	13.9	280	8	ADJ50292	Adj50292 Oil-assoc
67	68	13.9	285	4	AAB92683	Aab92683 Human pro
68	68	13.9	297	3	AAG31202	Aag31202 Arabidops
69	68	13.9	302	4	AAB88379	Aab88379 Human mem
70	68	13.9	302	9	ADY63123	Ady63123 Human clo
71	68	13.9	324	3	AAG31201	Aag31201 Arabidops
72	68	13.9	414	6	ABU11747	Abu11747 Human MDD
73	68	13.9	445	2	AAR24781	Aar24781 Human GNT
74	68	13.9	445	4	AAG67094	Aag67094 Human bet
75	68	13.9	445	7	ADE55946	Ades5946 Human Pro

ALIGNMENTS

RESULT 1
ABB78161
ID ABB78161 standard; protein; 91 AA.
XX
AC ABB78161;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX
KW hydroxyl radical; DNA damage; YggX homologue.
OS
XX Unidentified.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 98.2%; Score 481; DB 5; Length 91;
Best Local Similarity 98.9%; Pred. No. 2e-48;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNA 60
|||
1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNA 60
Db

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db

RESULT 2
ABB78159
ID ABB78159 standard; protein; 91 AA.
XX
AC ABB78159;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 98.2%; Score 481; DB 5; Length 91;
Best Local Similarity 98.9%; Pred. No. 2e-48;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MSPTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNA 60
|||
1 MSRTIFCTYLQRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLMMNA 60
Db

QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
|||||
61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db

RESULT 3
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Salmonella typhi.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502a-16

Perfect score: 490
Sequence: 1 MSPTIFCTYLGRDAEGQDFQ.....SPFPEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	481	98.2	91	2	AH0879	conserved hypothet
2	462	94.3	91	2	A85954	hypothetical prote
3	462	94.3	91	2	A65082	hypothetical prote
4	462	94.3	91	2	F91108	hypothetical prote
5	386	78.8	90	2	A10116	conserved hypothet
6	382	78.0	90	2	C82320	hypothetical prote
7	378	77.1	90	2	C64013	hypothetical prote
8	252	51.4	93	2	E84994	hypothetical prote
9	225	45.9	105	2	C82624	conserved hypothet
10	221	45.1	90	2	H83003	conserved hypothet
11	204	41.6	88	2	H81014	conserved hypothet
12	79.5	16.2	1638	2	D87749	protein unc-73b [i
13	79.5	16.2	2488	2	T42739	guanine nucleotide
14	78	15.9	1260	2	T04440	hypothetical prote
15	73.5	15.0	495	2	AH0985	probable zinc-prot
16	71.5	14.6	209	2	I64172	hypothetical prote
17	71	14.5	447	2	JC2076	alpha-1,3-mannosyl
18	71	14.5	507	2	C81063	fumarate hydratase
19	71	14.5	546	2	A81807	thiosulfate reduct
20	70	14.3	758	2	AD0763	thiosulfate-dithio
21	70	14.3	758	2	A57143	hypothetical prote
22	69.5	14.2	859	2	T29630	hypothetical prote
23	69	14.1	265	2	T46013	hypothetical prote
24	69	14.1	447	2	T16527	hypothetical prote
25	68.5	14.0	683	2	AC2256	hypothetical prote
26	68	13.9	324	2	T05429	hypothetical prote
27	68	13.9	445	1	XUHUMB	alpha-1,3-mannosyl
28	68	13.9	689	2	F83902	beta-galactosidase
29	67.5	13.8	166	2	F70562	hypothetical prote

30	67	13.7	447	1	A38561	alpha-1,3-mannosyl
31	67	13.7	1111	2	T23047	hypothetical prote
32	66.5	13.6	548	2	A54510	63K antigen - nema
33	66.5	13.6	618	2	A71364	probable phosphoen
34	66	13.5	447	1	A42500	alpha-1,3-mannosyl
35	66	13.5	1085	2	S62516	hypothetical coile
36	65.5	13.4	287	2	F82265	conserved hypothet
37	65.5	13.4	365	2	B54128	Fe-binding protein
38	65	13.3	251	2	E90428	hypothetical prote
39	65	13.3	433	2	A70465	probable GTP bindi
40	65	13.3	507	2	A83105	probable fumarase
41	65	13.3	511	2	A99574	ABC transporter at
42	65	13.3	593	2	AF2393	probable soluble l
43	65	13.3	628	2	AF2393	hypothetical prote
44	65	13.3	1230	2	S56850	SMC1 protein homol
45	64.5	13.2	401	2	AB1978	hypothetical prote
46	64.5	13.2	544	2	T40058	probable chromatin
47	64.5	13.2	1119	2	T15842	hypothetical prote
48	64.5	13.2	1197	2	S26947	DNA-directed DNA p
49	64	13.1	643	2	A43647	parasporeal crystal
50	63.5	13.0	327	2	AD2129	transcription regu
51	63.5	13.0	379	2	S70709	type II site-speci
52	63.5	13.0	410	1	KHMSD	cathepsin D (EC 3.
53	63.5	13.0	2672	2	A48126	translation activa
54	63	12.9	205	2	C26135	keratin, 50K type
55	63	12.9	235	2	G65212	hypothetical 26.7K
56	63	12.9	258	2	A97991	hypothetical prote
57	63	12.9	258	2	E95121	phosphoesterase, p
58	63	12.9	483	2	G64799	ybeV protein - Esc
59	63	12.9	543	2	T16015	hypothetical prote
60	63	12.9	549	2	T16016	hypothetical prote
61	63	12.9	703	2	B82148	ATP-dependent heli
62	63	12.9	1166	2	H71609	hypothetical prote
63	63	12.9	1209	2	T46027	hypothetical prote
64	63	12.9	1327	2	T14594	guanidine nucleoti
65	63	12.9	1572	2	S45251	SNF2alpha protei
66	63	12.9	1586	2	S39580	HBRM protein - hum
67	62.5	12.8	165	2	A81382	shikimate kinase (
68	62.5	12.8	259	2	G83203	conserved hypothet
69	62.5	12.8	305	2	A75211	asparaginase (EC 3
70	62.5	12.8	375	2	T37245	GTP-binding regula
71	62.5	12.8	385	2	D87723	protein R06A10.2 l
72	62.5	12.8	498	2	G91179	hypothetical prote
73	62.5	12.8	498	2	H86025	hypothetical prote
74	62.5	12.8	498	2	S47748	53.1K protein prec
75	62.5	12.8	629	2	B83107	chemotactic transd

ALIGNMENTS

RESULT 1
AH0879
C/Species: hypothetical protein STY3266 [imported] - Salmonella enterica subsp. enterica
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0879
R/Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A/Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.,
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
C/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:g16504189;
C/Genetics:
A/Gene: STY3266
C/Superfamily: fe(II) trafficking protein YggX

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Query Match      98.2%; Score 481; DB 2; Length 91;  
Best Local Similarity   98.9%; Pred. No. 7.8e-42;  
Matches    90; Conservative     0; Mismatches    1; Indels       0; Gaps        0;
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OY          1 MSPTIFCTYLQRDAEGQDFQLYPGELGKRIYN EISKDWAQAOMHKOTMLINEKKLNMNNA 60  
||| |||||||  
Db         1 MSRTIFCTYLQRDAEGQDPFLYPGELGKRIYN EISKDWAQAOMHKOTMLINEKKLNMNNA 60
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OY 61 EHRLLEQEWMVSFLFEGKDVIHIEGYTPEDCK 91
|||||
Db 61 EHRLLEQEWMVSFLFEGKDVIHIEGYTPEDCK 91

RESULT 2

A85954

hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;/Species: Escherichia coli
C;/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;/Accession: A85954
R;/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, B.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;/Reference number: A85480; PMID:11206551
A;/Accession: A85954
A;/Status: preliminary
A;/Molecule type: DNA
A;/Residues: 1-91 <STO>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A;/Experimental source: strain O157.H7, substrain EDL933
C;/Genetics:
A;/Gene: yggX
C;/Superfamily: fe(II) trafficking protein YggX

Query Match 94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSPTIFCTYLQRDAEGQDFQLYPGELGKRIYN EISKDWAQAOMHKOTMLINEKKLNMMNA 60
||| |||||||
Db 1 MSRTIFCTPLQREAAGQDFLYPGELGKRIYN EISKEAWAQMHKOTMLINEKKLNMMNA 60

OY 61 EHRLLEQEWMVSFLFEGKDVIHIEGYTPEDCK 91
|||||
Db 61 EHRLLEQEWMVNFLFEKGVEVHIETGPEDCK 91

RESULT 3

A65082

hypothetical protein b2962 - Escherichia coli (strain K-12)

C;/Species: Escherichia coli
C;/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;/Accession: A65082
R;/Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;/Title: The complete genome sequence of Escherichia coli K-12.
A;/Reference number: A64720; PMID:97426617; PMID:9278503
A;/Accession: A65082
A;/Status: preliminary; nucleic acid sequence not shown; translation not shown
A;/Molecule type: DNA
A;/Residues: 1-91 <BLAT>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g
C;/Experimental source: strairn K-12, substrain MG1655
C;/Superfamily: fe(II) trafficking protein YggX

Query Match 94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 MSPTIFCTYLQRDAEGQDFQLYPGELGKRIYN EISKDWAQAOMHKOTMLINEKKLNMMNA 60
||| |||||||
||| :|||:

```

Db      1 MSRTIFCTFLQREAGQDFQLYPGEIGKRIYNEISKEAWAQWQHQTMLINEKKLMMNA 60
QY      61 EHRKLLIQEMVSVFLFEGKDVHIEGYTPEDKK 91
        |||||:||||:|||||
Db      61 EHRKLLIQEMVSVFLFEGKEVHIEGYTPEDKK 91

RESULT 4
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno-
A;Reference number: A99629, MUID:21156231; PMID:11258796
A;Accession: F91108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <HAY>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;
C;Genetics:
A;Gene: ECs3838
C;Superfamily: fe(II) trafficking protein YggX

Query Match      94.3%; Score 462; DB 2; Length 91;
Best Local Similarity 93.4%; Pred. No. 6.5e-40;
Matches 85; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 MSPTIFCTYLQDAEGQDFQLYPGEIGKRIYNEISKDAWAQWQHQTMLINEKKLMMNA 60
        |||||:||||:|||||
Db      1 MSRTIFCTFLQREAGQDFQLYPGEIGKRIYNEISKEAWAQWQHQTMLINEKKLMMNA 60
QY      61 EHRKLLIQEMVSVFLFEGKDVHIEGYTPEDKK 91
        |||||:||||:|||||
Db      61 EHRKLLIQEMVSVFLFEGKEVHIEGYTPEDKK 91

RESULT 5
A10116
conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004
A;Accession: A10116
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
ll, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: A10116
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <KUR>
A;Cross-references: UNIPARC:UPI00000DCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;
C;Genetics:
A;Gene: YPO0953
C;Superfamily: fe(II) trafficking protein YggX

Query Match      78.8%; Score 386; DB 2; Length 90;
Best Local Similarity 80.0%; Pred. No. 3.2e-32;
Matches 72; Conservative 9; Mismatches 9; Indels 0; Gaps 0;

QY      1 MSPTIFCTYLQDAEGQDFQLYPGEIGKRIYNEISKDAWAQWQHQTMLINEKKLMMNA 60
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Db      1 MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKQTMLINEKKLSMNNI 60
QY      61 EHRKLLIQEMVSVFLFEGKDVHIEGYTPEDK 90
        |||||:||||:|||||
Db      61 EDRKLLIQEMVSVFLFEGQDVHIEGYTPPSK 90

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502a-16
Perfect score: 490
Sequence: 1 MSPTICTYTLQRDAGQDFQ.....SFLFEGKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	476	97.1	90	1 FETP_SALCH	Q57K04 salmonella
2	476	97.1	90	1 FETP_SALPA	Q5pmn1 salmonella
3	476	97.1	90	1 FETP_SALTI	P67618 salmonella
4	476	97.1	90	1 FETP_SALTY	P67617 salmonella
5	457	93.3	90	1 FETP_ECOS7	P0a8p4 escherichia
6	457	93.3	90	1 FETP_ECOLI	P0a8p3 escherichia
7	457	93.3	90	1 FETP_SHIFL	P0a8p5 shigella fl
8	453	92.4	90	1 FETP_ECOL6	Q6fe19 escherichia
9	409	83.5	90	1 FETP_ERWCT	Q6d8j9 erwinia car
10	394	80.4	90	1 FETP_YERPS	Q666m3 yersinia ps
11	386	78.8	90	1 FETP_VIBPA	Q871i5 vibrio para
12	386	78.8	90	1 FETP_YERPE	Q8zhe7 yersinia pe
13	382	78.0	90	1 FETP_VIBCH	Q9kur4 vibrio chol
14	382	78.0	90	1 FETP_VIBVU	Q8dcs5 vibrio vuln
15	382	78.0	90	1 FETP_VIBVY	Q7mb14 vibrio vuln
16	380	77.6	91	1 FETP_MANSN	Q65vt7 mannheimia
17	378	77.1	90	1 FETP_HA8IN	P44048 haemophilus
18	378	77.1	90	2 Q4QMD9_HAEI8	Q4qmd9 haemophilus
19	376	76.7	90	1 FETP_PHOPR	Q6lmk7 photobacter
20	370	75.5	90	1 FETP_PASMU	Q9c1b9 pasteurella
21	369	75.3	90	1 FETP_PHOLL	Q7n711 photorhabdu
22	364	74.3	94	1 FETP_HABDU	Q7vkb6 haemophilus
23	358	73.1	90	1 FETP_VIBF1	Q5e7t0 vibrio fisc
24	334	68.2	90	1 FETP_IDILO	Q5qy58 idiomarina
25	329	67.1	92	1 FETP_SH8ON	Q8ebx6 shewanella
26	252	51.4	77	1 FETP_BUCAI	P57618 buchnera ap
27	242	49.4	90	1 FETP_BORBR	Q7wh06 bordetella
28	242	49.4	90	1 FETP_BORPA	Q7w9q2 bordetella
29	242	49.4	90	1 FETP_BORPE	Q7vwc4 bordetella
30	236	48.2	78	1 FETP_BUCAP	Q8k925 buchnera ap
31	232	47.3	91	1 FETP_XANAC	Q8pjh7 xanthomonas

32	225	45.9	90	1 FETP_XYLFA	Q9pc73 xylella fas
33	225	45.9	92	1 FETP_XANOR	Q5gy22 xanthomonas
34	221.5	45.2	89	1 FETP_LEGPL	Q5wvc4 legionella
35	221	45.1	90	1 FETP_PSEAB	Q9hu36 pseudomonas
36	221	45.1	90	1 FETP_XYLF1	Q87d06 xylella fas
37	221	45.1	92	1 FETP_XANCP	Q8p829 xanthomonas
38	221	45.1	92	2 Q4UWI4_XANCP	Q4uw14 xanthomonas
39	218	44.5	78	1 FETP_WIGBR	Q8d3c5 wiggleswort
40	217.5	44.4	89	1 FETP_LEGPA	Q5x3x9 legionella
41	217.5	44.4	89	1 FETP_LEGPH	Q5zu80 legionella
42	215	43.9	90	1 FETP_NITEU	Q82xf2 nitrosomona
43	215	43.9	90	1 FETP_PSESM	Q87uf5 pseudomonas
44	215	43.9	90	2 Q4ZLF3_PSESY	Q4zlp3 pseudomonas
45	211	43.1	90	1 FETP_COXBU	Q83d06 coxiella bu
46	211	43.1	90	1 FETP_PSEPK	Q88r49 pseudomonas
47	211	43.1	90	2 Q4J228_AZOV1	Q4j228 azotobacter
48	209	42.7	79	1 FETP_CANBF	Q7vrg9 candidatus
49	208	42.4	90	2 Q6T7F6_PSEFL	Q6t7f6 pseudomonas
50	206	42.0	90	1 FETP_CHRVO	Q7n8r4 chromobacte
51	204	41.6	88	1 FETP_NEIG1	Q5f553 neisseria g
52	204	41.6	88	1 FETP_NEIMA	P67615 neisseria m
53	204	41.6	88	1 FETP_NEIMB	P67616 neisseria m
54	201	41.0	87	1 FETP_BUCBP	Q89a44 buchnera ap
55	199	40.6	91	1 FETP_BURMA	Q62iur burkholderi
56	199	40.6	91	1 FETP_BURPS	Q63sj4 burkholderi
57	198	40.4	90	2 Q4KJT2_PSEF5	Q4kjt2 pseudomonas
58	198	40.4	91	1 FETP_RALSO	Q8y010 ralstonia s
59	196	40.0	91	2 Q4LS19_9BURK	Q4ls19 burkholderi
60	192	39.2	87	1 FETP_FRATT	Q5nhj8 francisella
61	188	38.4	90	1 FETP_METCA	Q60aj7 methylococc
62	183.5	37.4	90	1 FETP_AC1AD	Q6ffb3 acinetobact
63	145	29.6	96	2 Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	138	28.2	92	2 Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	82.5	16.8	482	2 Q5NUY1_9BURK	Q5nuyl ralstonia m
66	82.5	16.8	514	2 Q6AIZ9_DESPS	Q6aiz9 desulfolale
67	79.5	16.2	1638	2 Q7KBP4_CABEL	Q7kbp4 caenorhabdi
68	79.5	16.2	2140	2 Q6BEW2_CABEL	Q6bew2 caenorhabdi
69	79.5	16.2	2488	2 Q61528_CABEL	Q61528 caenorhabdi
70	78.5	16.0	337	2 Q81AR8_BACCR	Q81ar8 bacillus ce
71	78	15.9	1260	2 Q49677_ARATH	Q49677 arabidopsis
72	77.5	15.8	1047	2 Q5CJ53_CRYHO	Q5cj53 cryptospori
73	76.5	15.6	486	2 Q7WX51_ALCEU	Q7wx51 alcaligenes
74	75.5	15.4	1278	2 Q5CYM7_CRYPV	Q5cym7 cryptospori
75	75	15.3	385	2 Q734A2_BACCI	Q734a2 bacillus ce

ALIGNMENTS

RESULT 1
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=Y99X; Ordered locus names=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_Taxid=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.;
RT "The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.";
RL Nucleic Acids Res. 33:1690-1698(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or


```

CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; AB017220; AAX66958.1; -; Genomic_DNA.
CC      DR      HAMAP; MF 00686; -; 1.
CC      DR      InterPro; IPR007457; YggX.
CC      DR      ProDom; PD029191; DUF495; 1.
CC      KW      Complete proteome; Iron.
CC      FT      INIT MET 0
CC      FT      SEQUENCE 90 AA; 10768 MW; B3B6A1BE2255E3C CRC64;
CC      -----
CC      Query Match          97.1%; Score 476; DB 1; Length 90;
CC      Best Local Similarity 98.9%; Pred. No. 1.2e-41;
CC      Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC      -----
QY      2 SPTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQWQHQTMLINEKILNMNNAE 61
QY      1 SRTIFCTYLQDAEGQDFOLYPGELGKRIYNEISKDAMQWQHQTMLINEKILNMNNAE 60
QY      62 HRKLLQEMVSPFLFEGKDVHIEGYTPEDCK 91
QY      61 HRKLLQEMVSPFLFEGKDVHIEGYTPEDCK 90
QY      -----
Db      61 HRKLLQEMVSPFLFEGKDVHIEGYTPEDCK 90
Db      -----
RESULT 2
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ID      PFTP_SALPA          STANDARD;          PRT;          90 AA.
AC      Q5PMM1;
DT      13-SEP-2005 (Rel. 48, Created)
DT      13-SEP-2005 (Rel. 48, Last sequence update)
DT      13-SEP-2005 (Rel. 48, Last annotation update)
DE      Probable Fe(2+) trafficking protein.
OS      Name=yggX; Ordered locus Names=SPA2974;
OS      Salmonella paratyphi-a.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Salmonella.
OX      NCBI_TaxID=54388;
RX      [1]
RP      NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC      STRAIN=ATCC 9150 / SARB42;
RX      PubMed=15531882; DOI=10.1038/ng1470;
RA      McClelland M., Sanderson K.E., Clifton S.W., Latreille P.,
RA      Porwollik S., Sabo A., Meyer R., Bieri T., Ozersky P., Mclellan M.,
RA      Harkins C.R., Wang C., Nguyen C., Berghof A., Elliott G.,
RA      Kohlberg S., Strong C., Du F., Carter J., Kremizki C., Layman D.,
RA      Leonard S., Sun H., Fulton L., Nash W., Miner T., Mink P.,
RA      Delehaunty K., Fronick C., Magrini V., Nhan M., Warren W., Florea L.,
RA      Spieth J., Wilson R.K.;
RT      "Comparison of genome degradation in Paratyphi A and Typhi, human-
RT      restricted serovars of Salmonella enterica that cause typhoid.";
RL      Nat. Genet. 36:1268-1274(2004).
CC      -1- FUNCTION: Could be a mediator in iron transactions between iron
CC      acquisition and iron-requiring processes, such as synthesis and/or
CC      repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC      -1- SUBUNIT: Monomer (By similarity).
CC      -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC      -----
CC      This Swiss-Prot entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use as long as its content is in no way modified and this statement is not
CC      removed.
CC      -----
CC      EMBL; CP000026; AAV78812.1; -; Genomic_DNA.
CC      DR      SMR; Q5PMM1; 1-91.
CC      DR      HAMAP; MF 00686; -; 1.

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DR   InterPro; IPR007457; YggX.
DR   ProDom; PD029191; DUF495; 1.
KW   Complete proteome; Iron.
SQ   INIT MET      0
     SEQUENCE      90 AA; 10768 MW; B3B6A1BE22555E3C CRC64;
                                     By similarity.

Query Match      97.1%; Score 476; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 1.2e-41;
Matches 89; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 SPTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQOMQKQTMLINEKKLMMNNAE 61
      1 SRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQOMQKQTMLINEKKLMMNNAE 60
Db      62 HRKLLLEQEMVSLFPEGKDVHIEGYTPEDKK 91
      61 HRKLLLEQEMVSLFPEGKDVHIEGYTPEDKK 90

RESULT 3
FETP_SALTI
FETP_SALTI STANDARD; PRT; 90 AA.
AC P67618; Q8XFW6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; Ordered locus names=STY3266, t3024;
OS Salmonella typhi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBITaxID=601;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CT18;
RX MEDLINE=21534947; PubMed=11677608; DOI=10.1038/35101607;
RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA Churcher C.M., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,
RA Baker S., Basham D., Brooks K., Chillingworth T., Comerton P.,
RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA Feltwell T., Hamlin N., Hague A., Hien T.T., Holroyd S., Jagers K.,
RA Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Stevens K.,
RA Whitehead S., Barrell B.G.;
RT "Complete genome sequence of a multiple drug resistant Salmonella
RT enterica serovar Typhi CT18."
RL Nature 413:848-852(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Ty2 / ATCC 700931;
RX MEDLINE=22531367; PubMed=12644504;
RX DOI=10.1128/JB.185.7.2330-2337.2003;
RA Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT and CT18."
RL J. Bacteriol. 185:2330-2337(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL; AL627277; CAD02936.1; -; Genomic DNA.
CC EMBL; AE016844; AA070576.1; -; Genomic DNA.
CC SMR; P67618; 1-90.
DR HAMAP; MF 00686; -; 1.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-16
Perfect score: 490
Sequence: 1 MSPTIFCTYLQRDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	438	89.4	107	2	US-09-489-039A-11962 Sequence 11962, A
2	376	76.7	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	221	45.1	122	2	US-09-252-991A-23355 Sequence 23355, A
4	188.5	38.5	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	130	26.5	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	70.5	14.4	184	2	US-09-325-932A-66 Sequence 66, Appl
7	68.5	14.0	544	2	US-09-248-796A-18911 Sequence 18911, A
8	68	13.9	280	2	US-09-323-998E-37 Sequence 37, Appl
9	68	13.9	1214	2	US-10-164-595-24 Sequence 24, Appl
10	66.5	13.6	325	2	US-09-134-000C-4346 Sequence 4346, Ap
11	66.5	13.6	548	2	US-09-167-299-3 Sequence 3, Appli
12	66	13.5	292	2	US-09-328-352-5836 Sequence 5836, Ap
13	65	13.3	474	2	US-09-252-991A-24473 Sequence 24473, A
14	64	13.1	98	2	US-09-270-767-41085 Sequence 41085, A
15	64	13.1	98	2	US-09-270-767-56301 Sequence 56301, A
16	64	13.1	337	2	US-09-270-767-41746 Sequence 41746, A
17	64	13.1	569	2	US-09-107-532A-6689 Sequence 6689, Ap
18	64	13.1	644	2	US-08-793-331-7 Sequence 7, Appli
19	64	13.1	1176	2	US-09-489-039A-8879 Sequence 8879, Ap
20	63.5	13.0	921	2	US-09-248-796A-14950 Sequence 14950, A
21	63	12.9	1586	2	US-09-538-092-1171 Sequence 1171, Ap
22	62.5	12.8	260	2	US-09-252-991A-17498 Sequence 17498, A
23	62.5	12.8	419	2	US-09-543-681A-7295 Sequence 7295, Ap
24	62.5	12.8	662	2	US-09-583-110-5119 Sequence 5119, Ap
25	62.5	12.8	664	2	US-09-107-433-2775 Sequence 2775, Ap
26	62.5	12.8	701	2	US-09-252-991A-23288 Sequence 23288, A
27	62	12.7	227	2	US-09-270-767-58283 Sequence 58283, A

28	62	12.7	238	2	US-09-323-998E-41	Sequence 41, Appl
29	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
30	62	12.7	604	2	US-09-008-097-4	Sequence 4, Appli
31	62	12.7	604	2	US-09-472-667-4	Sequence 4, Appli
32	62	12.7	898	2	US-09-583-110-3750	Sequence 3750, Ap
33	62	12.7	899	2	US-09-107-433-3196	Sequence 3196, Ap
34	62	12.7	1167	2	US-09-008-097-6	Sequence 6, Appli
35	62	12.7	1167	2	US-09-472-667-6	Sequence 6, Appli
36	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appli
37	61	12.4	143	2	US-09-270-767-45872	Sequence 45872, A
38	61	12.4	184	2	US-09-270-767-61671	Sequence 61671, A
39	61	12.4	271	2	US-09-248-796A-19265	Sequence 19265, A
40	61	12.4	389	2	US-09-270-767-46116	Sequence 46116, A
41	61	12.4	1394	2	US-09-248-796A-19555	Sequence 19555, A
42	60.5	12.3	223	2	US-09-543-681A-5667	Sequence 5667, Ap
43	60.5	12.3	504	2	US-10-104-047-3467	Sequence 3467, Ap
44	60.5	12.3	525	2	US-09-540-236-2250	Sequence 2250, Ap
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46	60	12.2	232	2	US-09-201-641-8	Sequence 8, Appli
47	60	12.2	232	2	US-09-323-998E-36	Sequence 36, Appl
48	60	12.2	421	2	US-09-489-039A-7512	Sequence 7512, Ap
49	59.5	12.1	139	2	US-09-513-999C-4802	Sequence 4802, Ap
50	59.5	12.1	209	2	US-09-252-991A-20905	Sequence 20905, A
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52	59.5	12.1	264	2	US-09-949-016-6012	Sequence 6012, Ap
53	59.5	12.1	276	2	US-09-949-016-11703	Sequence 11703, A
54	59.5	12.1	434	2	US-09-303-518D-334	Sequence 334, App
55	59.5	12.1	680	2	US-09-298-924-4	Sequence 4, Appli
56	59.5	12.1	687	2	US-09-538-092-539	Sequence 539, App
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65	59	12.0	284	2	US-09-323-998E-16	Sequence 16, Appl
66	59	12.0	331	2	US-09-328-352-6400	Sequence 6400, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Db      77 EHRKLLLEQEMVSVFLFPEGKDVHIEGYTPPEKQ 107

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RESULT 2
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; Sequence 5443, Application US/09543681A

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; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A

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; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
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; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Qy 61 EHRKLLQEMVSVLFEGKD-VHIEGYTP 87

Db 93 EDRKFLQEMDKFL-SGEDYAKADGYVP 119

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RESULT 4
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; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
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; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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RESULT 5
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; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

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Db 85 YLNEOREKFLDNGDYEKAPAGYKP 107

RESULT 6
US-09-325-932A-66
; Sequence 66, Application US/09325932A

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
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Title: US-09-955-502A-16

Perfect score: 490
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Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	481	98.2	91	3	US-09-955-502-17 Sequence 17, Appl
4	467	95.3	91	3	US-09-955-502-18 Sequence 18, Appl
5	465	94.9	88	3	US-09-955-502-15 Sequence 15, Appl
6	462	94.3	91	3	US-09-955-502-11 Sequence 11, Appl
7	462	94.3	91	3	US-09-955-502-12 Sequence 12, Appl
8	462	94.3	91	3	US-09-955-502-13 Sequence 13, Appl
9	386	78.8	90	3	US-09-955-502-20 Sequence 20, Appl
10	382	78.0	90	3	US-09-955-502-10 Sequence 10, Appl
11	379	77.3	78	3	US-09-955-502-19 Sequence 19, Appl
12	378	77.1	87	3	US-09-955-502-7 Sequence 7, Appl
13	376	76.7	91	3	US-09-955-502-5 Sequence 5, Appl
14	370	75.5	87	3	US-09-955-502-6 Sequence 6, Appl
15	364	74.3	87	3	US-09-955-502-8 Sequence 8, Appl
16	329	67.1	88	3	US-09-955-502-9 Sequence 9, Appl
17	252	51.4	76	3	US-09-955-502-21 Sequence 21, Appl
18	242	49.4	87	3	US-09-955-502-2 Sequence 2, Appl
19	242	49.4	87	3	US-09-955-502-3 Sequence 3, Appl
20	228	46.5	86	3	US-09-955-502-4 Sequence 4, Appl
21	225	45.9	89	3	US-09-955-502-22 Sequence 22, Appl
22	221	45.1	87	3	US-09-955-502-25 Sequence 25, Appl
23	215	43.9	90	3	US-09-955-502-23 Sequence 23, Appl
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25	211	43.1	88	3	US-09-955-502-33 Sequence 33, Appl
26	204	41.6	88	3	US-09-955-502-26 Sequence 26, Appl
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28	204	41.6	88	3	US-09-955-502-28	Sequence 28, Appl
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32	188	38.4	87	3	US-09-955-502-32	Sequence 32, Appl
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36	72	14.7	1261	4	US-10-437-963-189166	Sequence 189166,
37	71.5	14.6	184	4	US-10-393-840-52	Sequence 52, Appl
38	71	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
39	70.5	14.4	184	4	US-10-219-220-66	Sequence 66, Appl
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41	69	14.1	503	5	US-10-450-763-46936	Sequence 46936, A
42	69	14.1	679	5	US-10-805-684-105	Sequence 105, App
43	68.5	14.0	449	4	US-10-424-599-279212	Sequence 279212,
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46	68	13.9	280	3	US-09-323-998D-37	Sequence 37, Appl
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48	68	13.9	445	4	US-10-844-874-14	Sequence 14, Appl
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51	68	13.9	689	4	US-10-369-493-17280	Sequence 17280, A
52	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
53	68	13.9	764	5	US-10-491-467-15	Sequence 15, Appl
54	68	13.9	1206	4	US-10-085-198-144	Sequence 144, Appl
55	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
56	67.5	13.8	166	5	US-10-482-706-269	Sequence 269, App
57	67.5	13.8	593	5	US-10-450-763-50306	Sequence 50306, A
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70	65.5	13.4	221	4	US-10-767-701-41912	Sequence 41912, A
71	65.5	13.4	306	4	US-10-424-599-241560	Sequence 241560,
72	65.5	13.4	481	5	US-10-732-923-982	Sequence 982, App
73	65.5	13.4	1588	4	US-10-437-963-189741	Sequence 189741,
74	65	13.3	290	4	US-10-389-566-2247	Sequence 2247, Ap
75	65	13.3	311	4	US-10-029-386-33838	Sequence 33838, A

ALIGNMENTS

RESULT 1
US-09-955-502-14
; Sequence 14, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi

US-09-955-502-14

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Best Local Similarity 98.9%; Pred. No. 4.8e-48;
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RESULT 2

US-09-955-502-16

; Sequence 16, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella dublin
US-09-955-502-16

Query Match 98.2%; Score 481; DB 3; Length 91;
Best Local Similarity 98.9%; Pred. No. 4.8e-48;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3

US-09-955-502-17

; Sequence 17, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 17
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella typhi CT18
US-09-955-502-17

Query Match 98.2%; Score 481; DB 3; Length 91;

Best Local Similarity 98.9%; Pred. No. 4.8e-48;
Matches 90; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 4

US-09-955-502-18

; Sequence 18, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 18
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella typhimurium
US-09-955-502-18

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DB 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 5

US-09-955-502-15

; Sequence 15, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 15
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-09-955-502-15

Query Match 94.9%; Score 465; DB 3; Length 88;
Best Local Similarity 98.9%; Pred. No. 3.3e-46;
Matches 87; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.7
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Title: US-09-955-502A-16
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5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	41.6	88	US-10-467-657-968	Sequence 968, App
2	68	13.9	478	US-10-821-234-915	Sequence 915, App
3	65	13.3	593	US-11-194-246-317	Sequence 317, App
4	64.5	13.2	177	US-10-467-657-1658	Sequence 1658, App
5	63.5	13.0	1432	US-10-510-386-218	Sequence 218, App
6	63	12.9	251	US-11-054-515-1496	Sequence 1496, App
7	62	12.7	604	US-10-942-072-4	Sequence 4, Appli
8	62	12.7	1167	US-10-942-072-6	Sequence 6, Appli
9	60.5	12.3	504	US-11-072-512-3467	Sequence 3467, App
10	59.5	12.1	264	US-10-821-234-1555	Sequence 1555, App
11	59.5	12.1	650	US-10-467-657-1948	Sequence 1948, App
12	59.5	12.1	834	US-10-453-372-658	Sequence 658, App
13	59.5	12.1	1995	US-11-069-834-60	Sequence 60, Appl
14	59	12.0	697	US-10-485-517-202	Sequence 202, App
15	59	12.0	1168	US-10-942-072-11	Sequence 11, Appl
16	59	12.0	1450	US-10-485-517-152	Sequence 152, Appl
17	58.5	11.9	285	US-10-467-657-222	Sequence 222, App
18	58.5	11.9	285	US-10-467-657-8230	Sequence 8230, App
19	58.5	11.9	695	US-10-453-372-648	Sequence 648, App
20	58.5	11.9	700	US-10-995-561-922	Sequence 922, App
21	58.5	11.9	700	US-10-995-561-924	Sequence 924, App
22	58.5	11.9	749	US-11-098-686-10505	Sequence 10505, A
23	58.5	11.9	782	US-10-793-626-2352	Sequence 2352, App
24	58	11.8	257	US-11-054-515-1710	Sequence 1710, App
25	58	11.8	448	US-10-618-320A-25	Sequence 25, Appl

26	58	11.8	480	6	US-10-510-386-12	Sequence 12, Appl
27	58	11.8	1501	6	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.7	336	7	US-10-453-372-640	Sequence 640, App
29	57.5	11.7	752	6	US-11-072-512-3003	Sequence 3003, App
30	57.5	11.7	775	6	US-10-453-372-656	Sequence 656, App
31	57.5	11.7	793	6	US-10-995-561-925	Sequence 925, App
32	57.5	11.7	804	6	US-10-453-372-650	Sequence 650, App
33	57.5	11.7	847	6	US-10-453-372-654	Sequence 654, App
34	57.5	11.7	857	6	US-10-453-372-652	Sequence 652, App
35	57.5	11.7	905	6	US-10-453-372-638	Sequence 638, App
36	57.5	11.7	905	6	US-10-453-372-662	Sequence 662, App
37	57.5	11.7	905	6	US-10-453-372-664	Sequence 664, App
38	57.5	11.7	963	6	US-10-995-561-923	Sequence 923, App
39	57.5	11.7	963	6	US-10-453-372-660	Sequence 660, App
40	57.5	11.7	1012	6	US-10-453-372-646	Sequence 646, App
41	57.5	11.7	3803	6	US-10-995-561-773	Sequence 773, App
42	57.5	11.7	3960	6	US-10-995-561-771	Sequence 771, App
43	57.5	11.7	5335	6	US-10-995-561-777	Sequence 777, App
44	57.5	11.7	5406	6	US-10-995-561-774	Sequence 774, App
45	57.5	11.7	5415	6	US-10-995-561-779	Sequence 779, App
46	57.5	11.7	5464	6	US-10-995-561-775	Sequence 775, App
47	57.5	11.7	5935	6	US-10-995-561-776	Sequence 776, App
48	57	11.6	234	6	US-10-524-647-120	Sequence 120, App
49	57	11.6	234	6	US-10-524-972-108	Sequence 108, App
50	57	11.6	432	6	US-10-821-234-1463	Sequence 1463, App
51	56.5	11.5	440	7	US-11-072-512-3856	Sequence 3856, App
52	56.5	11.5	242	7	US-11-022-562-220	Sequence 220, App
53	56.5	11.5	647	7	US-11-000-463-722	Sequence 722, App
54	56.5	11.5	692	7	US-11-038-284-33	Sequence 33, Appl
55	56.5	11.5	873	7	US-11-038-284-35	Sequence 35, Appl
56	56.5	11.5	889	7	US-11-038-284-15	Sequence 15, Appl
57	56.5	11.5	1254	6	US-10-528-031-47	Sequence 47, Appl
58	56.5	11.5	1897	6	US-10-821-234-1635	Sequence 1635, App
59	56.5	11.5	1907	7	US-11-000-463-250	Sequence 250, App
60	56.5	11.5	3433	6	US-10-714-781A-316	Sequence 316, Appl
61	56	11.4	206	7	US-11-124-367A-316	Sequence 10257, A
62	56	11.4	1011	7	US-11-098-686-10257	Sequence 580, App
63	55.5	11.3	136	6	US-10-793-626-580	Sequence 10812, A
64	55.5	11.3	279	7	US-11-098-686-10812	Sequence 42, Appl
65	55.5	11.3	1188	7	US-11-115-639-42	Sequence 43, Appl
66	55.5	11.3	1188	7	US-11-115-639-43	Sequence 1, Appli
67	55	11.2	189	7	US-11-071-262-1	Sequence 198, App
68	55	11.2	667	6	US-10-793-626-198	Sequence 67, Appl
69	55	11.2	783	7	US-11-037-243-67	Sequence 22, Appl
70	55	11.2	1142	7	US-11-109-156-22	Sequence 74, Appl
71	54.5	11.1	317	6	US-10-523-503-74	Sequence 26, Appl
72	54.5	11.1	450	6	US-10-618-320A-26	Sequence 20, Appl
73	54.5	11.1	496	7	US-11-069-642-20	Sequence 187, App
74	54.5	11.1	577	7	US-11-072-175-187	Sequence 34, Appl
75	54	11.0	111	6	US-10-771-257-34	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:38:11 ; Search time 74.7278 Seconds
(without alignments)
535.055 Million cell updates/sec

Title: US-09-955-502A-17
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAEGQDFQ.....SFLPEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	488	100.0	91	5	ABB78161	Abb78161 Amino aci
2	488	100.0	91	5	ABB78159	Abb78159 Amino aci
3	488	100.0	91	5	ABB78162	Abb78162 Amino aci
4	474	97.1	91	5	ABB78163	Abb78163 Amino aci
5	472	96.7	88	5	ABB78160	Abb78160 Amino aci
6	469	96.1	91	5	ABB78158	Abb78158 Amino aci
7	469	96.1	91	5	ABB78157	Abb78157 Amino aci
8	469	96.1	91	5	ABB78156	Abb78156 Amino aci
9	445	91.2	107	7	ABO65445	ABO65445 Klebsiell
10	393	80.5	90	5	ABB78165	Abb78165 Amino aci
11	389	79.7	90	5	ABB78155	Abb78155 Amino aci
12	386	79.1	78	5	ABB78164	Abb78164 Amino aci
13	385	78.9	87	5	ABB78152	Abb78152 Amino aci
14	383	78.5	91	5	ABB78150	Abb78150 Amino aci
15	383	78.5	93	7	ADF05158	Adf05158 Bacteri
16	377	77.3	87	5	ABB78151	Abb78151 Amino aci
17	371	76.0	87	5	ABB78153	Abb78153 Amino aci
18	336	68.9	88	5	ABB78154	Abb78154 Amino aci
19	259	53.1	76	5	ABB78166	Abb78166 Amino aci
20	249	51.0	87	5	ABB78148	Abb78148 Amino aci
21	249	51.0	87	5	ABB78147	Abb78147 Amino aci
22	235	48.2	86	5	ABB78149	Abb78149 Amino aci
23	228	46.7	87	5	ABB78170	Abb78170 Amino aci
24	228	46.7	122	7	ABO74609	ABO74609 Pseudomon

25	224.5	46.0	89	9	ABB41576	Aeb41576 L. pneumo
26	224.5	46.0	95	9	ABB38294	Aeb38294 L. pneumo
27	222.5	45.6	90	5	ABB78167	Abb78167 Amino aci
28	222	45.5	90	5	ABB78168	Abb78168 Amino aci
29	218	44.7	87	5	ABB78169	Abb78169 Amino aci
30	218	44.7	88	5	ABB78178	Abb78178 Amino aci
31	211	43.2	88	5	ABB78171	Abb78171 Amino aci
32	211	43.2	88	5	ABB78172	Abb78172 Amino aci
33	211	43.2	88	5	ABB78173	Abb78173 Amino aci
34	211	43.2	88	6	ABP77219	Abp77219 N. gonorr
35	206	42.2	87	5	ABB78175	Abb78175 Amino aci
36	200	41.0	87	5	ABB78174	Abb78174 Amino aci
37	197	40.4	87	5	ABB78176	Abb78176 Amino aci
38	195.5	40.1	92	6	ADA34169	Ada34169 Acinetoba
39	195	40.0	87	5	ABB78177	Abb78177 Amino aci
40	130	26.6	110	8	ADL05173	Adl05173 M. catarr
41	77	15.8	1647	4	ABG10750	Abg10750 Novel hum
42	72	14.8	309	8	ADN46828	Adn46828 Thermococ
43	72	14.8	506	3	AAV74371	Aay74371 Neisseria
44	72	14.8	507	6	ABU40210	Abu40210 Proteina
45	71.5	14.7	184	3	AAB16290	Aab16290 Pinus rad
46	71	14.5	447	2	AAR52657	Aar52657 Rat N-ace
47	71	14.5	447	7	ADE55944	Ade55944 Rat Prote
48	71	14.5	507	3	AAV74372	Aay74372 Neisseria
49	71	14.5	507	3	AAV74373	Aay74373 Neisseria
50	71	14.5	546	6	ABU38097	Abu38097 Protein e
51	71	14.5	548	4	AAE04737	Aae04737 Brugia ma
52	70.5	14.4	184	3	AAB16325	Aab16325 Pinus rad
53	70.5	14.4	184	4	AAB65734	Aab65734 Annexin-1
54	70.5	14.4	184	7	ADB94702	Adb94702 Programme
55	70.5	14.4	593	4	ABG19947	Abg19947 Novel hum
56	70	14.3	257	3	AAG31203	Aag31203 Arabidops
57	70	14.3	297	3	AAG31202	Aag31202 Arabidops
58	70	14.3	324	3	AAG31201	Aag31201 Arabidops
59	70	14.3	758	9	ADW71760	Adw71760 Salmonell
60	69.5	14.2	227	8	AAQ38052	Aaq38052 Streptoco
61	69.5	14.2	1377	3	ADV81847	Adv81847 Streptoco
62	69.5	14.2	1387	8	ADV88434	Adv88434 Streptoco
63	69.5	14.2	1387	8	ADV79687	Adv79687 Streptoco
64	69	14.1	503	4	ABG16577	Abg16577 Novel hum
65	69	14.1	679	9	ADZ85056	Adz85056 Partial F
66	68.5	14.0	608	5	ABP73745	Abp73745 Candida a
67	68.5	14.0	632	8	ADS29711	Ads29711 Bacterial
68	68	13.9	239	3	ADT07537	Adt07537 Human col
69	68	13.9	280	3	AAV54294	Aav54294 Amino aci
70	68	13.9	280	5	ABG93905	Abg93905 Lactuca s
71	68	13.9	280	8	ADJ50292	Adj50292 Oll-a88oc
72	68	13.9	285	4	AAV92683	Aav92683 Human pro
73	68	13.9	302	4	AAV88379	Aav88379 Human mem
74	68	13.9	302	9	ADY63123	Ady63123 Human clo
75	68	13.9	414	6	ABU11747	Abu11747 Human MDD

ALIGNMENTS

RESULT 1
ABB78161
ID ABB78161 standard; protein; 91 AA.
XX
AC ABB78161;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKKLNMMNA 60
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 2
ABB78159
ID ABB78159 standard; protein; 91 AA.
XX
AC ABB78159;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

XX Unidentified.

XX US2002072118-A1.

XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX

SQ Sequence 91 AA;

Query Match 100.0%; Score 488; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 2.3e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKKLNMMNA 60
Db 1 MSRTIFCTYLQDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHQTMLINEKKLNMMNA 60
QY 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91
Db 61 EHRKLEQEMVSFLFEGKDVHIEGYTPEDKK 91

RESULT 3
ABB78162
ID ABB78162 standard; protein; 91 AA.
XX
AC ABB78162;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

XX Salmonella typhi.

XX US2002072118-A1.

XX 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.

XX 22-SEP-2000; 2000US-0234588P.

XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

XX Downs D, Gralnick JA;

XX WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.

XX Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:12:27 ; Search time 9.94989 Seconds
(without alignments)
879.982 Million cell updates/sec

Title: US-09-955-502A-17
Perfect score: 488
Sequence: 1 MSRTIFCTYLQRDAGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB	ID	Description
1	488	100.0	91	2	AH0879	conserved hypothet
2	469	96.1	91	2	A85954	hypothetical prote
3	469	96.1	91	2	A65082	hypothetical prote
4	469	96.1	91	2	F91108	hypothetical prote
5	393	80.5	90	2	A10116	conserved hypothet
6	389	79.7	90	2	C82320	conserved hypothet
7	385	78.9	90	2	C64013	hypothetical prote
8	259	53.1	93	2	B84994	hypothetical prote
9	232	47.5	105	2	C82624	conserved hypothet
10	228	46.7	90	2	H83003	conserved hypothet
11	211	43.2	88	2	H81014	conserved hypothet
12	79.5	16.3	1638	2	D87749	protein unc-73b [i
13	79.5	16.3	2488	2	T42739	guanine nucleotide
14	78	16.0	1260	2	T04440	hypothetical prote
15	73.5	15.1	495	2	AH0985	probable zinc-prot
16	71.5	14.7	209	2	I64172	hypothetical prote
17	71	14.5	447	2	JC2076	alpha-1,3-mannosyl
18	71	14.5	507	2	C81063	fumarate hydratase
19	71	14.5	546	2	A81807	fumarate hydratase
20	71	14.5	548	2	A54510	63K antigen - nema
21	70	14.3	324	2	T05429	hypothetical prote
22	70	14.3	758	2	AD0763	thiosulfate reduct
23	70	14.3	758	2	A57143	thiosulfate-dithio
24	69.5	14.2	859	2	T29630	hypothetical prote
25	69	14.1	265	2	T46013	hypothetical prote
26	69	14.1	447	2	T16527	hypothetical prote
27	68.5	14.0	683	2	AC2256	hypothetical prote
28	68	13.9	445	1	XUHUMB	alpha-1,3-mannosyl
29	68	13.9	689	2	F83902	beta-galactosidase

30	67.5	13.8	166	2	F70562	hypothetical prote
31	67	13.7	447	1	A38561	alpha-1,3-mannosyl
32	67	13.7	1111	2	T23047	hypothetical prote
33	66.5	13.6	410	1	KHMSD	cathepsin D (EC 3.
34	66	13.5	447	1	A42500	alpha-1,3-mannosyl
35	66	13.5	703	2	B82148	ATP-dependent heil
36	66	13.5	1085	2	S62516	hypothetical coile
37	65.5	13.4	287	2	F82265	conserved hypothet
38	65.5	13.4	365	2	B54128	Fe-binding protein
39	65	13.3	433	2	A70465	probable GTP bindi
40	65	13.3	507	2	A83105	probable fumarase
41	65	13.3	511	2	A99574	ABC transporter at
42	65	13.3	593	2	C64097	probable soluble l
43	65	13.3	1230	2	S56850	SMC1 protein homol
44	64.5	13.2	327	2	AD2129	transcription regu
45	64.5	13.2	385	2	D87723	protein R06A10.2 l
46	64.5	13.2	401	2	AB1978	hypothetical prote
47	64.5	13.2	544	2	T40058	probable chromatin
48	64.5	13.2	1197	2	S26947	DNA-directed DNA p
49	64	13.1	251	2	E90428	hypothetical prote
50	64	13.1	548	2	A28309	60K filarial antig
51	64	13.1	643	2	A43647	parasporel crystal
52	63.5	13.0	379	2	S70709	type II site-speci
53	63.5	13.0	438	2	T37786	probable RNA-bindi
54	63.5	13.0	2672	2	A48126	translation activa
55	63	12.9	205	2	C26135	keratin, 50K type
56	63	12.9	235	2	G65212	hypothetical 26.7K
57	63	12.9	258	2	A97991	hypothetical prote
58	63	12.9	258	2	E95121	phosphoesterase, p
59	63	12.9	483	2	G64799	ybeV protein - Bac
60	63	12.9	543	2	T16015	hypothetical prote
61	63	12.9	549	2	T16016	hypothetical prote
62	63	12.9	1119	2	T15842	hypothetical prote
63	63	12.9	1166	2	H71609	hypothetical prote
64	63	12.9	1209	2	T46027	guanidine nucleoti
65	63	12.9	1327	2	T14594	SNF2alpha protein
66	63	12.9	1572	2	S45251	HBRM protein - hum
67	63	12.9	1586	2	S39580	shikimate kinase (
68	62.5	12.8	165	2	A81382	conserved hypothet
69	62.5	12.8	259	2	G83203	asparaginase (EC 3
70	62.5	12.8	305	2	A75211	GTP-binding regula
71	62.5	12.8	375	2	T37245	hypothetical prote
72	62.5	12.8	498	2	G91179	hypothetical prote
73	62.5	12.8	498	2	H86025	hypothetical prote
74	62.5	12.8	498	2	S47748	53.1K protein prec
75	62.5	12.8	629	2	B83107	chemotactic transd

ALIGNMENTS

RESULT 1
AH0879
conserved hypothetical protein SRY3266 [imported] - Salmonella enterica subsp. enterica
C/Species: Salmonella enterica subsp. enterica serovar Typhi
A/Note: this species has also been called Salmonella typhi
C/Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 05-Oct-2004
C/Accession: AH0879
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Conerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A/Title: Complete genome sequence of a multiple drug resistant Salmonella enterica sero
A/Reference number: AB0502; MUID:21534947; PMID:11677608
A/Accession: AH0879
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <PAR>
A/Cross-references: UNIPARC:UPI000005A44C; GB:AL513382; PIDN:CAD02936.1; PID:gl6504189;
C/Genetics:
A;Gene: STY3266
C;Superfamily: fe(II) trafficking protein YggX

Query Match		100.0%;	Score 488;	DB 2;	Length 91;
Best Local Similarity		100.0%;	Pred. No. 2.1e-42;		
Matches		91;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60			
Db	1 MSRTIFCTYLRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60			
OY	61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK	91			
Db	61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK	91			
RESULT 2					
A85954					
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)					
C/Species: Escherichia coli					
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004					
C/Accession: A85954					
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew					
Miller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,					
Nature 409, 529-533, 2001					
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.					
A/Reference number: A85480; MUID:21074935; PMID:11206551					
A/Accession: A85954					
A/Status: preliminary					
A/Molecule type: DNA					
A/Residues: 1-91 <STO>					
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; E					
C/Experimental source: strain O157:H7, substrain EDL933					
C/Genetics:					
A/Gene: yggX					
C;Superfamily: fe(II) trafficking protein YggX					
Query Match		96.1%;	Score 469;	DB 2;	Length 91;
Best Local Similarity		94.5%;	Pred. No. 1.8e-40;		
Matches		86;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60			
Db	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNA	60			
OY	61 EHRKLEQEMVSLFEGKDVHIEGYTPEDKK	91			
Db	61 EHRKLEQEMVSLFEGKEVHIEGYTPEDKK	91			
RESULT 3					
A65082					
hypothetical protein b2962 - Escherichia coli (strain K-12)					
C/Species: Escherichia coli					
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004					
C/Accession: A65082					
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co					
.A.; Rose, D.J.; Mau, B.; Shao, Y.					
Science 277, 1453-1462, 1997					
A/Title: The complete genome sequence of Escherichia coli K-12.					
A/Reference number: A64720; MUID:97426617; PMID:9278503					
A/Accession: A65082					
A/Status: preliminary; nucleic acid sequence not shown; translation not shown					
A/Molecule type: DNA					
A/Residues: 1-91 <BLAT>					
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g					
A/Experimental source: strain K-12, substrain MG1655					
C;Superfamily: fe(II) trafficking protein YggX					
Query Match		96.1%;	Score 469;	DB 2;	Length 91;
Best Local Similarity		94.5%;	Pred. No. 1.8e-40;		
Matches		86;	Conservative	5;	Mismatches 0; Indels 0; Gaps 0;
OY	1 MSRTIFCTYLRDAEGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60			

Db	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNA	60
OY	61 EHRKLLSEQEMVSLFEGKDVHIEGYTPEDKK	91
Db	61 EHRKLLSEQEMVSLFEGKEVHIEGYTPEDKK	91

RESULT 4

F91108

hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R

C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004

C/Accession: F91108

R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G

gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen

A/Reference number: A99629; MUID:21156231; PMID:11258796

A/Accession: F91108

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <HAY>

A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: ECs3838

C;Superfamily: fe(II) trafficking protein YggX

Query Match	96.1%;	Score 469;	DB 2;	Length 91;
Best Local Similarity	94.5%;	Pred. No. 1.8e-40;		
Matches	86;	Conservative 5;	Mismatches 0;	Indels 0; Gaps 0;

OY	1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60
Db	1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKKLNMNNA	60
OY	61 EHRKLLSEQEMVSLFEGKDVHIEGYTPEDKK	91
Db	61 EHRKLLSEQEMVSLFEGKEVHIEGYTPEDKK	91

RESULT 5

A10116

conserved hypothetical protein YPO0953 [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 05-Oct-2004

C/Accession: A10116

R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: A10116

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-90 <KUR>

A/Cross-references: UNIPARC:UPI00000DCCC4; GB:AL590842; PIDN:CAC89796.1; PID:g15979022;

C/Genetics:

A/Gene: YPO0953

C;Superfamily: fe(II) trafficking protein YggX

Query Match	80.5%;	Score 393;	DB 2;	Length 90;
Best Local Similarity	81.1%;	Pred. No. 8.1e-33;		
Matches	73;	Conservative 9;	Mismatches 8;	Indels 0; Gaps 0;

OY	1 MSRTIFCTYLQRDAGQDFQLYPGELGKRIYNEISKDAWAQWQHKTMLINEKKLNMNNA	60
Db	1 MSRTIFCTFLKDAERQDFQLYPGEIGKRIYNEISKEAWSQWITKOTMLINEKKLNMNI	60
OY	61 EHRKLLSEQEMVSLFEGKDVHIEGYTPEDK	90
Db	61 EDRKLLSEQEMVSLFEGQDVHIAGYTPPSK	90

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:51:36 ; Search time 67.0581 Seconds
(without alignments)
957.425 Million cell updates/sec

Title: US-09-955-502A-17
Perfect score: 488
Sequence: 1 MSRTIFCTYLQDAEGQDFQ.....SFLFEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	length	DB ID	Description
1	483	99.0	90	1	FETP_SALCH Q57K04 salmonella
2	483	99.0	90	1	FETP_SALPA Q5pmml1 salmoneilla
3	483	99.0	90	1	FETP_SALTI P67618 salmoneilla
4	483	99.0	90	1	FETP_SALTY P67617 salmoneilla
5	464	95.1	90	1	FETP_BCO57 P0a8p4 escherichia
6	464	95.1	90	1	FETP_BCO1I P0a8p3 escherichia
7	464	95.1	90	1	FETP_SHIFL P0a8p5 shigella fl
8	460	94.3	90	1	FETP_BCOL6 Q6fel9 escherichia
9	416	85.2	90	1	FETP_ERWCT Q6d8j9 erwinia car
10	401	82.2	90	1	FETP_YERPS Q666m3 yersinia ps
11	393	80.5	90	1	FETP_VIBPA Q871l5 vibrio para
12	389	79.7	90	1	FETP_YERPS Q8zhe7 yersinia pe
13	389	79.7	90	1	FETP_VIBCH Q8dcs5 vibrio chol
14	389	79.7	90	1	FETP_VIBVU Q7mh14 vibrio vuln
15	389	79.7	90	1	FETP_VIBVY Q65vt7 manheimia
16	387	79.3	91	1	FETP_MANSM P44048 haemophilus
17	385	78.9	90	1	FETP_HAEIN P44048 haemophilus
18	385	78.9	90	2	Q4QMD9_HAEI8 Q4qmd9 haemophilus
19	383	78.5	90	1	FETP_PHOPR Q6lwk7 photobacter
20	377	77.3	90	1	FETP_PASMU Q9clb9 pasteurella
21	376	77.0	90	1	FETP_PASLU Q7n7b1 photorhabdu
22	371	76.0	94	1	FETP_HABDU Q5e7t0 vibrio fisc
23	365	74.8	90	1	FETP_VIBF1 Q5qy58 idiomarina
24	341	69.9	90	1	FETP_IDILO Q8ebx6 shewanella
25	336	68.9	92	1	FETP_SHON P57618 buchnera ap
26	259	53.1	77	1	FETP_BUCAI Q7w9g2 bordetella
27	249	51.0	90	1	FETP_BORBR Q7w9g2 bordetella
28	249	51.0	90	1	FETP_BORPA Q7vwc4 bordetella
29	249	51.0	90	1	FETP_BORPB Q8k925 buchnera ap
30	243	49.8	78	1	FETP_BUCAP Q8pjh7 xanthomonas
31	239	49.0	91	1	FETP_XANAC

32	232	47.5	90	1	FETP_XYLFA Q9pc73 xylella fas
33	232	47.5	92	1	FETP_XANOR Q5gy22 xanthomonas
34	228.5	46.8	89	1	FETP_LEGPL Q5wvc4 legioneilla
35	228	46.7	90	1	FETP_PSEAE Q9hu36 pseudomonas
36	228	46.7	90	1	FETP_XYLEFT Q87d06 xylella fas
37	228	46.7	92	1	FETP_XANCP Q8p829 xanthomonas
38	228	46.7	92	2	Q4UW14_XANCP Q4uw14 xanthomonas
39	225	46.1	78	1	FETP_WIGBR Q87u65 pseudomonas
40	224.5	46.0	89	1	FETP_LEGPA Q5x3x9 legionella
41	224.5	46.0	89	1	FETP_LEGPH Q82xf2 nitrosomona
42	222	45.5	90	1	FETP_NITEU Q87uf5 pseudomonas
43	222	45.5	90	1	FETP_PSESM Q4zlp3 pseudomonas
44	222	45.5	90	2	Q4ZLP3_PSESY Q83d06 coxiella bu
45	218	44.7	90	1	FETP_PSEPK Q88r49 pseudomonas
46	218	44.7	90	1	FETP_COXBU Q4j228 azotobacter
47	218	44.7	90	2	Q4J228_AZOVI Q6t7f6 pseudomonas
48	215	44.1	90	2	Q6T7F6_PSEFL Q7nsr4 chromobacte
49	213	43.6	90	1	FETP_CHRVO Q7vrg9 candidatus
50	212	43.4	79	1	FETP_CANBF Q5f553 neisseria g
51	211	43.2	88	1	FETP_NEIG1 P67615 neisseria m
52	211	43.2	88	1	FETP_NEIMA Q89a44 buchnera ap
53	211	43.2	88	1	FETP_NEIMB Q62lu9 burkholderi
54	207	42.4	87	1	FETP_BUCBP Q63sj4 burkholderi
55	206	42.2	91	1	FETP_BURMA Q4kjt2 pseudomonas
56	206	42.2	91	1	FETP_BURPS Q8y010 ralstonia s
57	205	42.0	90	2	Q4KJT2_PSEF5 Q4ls19 burkholderi
58	205	42.0	91	1	FETP_RALSO Q60a17 methylococc
59	203	41.6	91	2	Q4LS19_9BURK Q5nhj8 francisella
60	195	40.0	90	1	FETP_METCA Q6fbj3 acinetobact
61	192	39.3	87	1	FETP_METCA Q5nhj8 francisella
62	190.5	39.0	90	1	FETP_FRATT Q6fbj3 acinetobact
63	146	29.9	96	2	Q4FVU7_9GAMM Q4nwq4 anaeromyxob
64	145	29.7	92	2	Q4NWQ4_9DELT Q5nuyl1 ralstonia m
65	82.5	16.9	482	2	Q5NUY1_9BURK Q6aiz9 desulfocale
66	82.5	16.9	514	2	Q6AIZ9_DESPS Q7kpp4 caenorhabdi
67	79.5	16.3	1638	2	Q7KPP4_CAEBL Q6bew2 caenorhabdi
68	79.5	16.3	2140	2	Q6BEW2_CAEBL Q61528 caenorhabdi
69	79.5	16.3	2488	2	O61528_CAEBL Q61528 caenorhabdi
70	78.5	16.1	337	2	O81AR8_BACCR Q81ar8 bacillus ce
71	78	16.0	1260	2	Q49677_ARATH Q49677 arabidopsis
72	77.5	15.9	1047	2	O5CJ53_CRYHO Q5cj53 cryptospori
73	76.5	15.7	486	2	Q7WX51_ALCEU Q7wx51 alcalligenes
74	75.5	15.5	1278	2	O5CYM7_CRYPV Q5cym7 cryptospori
75	75	15.4	385	2	Q734A2_BACCI Q734a2 bacillus ce

ALIGNMENTS

RESULT 1
FETP_SALCH
ID FETP_SALCH STANDARD; PRT; 90 AA.
AC Q57K04;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=YggX; OrderedLocustNames=SC3052;
OS Salmonella choleraesuis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Salmonella.
OX NCBI_TaxID=591;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=SC-B67;
RX PubMed=15781495; DOI=10.1093/nar/gki297;
RA Chiu C.-H., Tang P., Chu C., Hu S., Bao Q., Yu J., Chou Y.-Y.,
Wang H.-S., Lee Y.-S.,
"The genome sequence of Salmonella enterica serovar Choleraesuis, a
highly invasive and resistant zoonotic pathogen.",
Nucleic Acids Res. 33:1690-1698(2005).
RT
RL
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
acquisition and iron-regulating processes, such as synthesis and/or

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:15:51 ; Search time 18.4487 Seconds
(without alignments)
407.805 Million cell updates/sec

Title: US-09-955-502A-17

Perfect score: 488

Sequence: 1 MSRTIFCTYLQRDABGQDFQ.....SFLPEKDVHIEGYTPEDKK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	445	91.2	107	2	US-09-489-039A-11962 Sequence 11962, A
2	383	78.5	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	228	46.7	122	2	US-09-252-991A-23355 Sequence 23355, A
4	195.5	40.1	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	130	26.6	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	71	14.5	548	2	US-09-167-299-3 Sequence 3, Appli
7	70.5	14.0	184	2	US-09-325-932A-66 Sequence 66, Appli
8	68.5	14.0	544	2	US-09-248-796A-18911 Sequence 18911, A
9	68	13.9	280	2	US-09-323-998E-37 Sequence 37, Appli
10	68	13.9	337	2	US-09-270-767-41746 Sequence 41746, A
11	68	13.9	1214	2	US-10-164-595-24 Sequence 24, Appli
12	66.5	13.6	325	2	US-09-134-000C-4346 Sequence 4346, Ap
13	66	13.5	292	2	US-09-328-352-5836 Sequence 5836, Ap
14	65.5	13.4	546	1	US-08-533-669A-2 Sequence 2, Appli
15	65.5	13.4	546	2	US-09-183-861-2 Sequence 2, Appli
16	65.5	13.4	546	2	US-09-022-765-2 Sequence 2, Appli
17	65.5	13.4	546	2	US-09-551-974A-2 Sequence 2, Appli
18	65.5	13.4	546	2	US-09-565-501A-2 Sequence 2, Appli
19	65.5	13.4	546	2	US-09-639-206A-2 Sequence 2, Appli
20	65.5	13.4	546	2	US-09-874-923-2 Sequence 2, Appli
21	65.5	13.4	546	2	US-08-798-841-2 Sequence 2, Appli
22	65.5	13.4	982	2	US-09-551-974A-95 Sequence 95, Appli
23	65.5	13.4	982	2	US-09-565-501A-95 Sequence 95, Appli
24	65.5	13.4	982	2	US-09-639-206A-95 Sequence 95, Appli
25	65.5	13.4	982	2	US-09-874-923-95 Sequence 95, Appli
26	65.5	13.4	1427	2	US-09-551-974A-97 Sequence 97, Appli
27	65.5	13.4	1427	2	US-09-565-501A-97 Sequence 97, Appli

28	65.5	13.4	1427	2	US-09-639-206A-97	Sequence 97, Appli
29	65.5	13.4	1427	2	US-09-874-923-97	Sequence 97, Appli
30	65.5	13.4	1641	2	US-09-551-974A-96	Sequence 96, Appli
31	65.5	13.4	1641	2	US-09-565-501A-96	Sequence 96, Appli
32	65.5	13.4	1641	2	US-09-639-206A-96	Sequence 96, Appli
33	65.5	13.4	1641	2	US-09-874-923-96	Sequence 96, Appli
34	65	13.3	474	2	US-09-252-991A-24473	Sequence 24473, A
35	64	13.1	98	2	US-09-270-767-41085	Sequence 41085, A
36	64	13.1	98	2	US-09-270-767-56301	Sequence 56301, A
37	64	13.1	569	2	US-09-107-532A-6689	Sequence 6689, Ap
38	64	13.1	644	2	US-08-793-331-7	Sequence 7, Appli
39	64	13.1	1176	2	US-09-489-039A-8879	Sequence 8879, Ap
40	63.5	13.0	921	2	US-09-248-796A-14950	Sequence 14950, A
41	63	12.9	1586	2	US-09-538-092-1171	Sequence 1171, Ap
42	62.5	12.8	260	2	US-09-252-991A-17498	Sequence 17498, A
43	62.5	12.8	419	2	US-09-543-681A-7295	Sequence 7295, Ap
44	62.5	12.8	662	2	US-09-583-110-5119	Sequence 5119, Ap
45	62.5	12.8	664	2	US-09-107-433-2775	Sequence 2775, Ap
46	62.5	12.8	701	2	US-09-252-991A-23288	Sequence 23288, A
47	62	12.7	227	2	US-09-270-767-58283	Sequence 58283, A
48	62	12.7	238	2	US-09-323-998E-41	Sequence 41, Appli
49	62	12.7	448	2	US-09-270-767-42959	Sequence 42959, A
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51	62	12.7	604	2	US-09-472-667-4	Sequence 4, Appli
52	62	12.7	898	2	US-09-583-110-3750	Sequence 3750, Ap
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55	62	12.7	1167	2	US-09-472-667-6	Sequence 6, Appli
56	61.5	12.6	591	2	US-09-370-368-8	Sequence 8, Appli
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74	59.5	12.2	276	2	US-09-949-016-11703	Sequence 11703, A
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:14:02 ; Search time 57.6264 Seconds
(without alignments)
659.810 Million cell updates/sec

Title: US-09-955-502A-17
Perfect score: 488
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Total number of hits satisfying chosen parameters: 1867569

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	472	96.7	88	3	US-09-955-502-15
6	469	96.1	91	3	US-09-955-502-11
7	469	96.1	91	3	US-09-955-502-12
8	469	96.1	91	3	US-09-955-502-13
9	393	80.5	90	3	US-09-955-502-20
10	389	79.7	90	3	US-09-955-502-10
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23	222	45.5	90	3	US-09-955-502-23
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26	211	43.2	88	3	US-09-955-502-26
27	211	43.2	88	3	US-09-955-502-27

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30	206	42.2	87	3	US-09-955-502-30	Sequence 30, Appl
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33	177	15.8	1647	5	US-10-450-763-41109	Sequence 41109, A
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45	68.5	14.0	608	4	US-10-032-585-7582	Sequence 7582, Ap
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47	68	13.9	280	3	US-09-323-998D-37	Sequence 37, Appl
48	68	13.9	280	4	US-10-389-566-2296	Sequence 2296, Ap
49	68	13.9	445	4	US-10-844-874-14	Sequence 14, Appl
50	68	13.9	445	5	US-10-713-970-13	Sequence 13, Appl
51	68	13.9	478	4	US-10-087-192-378	Sequence 378, App
52	68	13.9	689	4	US-10-369-493-17280	Sequence 17280, A
53	68	13.9	764	4	US-10-416-330-37	Sequence 37, Appl
54	68	13.9	764	5	US-10-491-467-15	Sequence 15, Appl
55	68	13.9	1206	4	US-10-085-198-144	Sequence 144, Appl
56	68	13.9	1214	5	US-10-717-665-24	Sequence 24, Appl
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; Sequence 14, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 14
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Salmonella paratyphi

GenCore version 5.1.7
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Title: US-09-955-502A-17
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SUMMARIES

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4	64.5	13.2	177	6	US-10-467-657-1658 Sequence 1658, App
5	63.5	13.0	1432	6	US-10-510-386-218 Sequence 218, App
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7	62	12.7	604	6	US-10-942-072-4 Sequence 4, Appli
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12	59.5	12.2	285	6	US-10-467-657-8230 Sequence 8230, App
13	59.5	12.2	650	6	US-10-467-657-1948 Sequence 1948, App
14	59.5	12.2	834	6	US-10-453-372-658 Sequence 658, App
15	59.5	12.2	1995	7	US-11-069-834-60 Sequence 60, Appli
16	59	12.1	257	7	US-11-054-515-1710 Sequence 1710, App
17	59	12.1	697	6	US-10-485-517-202 Sequence 202, App
18	59	12.1	1168	6	US-10-485-517-11 Sequence 11, Appli
19	59	12.1	1450	6	US-10-485-517-152 Sequence 152, App
20	58.5	12.0	695	6	US-10-453-372-648 Sequence 648, App
21	58.5	12.0	700	6	US-10-995-561-922 Sequence 922, App
22	58.5	12.0	700	6	US-10-995-561-924 Sequence 924, App
23	58.5	12.0	749	7	US-11-098-686-10505 Sequence 10505, A
24	58.5	12.0	782	6	US-10-793-626-2352 Sequence 2352, App
25	58	11.9	448	6	US-10-618-320A-25 Sequence 25, Appli

26	58	11.9	480	6	US-10-510-386-12	Sequence 12, Appli
27	58	11.9	1501	6	US-10-793-626-2850	Sequence 2850, App
28	57.5	11.8	242	7	US-11-022-562-220	Sequence 220, App
29	57.5	11.8	336	6	US-10-453-372-640	Sequence 640, App
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31	57.5	11.8	752	7	US-11-072-512-3003	Sequence 3003, App
32	57.5	11.8	775	6	US-10-453-372-656	Sequence 656, App
33	57.5	11.8	793	6	US-10-995-561-925	Sequence 925, App
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35	57.5	11.8	847	6	US-10-453-372-654	Sequence 654, App
36	57.5	11.8	857	6	US-10-453-372-652	Sequence 652, App
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38	57.5	11.8	905	6	US-10-453-372-662	Sequence 662, App
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43	57.5	11.8	3803	6	US-10-995-561-773	Sequence 773, App
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54	56.5	11.6	647	7	US-11-000-463-722	Sequence 722, App
55	56.5	11.6	1254	6	US-10-821-234-1635	Sequence 1635, App
56	56.5	11.6	1897	7	US-11-000-463-250	Sequence 250, App
57	56.5	11.6	1907	7	US-10-714-781A-67	Sequence 67, Appli
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ALIGNMENTS

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; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

GenCore version 5.1.7
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and is derived by analysis of the total score distribution.

SUMMARIES

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4	295.5	65.1	91	1	FETP_RALSO	Q8y010 ralstonia s
5	286.5	63.1	91	2	Q4LS19 9BURK	Q4ls19 burkholderi
6	283	62.3	90	1	FETP_CHRVO	Q7n8r4 chromobacte
7	282.5	62.2	91	1	FETP_BURMA	Q62iu9 burkholderi
8	282.5	62.2	91	1	FETP_BURPS	Q63sj4 burkholderi
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10	272.5	60.0	88	1	FETP_NEIMA	P67615 neisseria m
11	272.5	60.0	88	1	FETP_NEIMB	P67616 neisseria m
12	269	59.3	90	1	FETP_NITEU	Q82xf2 nitrosomona
13	242.5	53.4	90	1	FETP_METCA	Q60aj7 methylcoccc
14	242.5	53.4	92	1	FETP_SHON	Q8ebx6 shewanella
15	242	53.3	89	1	FETP_LEGPA	Q5x3x9 legionella
16	242	53.3	89	1	FETP_LEGPH	Q5zu80 legionella
17	241	53.1	89	1	FETP_LEGPL	Q5wvc4 legionella
18	241	53.1	90	1	FETP_VIBPA	Q87li5 vibrio para
19	240	52.9	90	1	FETP_IDILO	Q5qy58 idiomarina
20	239	52.6	91	1	FETP_MANSN	Q65vt7 manheimia
21	238.5	52.5	90	1	FETP_HABIN	P44048 haemophilus
22	238.5	52.5	90	2	Q4QMD9 HAB18	Q4qmd9 haemophilus
23	238	52.4	90	1	FETP_VIBF1	Q5e7c0 vibrio fisc
24	236	52.0	90	1	FETP_ECOL6	P0a8p4 escherichia
25	236	52.0	90	1	FETP_ECOL6	P0a8p4 escherichia
26	236	52.0	90	1	FETP_ECOL1	P0a8p3 escherichia
27	236	52.0	90	1	FETP_SHIFL	P0a8p5 shigella fl
28	236	52.0	90	1	FETP_VIBVU	Q8dc55 vibrio vuln
29	236	52.0	90	1	FETP_VIBVU	Q7mhi4 vibrio vuln
30	235	51.8	90	1	FETP_VIBVY	Q9kura4 vibrio chol
31	233.5	51.4	90	1	FETP_PASMU	Q9c1b9 pasteurella

32	233	51.3	90	1	FETP_PROPR	Q6lmk7 photobacter
33	232	51.1	90	1	FETP_PHOL	Q7n7i1 photorhabdu
34	230	50.7	90	1	FETP_SALCH	Q57k04 salmonella
35	230	50.7	90	1	FETP_SALPA	Q5pmm1 salmonella
36	230	50.7	90	1	FETP_SALTI	P67618 salmonella
37	230	50.7	90	1	FETP_SALTY	P67617 salmonella
38	228	50.2	90	2	Q4J228 AZOVI	Q4j228 azotobacter
39	225.5	49.7	94	1	FETP_HAEDU	Q7vkb6 haemophilus
40	225	49.6	90	1	FETP_ERWCT	Q6d8j9 erwina car
41	224.5	49.4	90	1	FETP_AC1AD	Q6f6b3 acinetobact
42	223	49.1	90	1	FETP_COXBU	Q83d06 coxiella bu
43	222.5	49.0	90	1	FETP_PSEAE	Q9hu36 pseudomonas
44	220	48.5	78	1	FETP_BUCAP	Q8k925 buchnera ap
45	220	48.5	90	1	FETP_YERPS	Q666m3 yersinia ps
46	220	48.5	91	1	FETP_XANAC	Q8bjh7 xanthomonas
47	214	47.1	92	1	FETP_XANOR	Q5gy22 xanthomonas
48	213	46.9	79	1	FETP_CANBP	Q7vrg9 candidatus
49	212	46.7	90	1	FETP_YERPE	Q8zhe7 yersinia pe
50	211	46.5	92	1	FETP_XANCP	Q8p829 xanthomonas
51	211	46.5	92	2	Q4UW14 XANCP	Q4uw14 xanthomonas
52	204.5	45.0	90	1	FETP_PSEPK	Q88r49 pseudomonas
53	202	44.5	90	1	FETP_XYLF1	Q87d06 xylella fas
54	200.5	44.2	90	1	FETP_PSESM	Q87uif5 pseudomonas
55	200.5	44.2	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
56	200	44.1	77	1	FETP_BUCAI	P57618 buchnera ap
57	196.5	43.3	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
58	196.5	43.3	90	2	Q4KJ22_PSEFS	Q4kjc2 pseudomonas
59	195	43.0	90	1	FETP_XYLF1	Q9pc73 xylella fas
60	193	42.5	78	1	FETP_WIGBR	Q8d3c5 wiggleswort
61	184	40.5	87	1	FETP_FRATF	Q5nhj8 francisella
62	175	38.5	92	2	Q4NW04_9DELT	Q4nwq4 anaeromyxob
63	166	36.6	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	157	34.6	87	1	FETP_BUCBP	Q89a44 buchnera ap
65	79.5	17.5	116	2	Q6UPK7_9H1V1	Q6ufk7 human immun
66	77.5	17.1	913	2	Q61IV8_CABBR	Q61iv8 caenorhabdi
67	77	17.0	330	2	Q5DA35_SCHJA	Q5da35 schistosoma
68	77	17.0	2410	2	Q5AZ49_EMENT	Q5az49 aspergillus
69	76.5	16.9	749	2	Q9CGA2_LACLA	Q9cga2 lactococcus
70	75.5	16.6	116	2	Q6WS71_9H1V1	Q6ws71 human immun
71	74.5	16.4	116	2	Q596M7_9H1V1	Q596m7 human immun
72	71.5	15.7	207	1	COAB_STAAM	P63830 staphylococ
73	71.5	15.7	207	1	COAB_STAAN	P63831 staphylococ
74	71.5	15.7	207	1	COAB_STAAR	Q6ggj8 staphylococ
75	71.5	15.7	207	1	COAB_STAAS	Q6ggn8 staphylococ

ALIGNMENTS

RESULT 1
FETP_BORBR
ID FETP_BORBR STANDARD; PRT; 90 AA.
AC Q7WH06;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BB3405;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebatina M., Preston A., Murphy L.D., Thomson N.R.,
Harris D.B., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
Achman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,

RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX640447; CAB33897.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.7%; Score 443.5; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6.9e-39;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIMQOISKEAWEEWKQIQTRLVNNENRLNLADA 60
Db 1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIMQOISKEAWEEWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLOQOMERFLFEDGTVEAQC-VP 86
Db 61 RARKYLOQOMERFLFEDGTVEAQQYVP 87

RESULT 2
FETP_BORPA
ID FETP_BORPA STANDARD; PRT; 90 AA.
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BPPI703;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 97.7%; Score 443.5; DB 1; Length 90;
Best Local Similarity 98.9%; Pred. No. 6.9e-39;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIMQOISKEAWEEWKQIQTRLVNNENRLNLADA 60
Db 1 MSRIVNCVKLKREAEGLDFPPYPGELGTRIMQOISKEAWEEWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLOQOMERFLFEDGTVEAQC-VP 86
Db 61 RARKYLOQOMERFLFEDGTVEAQQYVP 87

RESULT 3
FETP_BORPE
ID FETP_BORPE STANDARD; PRT; 90 AA.
AC Q7VWC4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP2336;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tobama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
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CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC removed.
CC -----
DR EMBL; BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.109 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-4
Perfect score: 454
Sequence: 1 MSRIVNCVKIKREAGLDLP.....QQQMERFLFEDGTVEAGVP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RB_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfilest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	229	50.4	107	2	US-09-489-039A-11962
2	228	50.2	93	2	US-09-543-681A-5443
3	223.5	49.2	92	2	US-09-328-352-5456
4	222.5	49.0	122	2	US-09-252-991A-23355
5	157.5	34.7	110	2	US-09-540-236-2859
6	72.5	16.0	303	2	US-09-902-540-13601
7	70.5	15.5	200	2	US-09-710-279-1186
8	70.5	15.5	200	2	US-09-134-001C-3785
9	70.5	15.5	208	2	US-09-134-001C-3785
10	70.5	15.5	366	2	US-08-928-213B-59
11	69	15.2	219	2	US-08-928-213B-61
12	69	15.2	504	1	US-08-441-139-18
13	69	15.2	521	1	US-08-557-122A-32
14	69	15.2	521	2	US-09-262-666-32
15	69	15.2	522	2	US-09-368-588-2
16	69	15.2	530	1	US-08-557-122A-35
17	69	15.2	530	2	US-09-262-666-35
18	67	14.8	381	2	US-09-949-016-9788
19	67	14.8	381	2	US-09-964-899-13
20	66.5	14.6	591	2	US-09-370-368-8
21	66.5	14.6	1242	2	US-09-107-532A-5241
22	66.5	14.6	1245	2	US-09-716-964B-87
23	66	14.5	503	2	US-09-058-260-26
24	64	14.1	1493	2	US-09-713-273A-20
25	63.5	14.0	498	2	US-09-058-260-16
26	63.5	14.0	503	1	US-08-781-802-2
27	63.5	14.0	503	1	US-08-781-802-10

28	63.5	14.0	503	1	US-08-781-802-12	Sequence 12, Appl
29	63.5	14.0	503	2	US-08-694-078-2	Sequence 2, Appli
30	63.5	14.0	503	2	US-09-058-260-2	Sequence 2, Appli
31	63.5	14.0	503	2	US-09-058-260-10	Sequence 10, Appl
32	63.5	14.0	503	2	US-09-058-260-12	Sequence 12, Appl
33	63.5	14.0	503	2	US-09-058-260-28	Sequence 28, Appl
34	63.5	14.0	503	1	US-09-058-260-30	Sequence 30, Appl
35	63.5	14.0	805	2	US-08-045-806-2	Sequence 2, Appli
36	63.5	14.0	805	1	US-08-366-051B-2	Sequence 2, Appli
37	63	13.9	581	2	US-09-713-273A-12	Sequence 12, Appl
38	63	13.9	979	2	US-09-543-681A-5465	Sequence 5465, Ap
39	63	13.9	2532	2	US-09-215-694-10	Sequence 10, Appl
40	63	13.9	2532	2	US-10-109-310-10	Sequence 10, Appl
41	62.5	13.8	666	2	US-09-270-767-62249	Sequence 62249, A
42	62.5	13.8	721	2	US-09-270-767-46645	Sequence 46645, A
43	61.5	13.5	292	2	US-09-328-352-5836	Sequence 5836, Ap
44	61.5	13.5	516	2	US-09-248-796A-19517	Sequence 19517, A
45	61.5	13.5	518	2	US-09-045-360-4	Sequence 4, Appli
46	61.5	13.5	518	2	US-09-746-390-4	Sequence 4, Appli
47	61.5	13.5	623	2	US-10-104-047-3378	Sequence 3378, Ap
48	61.5	13.5	1464	2	US-09-045-360-2	Sequence 2, Appli
49	61.5	13.5	1464	2	US-09-713-273A-21	Sequence 21, Appli
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51	61.5	13.5	1464	2	US-09-746-390-2	Sequence 2, Appli
52	61	13.4	312	2	US-09-605-703B-2656	Sequence 2656, Ap
53	61	13.4	563	2	US-09-949-016-10801	Sequence 10801, A
54	61	13.4	713	2	US-09-540-236-3595	Sequence 3595, Ap
55	61	13.4	856	2	US-09-252-991A-17850	Sequence 17850, A
56	61	13.4	862	1	US-08-685-118-2	Sequence 2, Appli
57	61	13.4	862	1	US-08-915-495-2	Sequence 2, Appli
58	61	13.4	862	1	US-08-914-520-2	Sequence 2, Appli
59	61	13.4	862	2	US-09-853-180B-4	Sequence 4, Appli
60	61	13.4	864	2	US-09-949-016-7758	Sequence 7758, Ap
61	60.5	13.3	81	2	US-10-290-579A-138	Sequence 138, App
62	60	13.2	1308	2	US-09-862-027-79	Sequence 79, Appl
63	59.5	13.1	447	2	US-09-902-540-13195	Sequence 13195, A
64	59.5	13.1	5037	2	US-09-424-783-4	Sequence 4, Appli
65	59	13.0	226	2	US-10-104-047-3820	Sequence 3820, Ap
66	59	13.0	265	2	US-09-710-279-174	Sequence 174, App
67	59	13.0	309	2	US-09-248-796A-14939	Sequence 14939, A
68	59	13.0	371	2	US-10-104-047-3421	Sequence 3421, Ap
69	59	13.0	435	2	US-09-248-796A-15070	Sequence 15070, A
70	59	13.0	437	2	US-09-134-001C-5342	Sequence 5342, Ap
71	59	13.0	805	2	US-09-598-401C-77	Sequence 77, Appl
72	59	13.0	1612	2	US-08-545-860D-48	Sequence 48, Appl
73	59	13.0	1612	4	PCT-US94-04496-48	Sequence 48, Appl
74	58.5	12.9	314	2	US-09-252-991A-18752	Sequence 18752, A
75	58.5	12.9	318	1	US-08-695-412B-12	Sequence 12, Appl

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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Query Match          50.4%; Score 229; DB 2; Length 107;
Best Local Similarity 51.2%; Pred. No. 5.3e-22;
Matches 43; Conservative 16; Mismatches 25; Indels 0; Gaps 0;

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      17 MSRTFCTFLQREADGDFQLYPGLGKRIYNEISKEAWAQWQHQTMLINEKLSMWNP 76
DB      61 RARKYLQOQMERFLFEDGTVEAOG 84
      77 EHRKLLQEQEMVQFLFEGKDVHIEG 100

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match          50.2%; Score 228; DB 2; Length 93;
Best Local Similarity 53.6%; Pred. No. 5.9e-22;
Matches 45; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY      1 MSRIVNCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNENRLNLADA 60
      4 MSRTFCTFLNKADGLDFQLYPGLGKRIYNEISKEAWQWMAKQTMLINEKLSMWNP 63
DB      61 RARKYLQOQMERFLFEDGTVEAOG 84
      64 DRRKLLQEQEMVRFLEFGHDVHIDG 87

QY      1 MSRIVNCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNENRLNLADA 60
      4 MSRTFCTFLNKADGLDFQLYPGLGKRIYNEISKEAWQWMAKQTMLINEKLSMWNP 63
DB      61 RARKYLQOQMERFLFEDGTVEAOG 84
      64 DRRKLLQEQEMVRFLEFGHDVHIDG 87

RESULT 3
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match          49.2%; Score 223.5; DB 2; Length 92;
Best Local Similarity 49.4%; Pred. No. 2.2e-21;
Matches 42; Conservative 18; Mismatches 24; Indels 1; Gaps 1;

QY      1 MSRIVNCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNENRLNLADA 60
      4 MSRIQVCRKRYQKEMEGLDFAFPFGAKQBEFFENVSKQAWQEWLQHTTLINERKLVNVEP 63
DB      61 RARKYLQOQMERFLFEDGTVEAOG 84
      61 RARKYLQOQMERFLFEDGTVEAOG 84
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Db      64 EAKKFLBEQREKFFNNDESVEKAEG 88

RESULT 4
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match          49.0%; Score 222.5; DB 2; Length 122;
Best Local Similarity 49.4%; Pred. No. 4.4e-21;
Matches 43; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY      1 MSRIVNCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNENRLNLADA 60
      33 MSRTVMCRKHYHEELPGLDRPPYPGAKGEDYNNVSRKAWDEWQKHQTMLINEKLSMWNNA 92
DB      61 RARKYLQOQMERFLFEDGTVEAOG-VP 86
      93 EDRKFLQEQEMDKFLSGEDYAKADGYVP 119

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

Query Match          34.7%; Score 157.5; DB 2; Length 110;
Best Local Similarity 39.7%; Pred. No. 1.1e-12;
Matches 31; Conservative 16; Mismatches 30; Indels 1; Gaps 1;

QY      4 IVNCVKLKREAGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNENRLNLADARAR 63
      24 MVFCRKYQQLPKLPNPPPNNAKGOEIQDTISAKAWNAMLELQTMLINEKLSMIDPOAK 83
DB      64 KYLQOQMERFLFEDGTVE 81
      84 KYLINEQREKFL-DNGDYE 100

RESULT 6
US-09-902-540-13601
; Sequence 13601, Application US/09902540
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 65.403 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-4
Perfect score: 454
Sequence: 1 MSRIVNCVKLKREAGLDLP.....QQQMERFLFDGTVEAQQVP 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_Main:*

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- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	454	100.0	86	3	US-09-955-502-4
2	443.5	97.7	87	3	US-09-955-502-2
3	443.5	97.7	87	3	US-09-955-502-3
4	282.5	62.2	87	3	US-09-955-502-29
5	282.5	62.2	87	3	US-09-955-502-30
6	272.5	60.0	88	3	US-09-955-502-26
7	272.5	60.0	88	3	US-09-955-502-27
8	272.5	60.0	88	3	US-09-955-502-28
9	257.5	56.7	87	3	US-09-955-502-31
10	246	54.2	91	3	US-09-955-502-5
11	242.5	53.4	87	3	US-09-955-502-32
12	242.5	53.4	88	3	US-09-955-502-9
13	241	53.1	91	3	US-09-955-502-11
14	241	53.1	91	3	US-09-955-502-12
15	241	53.1	91	3	US-09-955-502-13
16	241	53.1	91	3	US-09-955-502-18
17	238.5	52.5	87	3	US-09-955-502-7
18	235	51.8	88	3	US-09-955-502-15
19	235	51.8	90	3	US-09-955-502-10
20	235	51.8	91	3	US-09-955-502-14
21	235	51.8	91	3	US-09-955-502-16
22	233.5	51.4	87	3	US-09-955-502-6
23	225.5	49.7	87	3	US-09-955-502-8
24	223	49.1	88	3	US-09-955-502-33
25	222.5	49.0	87	3	US-09-955-502-25
26	222	48.9	78	3	US-09-955-502-19
27					

28	212	46.7	90	3	US-09-955-502-20	Sequence 20, Appl
29	204.5	45.0	87	3	US-09-955-502-24	Sequence 24, Appl
30	200.5	44.2	90	3	US-09-955-502-23	Sequence 23, Appl
31	200	44.1	76	3	US-09-955-502-21	Sequence 21, Appl
32	195	43.0	89	3	US-09-955-502-22	Sequence 22, Appl
33	71.5	15.7	207	5	US-10-857-625-698	Sequence 698, App
34	70.5	15.5	208	4	US-10-724-972A-6021	Sequence 6021, Ap
35	69.5	15.3	1733	4	US-10-437-963-181840	Sequence 181840,
36	69	15.2	428	4	US-10-437-963-146305	Sequence 146305,
37	69	15.2	527	5	US-10-501-282-46	Sequence 46, Appl
38	69	15.2	528	5	US-10-501-282-48	Sequence 48, Appl
39	68.5	15.1	87	4	US-10-424-599-281616	Sequence 281616,
40	68	15.0	558	4	US-10-425-115-217061	Sequence 217061,
41	67.5	14.9	559	4	US-10-425-115-338828	Sequence 338828,
42	67.5	14.9	714	4	US-10-369-493-2684	Sequence 2684, Ap
43	67	14.8	373	4	US-10-437-963-107538	Sequence 107538,
44	67	14.8	381	3	US-09-964-899-13	Sequence 13, Appl
45	67	14.8	381	5	US-10-975-523-13	Sequence 13, Appl
46	67	14.8	593	5	US-10-484-156-4	Sequence 4, Appli
47	67	14.8	1602	4	US-10-437-963-114183	Sequence 114183,
48	66.5	14.6	591	3	US-09-827-822-8	Sequence 8, Appli
49	66.5	14.6	1240	4	US-10-282-122A-57585	Sequence 57585, A
50	66.5	14.6	1245	4	US-10-671-403-87	Sequence 87, Appl
51	66.5	14.6	1245	4	US-10-671-419-87	Sequence 87, Appl
52	66.5	14.6	1245	4	US-10-671-844-87	Sequence 87, Appl
53	66.5	14.6	1245	4	US-10-671-134-87	Sequence 87, Appl
54	66.5	14.6	1245	4	US-10-673-098-87	Sequence 87, Appl
55	66.5	14.6	1245	4	US-10-672-638-87	Sequence 87, Appl
56	66.5	14.6	1245	4	US-10-673-127-87	Sequence 87, Appl
57	66.5	14.6	1245	4	US-10-670-817-87	Sequence 87, Appl
58	66.5	14.6	1245	4	US-10-673-119-87	Sequence 87, Appl
59	66.5	14.6	1245	4	US-10-671-207-87	Sequence 87, Appl
60	66.5	14.6	1245	5	US-10-673-120-87	Sequence 87, Appl
61	66.5	14.6	1245	5	US-10-671-412-87	Sequence 87, Appl
62	66.5	14.6	1245	5	US-10-671-859-87	Sequence 87, Appl
63	66.5	14.6	1245	5	US-10-671-106-87	Sequence 87, Appl
64	66.5	14.6	1406	4	US-10-437-963-129763	Sequence 129763,
65	66	14.5	318	4	US-10-047-260-20	Sequence 20, Appl
66	66	14.5	997	5	US-10-485-710-117	Sequence 117, App
67	65.5	14.4	348	4	US-10-437-963-121938	Sequence 121938,
68	65.5	14.4	596	4	US-10-437-963-130475	Sequence 130475,
69	65.5	14.4	1360	4	US-10-437-963-201860	Sequence 201860,
70	65	14.3	323	5	US-10-732-923-10030	Sequence 10030, A
71	65	14.3	323	5	US-10-732-923-10031	Sequence 10031, A
72	65	14.3	323	5	US-10-732-923-10032	Sequence 10032, A
73	65	14.3	1294	4	US-10-437-963-183026	Sequence 183026,
74	65	14.3	1626	4	US-10-437-963-113376	Sequence 113376,
75	65	14.3	1885	4	US-10-437-963-147331	Sequence 147331,

ALIGNMENTS

RESULT 1
US-09-955-502-4
; Sequence 4, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR FILING DATE: 2000-09-22
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Bordetella bronchiseptica

US-09-955-502-4

Query Match	100.0%;	Score 454;	DB 3;	Length 86;
Best Local Similarity	100.0%;	Pred. No. 5.7e-45;		
Matches	86;	Conservative	0;	Mismatches 0;
			Indels	0;
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Db 1 MSRI VNCV KLR EAGL DFP PYPG ELGTRI WQI SK EAW EEW KQI QTRL V NENR NLT LADA 600

Oy	61 RARKYLQOOMEKFLFEDGTVEAQGVP	86
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RESULT 2

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US-09-955-502-2
; Sequence 2, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Bordetella pertussis
US-09-955-502-2

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Query Match	97.7%;	Score 443.5;	DB 3;	Length 87;
Best Local Similarity	98.9%;	Pred. No. 9.6e-44;		
Matches 86;	Conservative 0;	Mismatches 0;	Indels 1;	Gaps 1

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Db 1 MSRIIVNCVKLKREAEGLDPPYPGELGTRIWMQISKEAWEEWKQIQTRLVNNENRNLNLADA 600

	61	RARKYLQOQMERRFLPEDGTVEAQG-VP	86
QY			
Db	61	RARKYLQOQMERRFLPEDGTVEAQQGYVP	87

RESULT 3

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US-09-955-502-3
; Sequence 3, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 3
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Bordetella parapertussis
US-09-955-502-3

Query Match          97.7%; Score 443.5; DB 3; Length 87;

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Best Local Similarity 98.9%; Pred. No. 9.6e-44;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db 1 MSRI VNCV LKREA EGLD PPPY PGELG TRLW QOISKEA WEEMK OIQTRL VNENR NLADA 600

Qy 61 RARKYLQOQMERFLFEDGTVEAQQ-V 86
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Db 61 RARKYLQOQMERFLFEDGTVEAQQGYV 87

RESULT 4

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US-09-955-502-29
; Sequence 29, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296, 97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 29
;
; LENGTH: 87
;
; TYPE: PRT
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; ORGANISM: Burkholderia mallei
US-09-955-502-29

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Query Match	62.2%;	Score 282.5;	DB 3;	length 87;
Best Local Similarity	56.3%;	Pred. No. 5.5e-25;		
Matches 49;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1

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Db 1 MARMIHCAKLGKEAEGIDFPPLPGLGKRLLYESVSCKAQAWODWLKKOQTMLINENNRNLNMA DP 600

Qy 61 RARKYLQQQMERFLFEDGTVEAQQ-V 86
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Db 61 RARQYLMKQTEKYFFGGADQASGYVP 87

RESULT 5

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US-09-955-502-30
; Sequence 30, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 30
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; LENGTH: 87
; TYPE: PRT
; ORGANISM: Burkholderia pseudomallei
US-09-955-502-30

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Query Match	62.2%;	Score 282.5;	DB 3;	Length 87;
Best Local Similarity	56.3%;	Pred. No. 5.5e-25;		
Matches 49;	Conservative 21;	Mismatches 16;	Indels 1;	Gaps 1

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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.85698 Seconds
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218.595 Million cell updates/sec

Title: US-09-955-502A-4
Perfect score: 454
Sequence: 1 MSRIYVNCVKIKREAGLDLP.....QQQMERFLPEDGTVEAQGV 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	272.5	60.0	88	6	US-10-467-657-968 Sequence 968, Appl
2	70.5	15.5	200	6	US-10-793-626-1186 Sequence 1186, Ap
3	70.5	15.5	200	6	US-10-793-626-2390 Sequence 2390, Ap
4	67	14.8	1320	7	US-11-098-686-10831 Sequence 10831, A
5	64.5	14.2	567	7	US-11-033-039-1279 Sequence 1279, Ap
6	63.5	14.0	805	7	US-11-108-539-2 Sequence 2, Appli
7	62.5	13.8	483	7	US-11-137-465-40 Sequence 40, Appl
8	62.5	13.8	832	7	US-11-098-686-10182 Sequence 10182, A
9	61.5	13.5	623	7	US-11-072-512-3378 Sequence 3378, Ap
10	60	13.2	240	7	US-11-044-111-10 Sequence 10, Appl
11	59	13.0	226	7	US-11-072-512-3820 Sequence 3820, Ap
12	59	13.0	265	6	US-10-793-626-174 Sequence 174, App
13	59	13.0	371	7	US-11-072-512-3421 Sequence 3421, Ap
14	59	13.0	805	6	US-10-927-641-77 Sequence 77, Appl
15	58.5	12.9	625	7	US-11-072-512-3210 Sequence 3210, Ap
16	58	12.8	662	7	US-11-072-175-184 Sequence 184, App
17	58	12.8	919	6	US-10-821-234-951 Sequence 951, App
18	57.5	12.7	398	6	US-10-793-626-44 Sequence 44, Appl
19	57.5	12.7	398	6	US-10-793-626-1498 Sequence 1498, Ap
20	57.5	12.7	897	6	US-10-821-234-1523 Sequence 1523, Ap
21	57	12.6	212	7	US-11-044-111-6 Sequence 6, Appli
22	57	12.6	212	7	US-11-044-111-26 Sequence 26, Appl
23	57	12.6	239	7	US-11-044-111-5 Sequence 5, Appli
24	57	12.6	239	7	US-11-044-111-25 Sequence 25, Appl
25	57	12.6	240	7	US-11-044-111-9 Sequence 9, Appli

26	57	12.6	464	6	US-10-959-322-5	Sequence 5, Appli
27	57	12.6	809	7	US-11-072-512-3367	Sequence 3367, Ap
28	57	12.6	1056	7	US-11-044-111-22	Sequence 22, Appl
29	56	12.3	183	7	US-11-072-512-3180	Sequence 3180, Ap
30	56	12.3	1076	6	US-10-467-657-7916	Sequence 7916, Ap
31	55.5	12.2	563	7	US-11-040-218-23	Sequence 23, Appl
32	55.5	12.2	3353	7	US-11-037-243-64	Sequence 64, Appl
33	55	12.1	519	7	US-11-099-691-10	Sequence 10, Appl
34	55	12.1	702	7	US-11-072-512-2154	Sequence 2154, Ap
35	54.5	12.0	356	7	US-11-143-986-8	Sequence 8, Appli
36	54.5	12.0	356	7	US-11-143-986-9	Sequence 9, Appli
37	54.5	12.0	1190	7	US-11-043-889-20	Sequence 20, Appl
38	54.5	12.0	1275	6	US-10-724-598-49	Sequence 49, Appli
39	54.5	12.0	1340	7	US-11-070-575-6	Sequence 6, Appli
40	54.5	12.0	1344	7	US-11-091-643-20	Sequence 20, Appl
41	54.5	12.0	1659	7	US-11-072-175-205	Sequence 205, App
42	54	11.9	331	7	US-11-098-686-10431	Sequence 10431, A
43	53.5	11.8	372	6	US-10-467-657-2318	Sequence 2318, Ap
44	53.5	11.8	599	7	US-11-109-157A-3	Sequence 3, Appli
45	53.5	11.8	618	6	US-10-454-437-396	Sequence 396, App
46	53.5	11.8	1373	7	US-11-098-686-11150	Sequence 11150, A
47	53.5	11.8	1686	7	US-11-109-157A-1	Sequence 1, Appli
48	53.5	11.8	1686	7	US-11-226-701-2	Sequence 2, Appli
49	53.5	11.8	2250	6	US-10-922-232B-57	Sequence 57, Appl
50	53.5	11.8	2630	7	US-11-186-731-2	Sequence 2, Appli
51	53.5	11.8	4060	6	US-10-922-232B-55	Sequence 55, Appl
52	53.5	11.8	6738	6	US-10-922-232B-56	Sequence 56, Appl
53	53.5	11.8	7968	7	US-11-186-731-5	Sequence 5, Appli
54	53	11.7	104	7	US-11-120-308-74	Sequence 74, Appl
55	53	11.7	200	7	US-11-194-246-402	Sequence 402, App
56	53	11.7	342	7	US-11-156-084-25	Sequence 25, Appl
57	53	11.7	342	7	US-11-156-084-44	Sequence 44, Appl
58	53	11.7	369	7	US-11-156-084-45	Sequence 45, Appl
59	53	11.7	384	7	US-11-098-686-10752	Sequence 10752, A
60	53	11.7	453	7	US-11-072-512-3394	Sequence 3394, Ap
61	53	11.7	619	7	US-11-156-084-24	Sequence 24, Appl
62	53	11.7	784	6	US-10-517-939-324	Sequence 324, App
63	52.5	11.6	143	6	US-10-793-626-1714	Sequence 1714, Ap
64	52.5	11.6	237	7	US-11-044-111-11	Sequence 11, Appl
65	52.5	11.6	362	6	US-10-517-939-88	Sequence 88, Appl
66	52.5	11.6	471	6	US-10-770-726-68	Sequence 68, Appl
67	52.5	11.6	471	7	US-11-152-366-31	Sequence 31, Appl
68	52.5	11.6	473	7	US-11-152-366-32	Sequence 32, Appl
69	52.5	11.6	552	7	US-11-019-711-69	Sequence 69, Appl
70	52.5	11.6	694	7	US-11-072-512-2469	Sequence 2469, Ap
71	52.5	11.6	863	6	US-10-793-626-2010	Sequence 2010, Ap
72	52.5	11.6	1043	6	US-10-821-234-1055	Sequence 1055, Ap
73	52.5	11.6	2871	7	US-11-124-367A-264	Sequence 264, App
74	52	11.5	230	7	US-11-072-512-3602	Sequence 3602, App
75	52	11.5	274	6	US-10-467-657-706	Sequence 706, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

```
; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
```

```
Query Match          60.0%; Score 272.5; DB 6; Length 88;
Best Local Similarity 59.8%; Pred. No. 4.6e-25;
Matches 52; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
```

```
OY      1 MSRIVNCVKLRKRAEGLDFPPYPGELGTRIMQISKEAWEEW-KQIQ-TRLVNRNLNADARPKY----- 60
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      1 MARMVFCVKLNKEAGMKFPPLPNELGKRIFENVSGEAWAATRHQTMLINENRSLADP 60
```

```
OY      61 PARKYLOQOMERFLFEDGTVEAQG-VP 86
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      61 RAREYLAQOMEQYFFGDGADAVQGYVP 87
```

RESULT 2

```
US-10-793-626-1186
; Sequence 1186, Application US/10793626
; Publication No. US20050255478A1
```

```
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1186
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-1186
```

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Query Match          15.5%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;
```

```
OY      17 LDFP-PYPGELGTRIMQISKEAWEEW-KQIQ-TRLVNRNLNADARPKY----- 65
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      109 MDIPLLYENEL-----QDTVDEWVWVYTSESIQIDRLMERNNLSLEDAKARYSQISIDK 163
```

```
OY      66 -----LQQOMERFLFEDGTVEAQ 83
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      164 KSRMADHVIDNLGDKLELKQNLQKLEEEGYIQSE 198
```

RESULT 3

```
US-10-793-626-2390
; Sequence 2390, Application US/10793626
; Publication No. US20050255478A1
```

```
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2390
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2390
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```
Query Match          15.5%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;
```

```
OY      17 LDFP-PYPGELGTRIMQISKEAWEEW-KQIQ-TRLVNRNLNADARPKY----- 65
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      109 MDIPLLYENEL-----QDTVDEWVWVYTSESIQIDRLMERNNLSLEDAKARYSQISIDK 163
```

```
OY      66 -----LQQOMERFLFEDGTVEAQ 83
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      164 KSRMADHVIDNLGDKLELKQNLQKLEEEGYIQSE 198
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RESULT 4

```
US-11-098-686-10831
; Sequence 10831, Application US/11098686
; Publication No. US20060024696A1
```

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; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10831
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10831
```

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Query Match          14.8%; Score 67; DB 7; Length 1320;
Best Local Similarity 31.5%; Pred. No. 9.2;
Matches 23; Conservative 11; Mismatches 25; Indels 14; Gaps 3;
```

```
OY      5 VNCVKLRKRAEGLDFPPYPGELGTRIMQISKEAWEEW-KQIQ-TRLVNRNLNADARPKY----- 61
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      217 LNLKSLSKSKLEEQOQYHLKKRLDIWHQ-----WEWRLLIQTRLHLPPISASFPQDGA 271
```

```
OY      62 ARKYLQOMERFL 74
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB      272 AR-----MERAL 278
```

RESULT 5

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US-11-033-039-1279
; Sequence 1279, Application US/11033039
; Publication No. US20060002947A1
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; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 86.765 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-5
Perfect score: 482
Sequence: 1 MARVFCERLKGAEGLDFQ.....NFLREGKDVHIEGYTPPEAK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	482	100.0	91 5	ABB78150	Abb78150 Amino aci
2	434	90.0	87 5	ABB78152	Abb78152 Amino aci
3	425	88.2	87 5	ABB78151	Abb78151 Amino aci
4	412	85.5	87 5	ABB78153	Abb78153 Amino aci
5	399	82.8	90 5	ABB78155	Abb78155 Amino aci
6	388	80.5	91 5	ABB78158	Abb78158 Amino aci
7	388	80.5	91 5	ABB78157	Abb78157 Amino aci
8	388	80.5	91 5	ABB78156	Abb78156 Amino aci
9	383	79.5	91 5	ABB78159	Abb78159 Amino aci
10	383	79.5	91 5	ABB78159	Abb78159 Amino aci
11	383	79.5	91 5	ABB78162	Abb78162 Amino aci
12	380	78.8	107 7	ABO65445	AbO65445 Klebsiell
13	378	78.4	88 5	ABB78160	Abb78160 Amino aci
14	377	78.2	93 7	ADF05158	Adf05158 Bacterial
15	369.5	76.7	91 5	ABB78163	Abb78163 Amino aci
16	357	74.1	90 5	ABB78165	Abb78165 Amino aci
17	344	71.4	88 5	ABB78154	Abb78154 Amino aci
18	316	65.6	78 5	ABB78164	Abb78164 Amino aci
19	260	53.9	87 5	ABB78148	Abb78148 Amino aci
20	260	53.9	87 5	ABB78147	Abb78147 Amino aci
21	246	51.0	76 5	ABB78166	Abb78166 Amino aci
22	246	51.0	86 5	ABB78149	Abb78149 Pseudomon
23	244	50.6	122 7	ABO74609	AbO74609 Amino aci
24	242	50.2	87 5	ABB78175	Abb78175 Amino aci

25	239	49.6	90 5	ABB78168	Abb78168 Amino aci
26	236.5	49.1	89 9	ABE41576	Aeb41576 L. pneumo
27	236.5	49.1	95 9	ABE38294	Aeb38294 L. pneumo
28	236	49.0	87 5	ABB78174	Abb78174 Amino aci
29	233	48.3	87 5	ABB78170	Abb78170 Amino aci
30	230	47.7	88 5	ABB78178	Abb78178 Amino aci
31	228	47.3	87 5	ABB78169	Abb78169 Amino aci
32	228	47.3	88 5	ABB78171	Abb78171 Amino aci
33	228	47.3	88 5	ABB78172	Abb78172 Amino aci
34	228	47.3	88 5	ABB78173	Abb78173 Amino aci
35	228	47.3	88 6	ABP77219	Abp77219 N. gonorr
36	224.5	46.6	90 5	ABB78167	Abb78167 Amino aci
37	223	46.3	87 5	ABB78177	Abb78177 Amino aci
38	215.5	44.7	92 6	ADA34169	Ada34169 Acinetoba
39	208	43.2	87 5	ABB78176	Abb78176 Amino aci
40	161	33.4	110 8	ADL05173	Adl05173 M. catarr
41	77.5	16.1	591 2	AAV41141	Aay41141 Mouse mam
42	77.5	16.1	860 2	AAV41140	Aay41140 Mouse mam
43	77.5	16.1	1755 2	AAV41139	Aay41139 Mouse mam
44	75	15.6	506 3	AAV74371	Aay74371 Neisseria
45	72	14.9	217 7	ADF07577	Adf07577 Bacterial
46	72	14.9	507 6	ABU40210	Abu40210 Protein e
47	70	14.5	474 7	ABO75727	AbO75727 Pseudomon
48	70	14.5	503 4	ABG16577	Abg16577 Novel hum
49	70	14.5	507 3	AAV74372	Aay74372 Neisseria
50	70	14.5	507 3	AAV74373	Aay74373 Neisseria
51	70	14.5	546 6	ABU38097	Abu38097 Protein e
52	70	14.5	883 8	ADN47233	Adn47233 Thermococ
53	69.5	14.4	507 6	ABU41973	Abu41973 Protein e
54	69	14.3	227 3	AAG38052	Aag38052 Arabidops
55	68.5	14.2	292 8	ADY08568	Ady08568 Plant ful
56	68	14.1	218 3	AAG45909	Aag45909 Arabidops
57	68	14.1	234 3	AAG45908	Aag45908 Arabidops
58	68	14.1	283 8	ADY12704	Ady12704 Plant ful
59	68	14.1	484 8	ADM90985	Adm90985 Human pha
60	68	14.1	557 3	AAV52446	Aay52446 Murine sy
61	68	14.1	557 5	AAO15046	Aao15046 Mouse syn
62	68	14.1	984 7	ADM26830	Adm26830 Hyperther
63	68	14.1	984 8	ADK72328	Adk72328 M. kandle
64	67.5	14.0	325 8	ADS30760	AdS30760 Bacterial
65	67.5	14.0	583 6	ABU89709	Abu89709 Protein d
66	67.5	14.0	583 7	ADB79911	AdB79911 Mouse put
67	67.5	14.0	583 7	ADC56738	Adc56738 Murine ra
68	67.5	14.0	583 8	ADO34029	AdO34029 Human MBC
69	67.5	14.0	583 8	ADP23797	Adp23797 PRO polyp
70	67.5	14.0	583 9	ADY16763	Ady16763 PRO polyp
71	67.5	14.0	583 9	ADY16765	Ady16765 PRO polyp
72	67.5	13.9	257 3	AAG31203	Aag31203 Arabidops
73	67	13.9	297 3	AAG31202	Aag31202 Arabidops
74	67	13.9	324 3	AAG31201	Aag31201 Arabidops
75	67	13.9	1356 7	ADC31390	Adc31390 Human nov

ALIGNMENTS

RESULT 1
ID ABB78150 standard; protein; 91 AA.
XX ABB78150;
DT 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
PN
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 482; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 1.4e-49;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARNVFCERLKQEAEGLDFOLYPGELGKRIFDSISKQAWGEWKKQTMLVNEKKLMMNNA 60
XX
DB 1 MARNVFCERLKQEAEGLDFOLYPGELGKRIFDSISKQAWGEWKKQTMLVNEKKLMMNNA 60
XX

QY 61 EHRKLEQEMVNFLEPGKDVHIEGYTPPEAK 91
XX
DB 61 EHRKLEQEMVNFLEPGKDVHIEGYTPPEAK 91
XX

RESULT 2
ABB78152
ID ABB78152 standard; protein; 87 AA.
XX
AC ABB78152;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Haemophilus influenzae.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;

Query Match 90.0%; Score 434; DB 5; Length 87;
Best Local Similarity 93.1%; Pred. No. 7.2e-44;
Matches 81; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MARNVFCERLKQEAEGLDFOLYPGELGKRIFDSISKQAWGEWKKQTMLVNEKKLMMNNA 60
XX
DB 1 MARTVFCEYLKKEAEGLDFOLYPGELGKRIFDSISKQAWGEWIKKQTMLVNEKKLMMNNA 60
XX

QY 61 EHRKLEQEMVNFLEPGKDVHIEGYTP 87
XX
DB 61 EHRKLEQEMVNFLEPGKDVHIEGYTP 87
XX

RESULT 3
ABB78151
ID ABB78151 standard; protein; 87 AA.
XX
AC ABB78151;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Pasteurella multocida.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
XX (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 14.0477 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-5

Perfect score: 482

Sequence: 1 MARWVFCERLKQEAAGLDFQ.....NFLPEGRDVHIEGYTPPEAK 91

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	441	91.5	90	2	C64013	hypothetical prote
2	399	82.8	90	2	C82320	conserved hypothet
3	388	80.5	91	2	A85954	hypothetical prote
4	388	80.5	91	2	A65082	hypothetical prote
5	388	80.5	91	2	F91108	hypothetical prote
6	383	79.5	91	2	AH0879	conserved hypothet
7	357	74.1	90	2	AI0116	conserved hypothet
8	246	51.0	93	2	B84994	hypothetical prote
9	244	50.6	90	2	H83003	conserved hypothet
10	238	49.4	105	2	C82624	conserved hypothet
11	228	47.3	88	2	H81014	conserved hypothet
12	78	16.2	935	2	T39389	probable DNA damag
13	77.5	16.1	591	1	FOMVMM	gag polypotein -
14	73.5	15.2	353	1	FOMVMM	gag polypotein -
15	70	14.5	182	2	C69416	hypothetical prote
16	70	14.5	507	2	A83105	probable fumarate
17	70	14.5	507	2	C81063	fumarate hydratase
18	70	14.5	546	2	A81807	fumarate hydratase
19	68.5	14.2	342	2	T13113	probable sopp prot
20	68	14.1	485	2	A84043	chromosome replica
21	68	14.1	593	2	C64097	probable soluble 1
22	68	14.1	946	2	T31488	hypothetical prote
23	67.5	14.0	583	1	A41129	radixin - mouse
24	67.5	14.0	583	1	A46127	radixin - human
25	67.5	14.0	583	1	S39805	radixin - pig
26	67.5	14.0	1206	2	B96507	hypothetical prote
27	67.5	14.0	1526	2	AC2239	WD-40 repeat prote
28	67	13.9	241	2	T27636	hypothetical prote
29	67	13.9	324	2	T05429	hypothetical prote

30	67	13.9	555	2	C96667	unknown protein, 7
31	67	13.9	2101	2	A42184	nuclear mitotic ap
32	66.5	13.8	152	2	B70423	transcription regu
33	66	13.7	225	2	C88939	protein C05B4.8 [1
34	66	13.7	324	2	C69261	2-hydroxyhepta-2,4
35	66	13.7	487	1	IQBP34	DNA ligase (ATP) (
36	66	13.7	583	2	T48365	hypothetical prote
37	66	13.7	720	2	JC5131	glycosyltransferas
38	66	13.7	1129	2	S00097	phytochrome 4 - oa
39	65.5	13.6	300	2	F84178	hypothetical prote
40	65.5	13.6	326	2	T20776	hypothetical prote
41	65.5	13.6	329	2	G88864	protein T04A11.11
42	65.5	13.6	329	2	S27787	gene Tc3 protein -
43	65.5	13.6	329	2	B87901	protein ZC247.4 [i
44	65.5	13.6	329	2	B87969	protein Y47H9C.3 [
45	65.5	13.6	329	2	G88210	protein R10H1.3 [i
46	65.5	13.6	329	2	H89382	protein ZK218.2 [i
47	65.5	13.6	329	2	H87991	protein Y6B3B.8 [i
48	65.5	13.6	329	2	H87720	protein F56A6.3 [i
49	65.5	13.6	329	2	D88198	protein T02G5.5 [i
50	65.5	13.6	329	2	A88892	protein Y45F10D.1
51	65.5	13.6	330	1	B64561	ketol-acid reducto
52	65.5	13.6	511	2	B39340	neurofilament prot
53	65.5	13.6	615	2	B39340	neurofilament prot
54	65.5	13.6	643	2	A43647	paraesporal crystal
55	65.5	13.6	1200	2	A46194	neurofilament prot
56	65.5	13.6	1454	2	S53398	hypothetical prote
57	65	13.5	106	2	F70081	hypothetical prote
58	65	13.5	258	2	S58159	hypothetical prote
59	65	13.5	310	2	F84578	1-aminocyclopropan
60	65	13.5	498	2	C90413	dihydropterolate 8y
61	64.5	13.4	146	2	S31638	hypothetical prote
62	64.5	13.4	242	2	D84422	60S ribosomal prot
63	64.5	13.4	996	2	A71080	hypothetical prote
64	64.5	13.4	1008	2	H72310	conserved hypothet
65	64	13.3	169	2	PN0560	phytochrome - long
66	64	13.3	171	2	PN0558	phytochrome - wild
67	64	13.3	300	2	T32681	hypothetical prote
68	64	13.3	356	2	E70032	two-component sens
69	64	13.3	358	2	T34382	hypothetical prote
70	64	13.3	375	2	T39364	probable galactosy
71	64	13.3	423	2	T45030	hypothetical prote
72	64	13.3	641	2	T38659	methylenetetrahydr
73	64	13.3	749	2	E86774	hypothetical prote
74	64	13.3	1024	2	T41415	probable leucine p
75	64	13.3	2672	2	A48126	translation activa

ALIGNMENTS

RESULT 1
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, C.
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:LA2023; NID:915;
C/Superfamily: fe(II) trafficking protein YggX

Query Match 91.5%; Score 441; DB 2; Length 90;
Best Local Similarity 93.2%; Pred. No. 4.8e-37;

Matches 82; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
QY 1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60
1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60
Db 1 MARTVFCEYLKKEAGLDFOLYPGLGKRIFDSVSKQAWGEMWIKKQTMVNEKKLNMNNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88
61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88

RESULT 2
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathavan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HIT>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
A/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 82.8%; Score 399; DB 2; Length 90;
Best Local Similarity 81.8%; Pred. No. 7.3e-33;
Matches 72; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
QY 1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60
1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNDP 60
Db 1 MARTVFCEYLKKEAGLDFOLYPGLGKRIFDSVSKQAWGEMWIKKQTMVNEKKLNMNNDP 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88
61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88

RESULT 3
A85954
hypothetical protein y9gx [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A/Experimental source: strain O157:H7, substrain EDL933
A/Genetics:
A/Gene: Y9GX
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 80.5%; Score 388; DB 2; Length 91;
Best Local Similarity 76.9%; Pred. No. 9.2e-32;
Matches 70; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60

Db 1 MSRTIFCTFLQREAGQDFOLYPGLGKRILYNEISKEAWAQOHKQTMVNEKKLNMNNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91

RESULT 4
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Col
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: A65082
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-91 <BLAT>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9J
A/Experimental source: strain K-12, substrain MG1655
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 80.5%; Score 388; DB 2; Length 91;
Best Local Similarity 76.9%; Pred. No. 9.2e-32;
Matches 70; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60
1 MSRTIFCTFLQREAGQDFOLYPGLGKRILYNEISKEAWAQOHKQTMVNEKKLNMNNA 60
Db 1 MSRTIFCTFLQREAGQDFOLYPGLGKRILYNEISKEAWAQOHKQTMVNEKKLNMNNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91

RESULT 5
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1;
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BA037261.1
A/Experimental source: strain O157:H7, substrain R1MD 0509952
A/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein Y9GX

Query Match 80.5%; Score 388; DB 2; Length 91;
Best Local Similarity 76.9%; Pred. No. 9.2e-32;
Matches 70; Conservative 11; Mismatches 10; Indels 0; Gaps 0;
QY 1 MARWVFCERLQKQAEGLDFOLYPGLGKRIFDSISKQAWGEMKKQTMVNEKKLNMNNA 60
1 MSRTIFCTFLQREAGQDFOLYPGLGKRILYNEISKEAWAQOHKQTMVNEKKLNMNNA 60
Db 1 MSRTIFCTFLQREAGQDFOLYPGLGKRILYNEISKEAWAQOHKQTMVNEKKLNMNNA 60

QY 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPPEAK 91

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: February 28, 2006, 18:23:46 ; Search time 83.6663 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-5
Perfect score: 482
Sequence: 1 MARWVFCERLKQKABGLDFQ.....NFLPEKDVHIEGYTPPEAK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	441	91.5	90	1	FETP_HAEIN	P44048 haemophilus
2	441	91.5	90	2	Q4QMD9_HAE18	Q4qmd9 haemophilus
3	432	89.6	90	1	FETP_PASMU	Q9clb9 pasteurella
4	429	89.0	91	1	FETP_MANSM	Q65vt7 manheimia
5	412	85.5	94	1	FETP_HAEDU	Q7vkb6 haemophilus
6	402	83.4	90	1	FETP_VIBPA	Q87l15 vibrio para
7	400	83.0	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
8	400	83.0	90	1	FETP_VIBVY	Q7mhl4 vibrio vuln
9	399	82.8	90	1	FETP_VIBCH	Q9kur4 vibrio chol
10	392	81.3	90	1	FETP_PHOPR	Q6lmk7 photobacter
11	383	79.5	90	1	FETP_ECO57	P0a8p4 escherichia
12	383	79.5	90	1	FETP_ECOLI	P0a8p3 escherichia
13	383	79.5	90	1	FETP_SHIFL	P0a8p5 shigella fl
14	379	78.6	90	1	FETP_ECOL6	Q8fel9 escherichia
15	378	78.4	90	1	FETP_SALCH	Q57K04 salmonella
16	378	78.4	90	1	FETP_SALPA	Q5pmml salmonella
17	378	78.4	90	1	FETP_SALTI	P67618 salmonella
18	378	78.4	90	1	FETP_SALTY	P67617 salmonella
19	374	77.6	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
20	365	75.7	90	1	FETP_YERPS	Q66m3 yersinia ps
21	360	74.7	90	1	FETP_ERWCT	Q6d8j9 erwinia car
22	357	74.1	90	1	FETP_PHOOL	Q7n7l1 photorhabdu
23	357	74.1	90	1	FETP_YERPE	Q8zhe7 yersinia pe
24	344	71.4	92	1	FETP_SHEON	Q8ebx6 shewanella
25	340	70.5	90	1	FETP_IDILO	Q5qy58 idiomarina
26	271	56.2	90	1	FETP_BORBR	Q7w9q2 bordetella
27	271	56.2	90	1	FETP_BORPA	Q7w9q2 bordetella
28	271	56.2	90	1	FETP_BORPE	Q7w9q2 bordetella
29	249	51.7	90	1	FETP_NITEU	Q82xf2 nitrosomona
30	249	51.7	91	1	FETP_BURMA	Q62i19 burkholderi
31	249	51.7	91	1	FETP_BURPS	Q63sj4 burkholderi

32	246	51.0	77	1	FETP_BUCAL	P57618 buchnera ap
33	244	50.6	90	1	FETP_PSEAE	Q9hu36 pseudomonas
34	242	50.2	90	1	FETP_XYLPF	Q87d06 xyloella fas
35	240.5	49.9	89	1	FETP_LEGPI	Q5wvc4 legionella
36	240	49.8	90	2	Q4J228_AZOVI	Q4j228 azotobacter
37	240	49.8	91	1	FETP_PALSO	Q8y010 ralstonia s
38	239	49.6	90	1	FETP_PSESM	Q87uf5 pseudomonas
39	239	49.6	90	2	Q4ZLB3_PSESY	Q4zlp3 pseudomonas
40	239	49.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
41	238	49.4	90	1	FETP_XYLPF	Q9pc73 xyloella fas
42	236.5	49.1	89	1	FETP_LEGPA	Q5x3x9 legionella
43	236.5	49.1	89	1	FETP_LEGPH	Q5zu80 legionella
44	235	48.8	90	1	FETP_PSEPK	Q88r49 pseudomonas
45	234	48.5	90	2	Q6T7F6_PSEPL	Q6t7f6 pseudomonas
46	232	48.1	91	1	FETP_XANAC	Q8pjh7 xanthomonas
47	231	47.9	90	1	FETP_METCA	Q60aj7 methylococc
48	230	47.7	90	1	FETP_COXBU	Q83d06 coxiella bu
49	228	47.3	88	1	FETP_NEIGI	Q5f553 neisseria g
50	228	47.3	88	1	FETP_NEIMA	P67615 neisseria m
51	228	47.3	88	1	FETP_NEIMB	P67616 neisseria m
52	227	47.1	92	1	FETP_XANOR	Q5gy22 xanthomonas
53	225	46.7	78	1	FETP_WIGBR	Q8d3c5 wigglewort
54	225	46.7	90	2	Q4KJT2_PSEF5	Q4kjt2 pseudomonas
55	224	46.5	90	1	FETP_CHRVO	Q7nsr4 chromobacte
56	223	46.3	92	1	FETP_XANCP	Q8p829 xanthomonas
57	223	46.3	92	1	Q4UW14_XANCP	Q4uw14 xanthomonas
58	222.5	46.2	90	1	FETP_AC1AD	Q6ffb3 acinetobact
59	207	42.9	78	1	FETP_BUCAP	Q8k925 buchnera ap
60	202	41.9	79	1	FETP_CANBF	Q7vir9 candidatus
61	202	41.9	87	1	FETP_BUCBP	Q89a44 buchnera ap
62	202	41.9	87	1	FETP_FRATP	Q5nhj8 francisella
63	176	36.5	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
64	152	31.5	96	2	Q4FVU7_9GAMM	Q4fvj7 psychrobact
65	86	17.8	2248	2	Q4UB40_THEAN	Q4ub40 theileria a
66	85	17.6	2249	2	Q4MYU4_THEPA	Q4myu4 theileria p
67	77.5	16.1	187	2	Q9HBF7_HUMAN	Q9hbf7 homo sapien
68	77.5	16.1	218	2	Q7SPV9_9BETR	Q7spv9 human betar
69	77.5	16.1	281	2	Q6PG71_MOUSEB	Q6pg71 mus musculu
70	77.5	16.1	372	2	Q85648_9BETR	Q85648 mouse mamma
71	77.5	16.1	452	2	Q7SPV8_9BETR	Q7spv8 human betar
72	77.5	16.1	590	1	GAG_MMTVB	P10258 mouse mamma
73	77.5	16.1	590	1	GAG_MMTVC	P11284 mouse mamma
74	77.5	16.1	591	2	Q83391_9BETR	Q83391 mouse mamma
75	77.5	16.1	591	2	Q91ZT6_9BETR	Q91zt6 exogenous m

ALIGNMENTS

RESULT 1
FETP_HAEIN
ID: FETP_HAEIN STANDARD; PRT; 90 AA.
AC P44048;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=HI0760;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fieischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.M.,
Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,


```

RA Gnehm C.L., McDonald L.A., Small K.V., Frazer C.M., Smith H.O.,
RA Venter J.C.;
RT "whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32760; AAC22419.1; -; Genomic_DNA.
DR PIR; G64013; G64013.
DR SMR; P44048; 1-87.
DR TIGR; HI0760; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
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SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;

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Best Local Similarity 93.2%; Pred. No. 1.6e-37;
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Db 1 MARTVFC EYLKKGAEGLDFOLYPGBLGKRIFDSVSKQAWGEMWIKQTMVNEKLLNMNNA 60
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Db 61 EHRKLLQEMVNFLEFGKDVHIEGYTPP 88

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AC Q4QMD9;
DT 13-SEP-2005 (TREMblrel. 31, Created)
DT 13-SEP-2005 (TREMblrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMblrel. 31, Last annotation update)
DE Hypothetical protein.
OS OrderedLocusNames=NTNHI0920;
ON Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaespy A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
d, strain KW20."
RL J. Bacteriol. 187:4627-4636(2005).
EMBL; CP000057; AAX87808.1; -; Genomic DNA.

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DR	pfam; PF04362; DUF495; 1.
DR	PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR	PRODOM; PD029191; DUF495; 1.
KW	Complete proteome; Hypothetical protein.
SQ	SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;

Query Match	91.5%;	Score 441;	DB 2;	Length 90;
Best Local Similarity	93.2%;	Pred. No. 1.6e-37;		
Matches	82;	Conservative 3;	Mismatches 3;	Indels 0; Gaps

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Dd	1 MARTVFCEYLKKEAEGDLFQLYPGELGRIFDVSVKQAQGEMIKQTMLVNEKCLNMNA	60
OY	61 EHRKLLEQENVNPLFEKGDVHIEGYTPP	88
Dd	61 EHRKLLEQENVNPLFEKGDVHIEGYTPP	88

[illegible]

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 21.2781 Seconds
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Title: US-09-955-502A-5
Perfect score: 482
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 572060

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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

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6	77.5	16.1	591	2	US-09-370-368-8
7	72	14.9	217	2	US-09-543-681A-7862
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23	66	13.7	292	2	US-09-328-352-5836
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25	66	13.7	720	1	US-08-840-236-1
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29	65.5	13.6	959	2	US-09-543-681A-6879	Sequence 6879, Ap
30	65	13.5	280	2	US-09-323-998E-37	Sequence 37, Appli
31	65	13.5	1401	2	US-09-750-590A-2	Sequence 2, Appli
32	64	13.3	361	2	US-09-328-352-7863	Sequence 7863, Ap
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34	63	13.1	116	2	US-09-562-737-125	Sequence 125, App
35	63	13.1	586	2	US-09-270-767-44373	Sequence 44373, A
36	63	13.1	1695	2	US-09-866-108A-15753	Sequence 15753, A
37	62.5	13.0	271	2	US-09-248-796A-19265	Sequence 19265, A
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55	61	12.7	674	2	US-09-536-784-200	Sequence 200, App
56	61	12.7	674	2	US-09-765-271-200	Sequence 200, App
57	61	12.7	674	2	US-09-765-272A-200	Sequence 200, App
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62	60.5	12.6	415	1	US-08-602-010A-10	Sequence 10, Appli
63	60.5	12.6	415	1	US-08-680-726A-10	Sequence 10, Appli
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ALIGNMENTS

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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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549.414 Million cell updates/sec

Title: US-09-955-502A-5
Perfect score: 482
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SUMMARIES

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5	399	82.8	90	3	US-09-955-502-10 Sequence 10, Appli
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14	357	74.1	90	3	US-09-955-502-20 Sequence 20, Appli
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36	70	14.5	503	5	US-10-450-763-46936	Sequence 46936, A
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ALIGNMENTS

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US-09-955-502-5
Sequence 5, Application US/099555502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE OF INVENTION: Oxygen-Labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 5
LENGTH: 91
TYPE: PRT
ORGANISM: Actinobacillus actinomycetemcomitans

GenCore version 5.1.7
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OM protein - protein search, using sw model

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218.595 Million cell updates/sec

Title: US-09-955-502A-5
Perfect score: 482
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7	62	12.9	793	US-10-995-561-925	Sequence 925, App
8	62	12.9	804	US-10-453-372-650	Sequence 650, App
9	62	12.9	847	US-10-453-372-654	Sequence 654, App
10	62	12.9	857	US-10-453-372-652	Sequence 652, App
11	62	12.9	905	US-10-453-372-638	Sequence 638, App
12	62	12.9	905	US-10-453-372-662	Sequence 662, App
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14	62	12.9	963	US-10-995-561-923	Sequence 923, App
15	62	12.9	963	US-10-453-372-660	Sequence 660, App
16	62	12.9	1012	US-10-453-372-646	Sequence 646, App
17	61.5	12.8	455	US-10-714-887-212	Sequence 212, App
18	60	12.4	583	US-11-080-991-64	Sequence 64, Appl
19	59	12.2	177	US-10-467-657-1658	Sequence 1658, Ap
20	59	12.2	342	US-11-156-084-25	Sequence 25, Appl
21	59	12.2	342	US-11-156-084-44	Sequence 44, Appl
22	59	12.2	369	US-11-156-084-45	Sequence 45, Appl
23	59	12.2	619	US-11-156-084-24	Sequence 24, Appl
24	59	12.2	695	US-10-453-372-648	Sequence 648, App
25	59	12.2	700	US-10-995-561-922	Sequence 922, App

26	59	12.2	700	6	US-10-995-561-924	Sequence 924, App
27	59	12.2	775	6	US-10-453-372-656	Sequence 656, App
28	58.5	12.1	465	6	US-10-873-528-164	Sequence 164, App
29	58.5	12.1	577	7	US-11-072-175-187	Sequence 187, App
30	58	12.0	296	7	US-11-087-227-10	Sequence 10, Appl
31	58	12.0	359	7	US-11-087-227-8	Sequence 8, Appli
32	58	12.0	359	7	US-11-192-450-6	Sequence 6, Appli
33	58	12.0	404	7	US-11-087-227-6	Sequence 6, Appli
34	58	12.0	404	7	US-11-192-450-3	Sequence 3, Appli
35	58	12.0	504	7	US-11-072-512-3467	Sequence 3467, Ap
36	57.5	11.9	285	6	US-10-467-657-222	Sequence 222, App
37	57.5	11.9	285	6	US-10-467-657-8230	Sequence 8230, Ap
38	57.5	11.9	349	7	US-11-098-686-10115	Sequence 10115, A
39	57.5	11.9	3803	6	US-10-995-561-773	Sequence 773, App
40	57.5	11.9	3960	6	US-10-995-561-771	Sequence 771, App
41	57.5	11.9	5335	6	US-10-995-561-777	Sequence 777, App
42	57.5	11.9	5406	6	US-10-995-561-774	Sequence 774, App
43	57.5	11.9	5415	6	US-10-995-561-779	Sequence 775, App
44	57.5	11.9	5464	6	US-10-995-561-775	Sequence 775, App
45	57.5	11.9	5935	6	US-10-995-561-776	Sequence 776, App
46	57	11.8	139	6	US-10-793-626-1310	Sequence 1310, Ap
47	57	11.8	319	6	US-10-793-626-2760	Sequence 2760, Ap
48	56.5	11.7	261	6	US-10-467-657-5896	Sequence 5896, Ap
49	56.5	11.7	299	7	US-11-156-084-288	Sequence 288, App
50	56.5	11.7	674	7	US-11-000-463-471	Sequence 471, App
51	56.5	11.7	782	6	US-10-793-626-2352	Sequence 2352, Ap
52	56	11.6	175	6	US-10-821-234-1522	Sequence 1522, Ap
53	56	11.6	234	6	US-10-524-972-108	Sequence 108, App
54	56	11.6	234	6	US-10-524-972-108	Sequence 436, App
55	56	11.6	246	6	US-10-131-826A-436	Sequence 57, Appl
56	56	11.6	246	7	US-11-240-769-57	Sequence 3198, Ap
57	56	11.6	254	7	US-11-072-512-3198	Sequence 2024, Ap
58	56	11.6	384	6	US-10-467-657-2024	Sequence 16, Appl
59	56	11.6	560	7	US-11-131-479-16	Sequence 1387, Ap
60	55.5	11.5	349	6	US-10-821-234-1387	Sequence 2877, Ap
61	55.5	11.5	351	7	US-11-072-512-2877	Sequence 85, Appl
62	55.5	11.5	497	7	US-11-010-239-85	Sequence 42, Appl
63	55.5	11.5	1188	7	US-11-115-639-42	Sequence 43, Appl
64	55.5	11.5	1188	7	US-11-115-639-43	Sequence 6, Appli
65	55	11.4	266	5	US-09-995-493-6	Sequence 2586, Ap
66	55	11.4	611	6	US-10-793-626-2586	Sequence 2472, Ap
67	55	11.4	619	7	US-11-072-512-2472	Sequence 28, Appl
68	55	11.4	724	7	US-11-126-313-28	Sequence 4, Appli
69	55	11.4	1219	7	US-11-032-236-4	Sequence 10784, A
70	54.5	11.3	165	7	US-11-098-686-10784	Sequence 718, App
71	54.5	11.3	268	6	US-10-995-561-718	Sequence 720, App
72	54.5	11.3	355	6	US-10-995-561-720	Sequence 4, Appli
73	54.5	11.3	524	6	US-10-507-106-4	Sequence 101, App
74	54.5	11.3	729	6	US-10-511-538-101	Sequence 7, Appli
75	54.5	11.3	774	7	US-11-070-627-7	

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

SEQ ID NO 968
LENGTH: 88
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 47.3%; Score 228; DB 6; Length 88;
Best Local Similarity 47.7%; Pred. No. 1e-19;
Matches 42; Conservative 20; Mismatches 24; Indels 2; Gaps 2;

QY 1 MARVFCERLKQAEGLDFQLYPGELGKRIKIPDSISKQAWGEMMKQTMVLVNEKKLNMWNA 60
1 MARVFCVTKLKEABGMKFPPLPNEIGKRIKIFENVSOEAWAATRHQTMLINENRLSLADP 60

QY 61 EHRKLEQEMVNFLEGGKDVHIEGYTP 87
61 RAREYLAQOMEQYFFGDGADA-VGGYVP 87

RESULT 2

US-11-194-246-317
Sequence 317, Application US/11194246
Publication No. US20050272089A1
GENERAL INFORMATION:
APPLICANT: Molt, John
APPLICANT: Trepod, Catherine
APPLICANT: Arvidson, Stefan
TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
TITLE OF INVENTION: USE
FILE REFERENCE: 00592.US1 (MER 268.05920101)
CURRENT APPLICATION NUMBER: US/11/194,246
CURRENT FILING DATE: 2005-08-01
PRIOR APPLICATION NUMBER: US/10/274,586
PRIOR FILING DATE: 2002-10-21
PRIOR APPLICATION NUMBER: US 60/345,438
PRIOR FILING DATE: 2001-10-19
NUMBER OF SEQ ID NOS: 621
SOFTWARE: PatentIn version 3.0
SEQ ID NO 317
LENGTH: 593
TYPE: PRT
ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317

Query Match 14.1%; Score 68; DB 7; Length 593;
Best Local Similarity 46.7%; Pred. No. 3.6;
Matches 14; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 32 DSISKQAWGEMMKQTMVLVNEKKLNMWNAE 61
293 ESKSKQEWRYWEAKQDILKNTKLTALSK 322

RESULT 3

US-10-857-780-23
Sequence 23, Application US/10857780
Publication No. US20050272043A1
GENERAL INFORMATION:
APPLICANT: ROTH, RICHARD B.
APPLICANT: BRAUN, ANDREAS
APPLICANT: KAMMERER, STEFAN M.
APPLICANT: NELSON, MATTHEW ROBERTS
APPLICANT: RENELAND, RIKARD HENRY
APPLICANT: HOYAL-WRIGHTSON, CAROLYN R.
TITLE OF INVENTION: METHODS FOR IDENTIFYING RISK OF BREAST CANCER AND TREATMENTS
TITLE OF INVENTION: THEREOF
FILE REFERENCE: SEQ-4069-CP
CURRENT APPLICATION NUMBER: US/10/857,780
CURRENT FILING DATE: 2004-05-28
PRIOR APPLICATION NUMBER: 10/723,681
PRIOR FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: 60/490,234
PRIOR FILING DATE: 2003-07-24

PRIOR APPLICATION NUMBER: 60/525,239
PRIOR FILING DATE: 2003-11-25
NUMBER OF SEQ ID NOS: 4962
SOFTWARE: PatentIn version 3.2
SEQ ID NO 23
LENGTH: 2101
TYPE: PRT
ORGANISM: Homo sapiens
US-10-857-780-23

Query Match 13.9%; Score 67; DB 6; Length 2101;
Best Local Similarity 24.1%; Pred. No. 23;
Matches 27; Conservative 26; Mismatches 27; Indels 32; Gaps 7;

QY 7 CERLKQAEGLDFQLYP-----GELG-----KRIKIPDSISK-----QAWGEMMK 45
299 CQDLKTEKSDMRKINQLSENGDLSFKLRBFASHLQQLQDALNELTEHSKATQEWLEK 358

QY 46 QTMVLVNEKKLNMWNAEHRKLEQEMVNFLEGGKDVHIEGY-----TPPEAK 91
359 QAQL-ERELSA-LQDKKCLEEK--NEILQKLSQLEHLSQLQDNPPQEK 405

RESULT 4

US-10-453-372-658
Sequence 658, Application US/10453372
Publication No. US20060003323A1
GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
FILE REFERENCE: 21402-589 A
CURRENT APPLICATION NUMBER: US/10/453,372
CURRENT FILING DATE: 2003-06-03
PRIOR APPLICATION NUMBER: 09/789390
PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: 09/823187
PRIOR FILING DATE: 2001-03-29
PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10
PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25
PRIOR APPLICATION NUMBER: 09/863776
PRIOR FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: 60/208263
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: 09/939398
PRIOR FILING DATE: 2001-08-24
PRIOR APPLICATION NUMBER: 60/227800
PRIOR FILING DATE: 2000-08-25
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1609
SOFTWARE: CuraseqList version 0.1
SEQ ID NO 658
LENGTH: 834
TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-658

Query Match 13.3%; Score 64; DB 6; Length 834;
Best Local Similarity 32.7%; Pred. No. 16;
Matches 17; Conservative 7; Mismatches 22; Indels 6; Gaps 2;

QY 39 WGEWMKKQTMVLVNEKKLNMWNAEHRKLEQEMVNFLEGGKDVHIEGYTPPEA 90
719 WRNWKRK-----NTKSNFANPVYRKTEEBEDEDELHGRTAQI-GHVPFAA 764

RESULT 5

US-11-072-512-2547

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-6
Perfect score: 462
Sequence: 1 MARTVFCEYLKQESGLDFQ.....QEMVNFLREGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp2003b8:*
8: geneseqp20048:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	87	5	ABB78151 Amino aci
2	435	94.2	87	5	ABB78152 Amino aci
3	425	92.0	91	5	ABB78150 Amino aci
4	416	90.0	87	5	ABB78153 Amino aci
5	379	82.0	91	5	ABB78158 Amino aci
6	379	82.0	91	5	ABB78157 Amino aci
7	379	82.0	91	5	ABB78156 Amino aci
8	377	81.6	88	5	ABB78160 Amino aci
9	377	81.6	91	5	ABB78161 Amino aci
10	377	81.6	91	5	ABB78159 Amino aci
11	377	81.6	91	5	ABB78162 Amino aci
12	375	81.2	90	5	ABB78155 Amino aci
13	370	80.1	91	5	ABB78163 Amino aci
14	364	78.8	107	7	ABO65445 Klebsiell
15	361	78.1	93	7	ADF05158 Bacteri
16	346	74.9	90	5	ABB78165 Amino aci
17	345	74.7	88	5	ABB78154 Amino aci
18	317	68.6	78	5	ABB78164 Amino aci
19	251	54.3	87	5	ABB78148 Amino aci
20	251	54.3	87	5	ABB78147 Amino aci
21	248	53.7	76	5	ABB78166 Amino aci
22	238	51.5	87	5	ABB78175 Amino aci
23	234.5	50.8	89	9	AEB41576 L. pneumo
24	234.5	50.8	95	9	AEB38294 L. pneumo

25	233.5	50.5	86	5	ABB78149 Amino aci
26	232	50.2	87	5	ABB78174 Amino aci
27	230	49.8	87	5	ABB78170 Amino aci
28	230	49.8	122	7	ABO74609 Pseudom
29	227.5	49.2	90	5	ABB78167 Amino aci
30	225	48.7	87	5	ABB78169 Amino aci
31	224	48.5	90	5	ABB78168 Amino aci
32	223	48.3	88	5	ABB78178 Amino aci
33	219	47.4	87	5	ABB78177 Amino aci
34	217	47.0	88	5	ABB78171 Amino aci
35	217	47.0	88	5	ABB78172 Amino aci
36	217	47.0	88	5	ABB78173 Amino aci
37	217	47.0	88	6	ABP77219 N. gonorr
38	205.5	44.5	92	6	ADA34169 Acinetoba
39	200	43.3	87	5	ABB78176 Amino aci
40	142	30.7	110	8	ADL05173 M. catarr
41	75	16.2	1144	8	ADS44344 Bacterial
42	74.5	16.1	591	2	AAV41141 Mouse mam
43	74.5	16.1	860	2	AAV41140 Mouse mam
44	74.5	16.1	1755	2	AAV41139 Mouse mam
45	73.5	15.9	593	4	ABG19947 Novel hum
46	72	15.6	506	3	AAV74371 Neisseria
47	71	15.4	975	5	ABP66068 Bifidobac
48	69.5	15.0	227	3	AG38052 Arabidops
49	69	14.9	474	7	ABO75727 Pseudomon
50	68.5	14.8	218	3	AGA45909 Arabidops
51	68.5	14.8	234	3	AGA45908 Arabidops
52	68.5	14.8	567	4	AAM00976 Human bon
53	68	14.7	330	4	AAU35726 Helicobac
54	68	14.7	330	6	ABU30763 Protein e
55	68	14.7	680	2	AAR90618 Sulfolobu
56	68	14.7	720	2	AAR92227 Thermosta
57	67	14.5	507	3	AAV74372 Neisseria
58	67	14.5	507	3	AAV74373 Neisseria
59	67	14.5	507	6	ABU40210 Protein e
60	67	14.5	546	6	ABU38097 Protein e
61	67	14.5	548	4	AAE04737 Brugia ma
62	66.5	14.4	367	7	ADB80348 Human MDD
63	66.5	14.4	383	5	AAM51460 Human CDV
64	66.5	14.4	427	3	AAV97292 Lipid ass
65	66.5	14.4	623	7	ADB64393 Human pro
66	66.5	14.4	723	7	ADB85144 Rat calci
67	66.5	14.4	723	8	ADI81552 Rat epith
68	66.5	14.4	723	8	ADI81556 Rat calci
69	66	14.3	1128	4	AA62367 AP4 relat
70	65.5	14.2	229	9	ADX07448 Cyclin-de
71	65.5	14.2	285	6	ABP80850 N. gonorr
72	65.5	14.2	285	6	ABP76846 N. gonorr
73	65.5	14.2	370	6	ABM71443 Staphyloc
74	65.5	14.2	507	6	ABU41973 Protein e
75	65.5	14.2	579	7	ADC77529 Mouse moe

ALIGNMENTS

RESULT 1	ABB78151	standard; protein; 87 AA.
ID	ABB78151	
XX	ABB78151	
AC	ABB78151	
XX	05-NOV-2002	(first entry)
DT	05-NOV-2002	(first entry)
XX	Amino acid sequence of a YggX homologue.	
DB	Amino acid sequence of a YggX homologue.	
XX	Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;	
KW	hydroxyl radical; DNA damage; YggX homologue.	
XX	Pasteurella multocida.	
OS	Pasteurella multocida.	
XX	US2002072118-A1.	
PN	US2002072118-A1.	
XX	US2002072118-A1.	

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-6
Perfect score: 462
Sequence: 1 MARTVFCVYLKQSEGLDFQ.....QEMVNFLEGGKVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	435	94.2	90	2	C64013	hypothetical prote
2	379	82.0	91	2	A85954	hypothetical prote
3	379	82.0	91	2	A65082	hypothetical prote
4	379	82.0	91	2	F91108	hypothetical prote
5	377	81.6	91	2	AH0879	conserved hypotet
6	375	81.2	90	2	C82320	conserved hypotet
7	346	74.9	90	2	A10116	conserved hypotet
8	248	53.7	93	2	B84994	hypothetical prote
9	237	51.3	105	2	C82624	conserved hypotet
10	230	49.8	90	2	H83003	conserved hypotet
11	217	47.0	88	2	H81014	conserved hypotet
12	75	16.2	1024	2	T41415	probable leucine p
13	74.5	16.1	591	1	FOMVMM	gag polypeptide -
14	74.5	16.1	1526	2	AC2239	WD-40 repeat prote
15	72	15.6	593	2	C64097	probable soluble 1
16	70.5	15.3	353	1	FOMVGR	gag polypeptide -
17	70	15.2	946	2	T31488	hypothetical prote
18	69	14.9	169	2	PN0560	phytochrome - long
19	69	14.9	171	2	PN0558	phytochrome - wild
20	69	14.9	225	2	C88939	protein C05E4.8 [i
21	69	14.9	241	2	T27636	hypothetical prote
22	69	14.9	507	2	A83105	probable fumarate
23	68.5	14.8	511	2	A39340	neurofilament prot
24	68.5	14.8	599	2	H64097	fumarate reductase
25	68.5	14.8	615	2	B39340	neurofilament prot
26	68.5	14.8	1200	2	A46194	neurofilament prot
27	68	14.7	338	2	T28363	ORF MSV202 hypothe
28	68	14.7	330	1	B64561	ketol-acid reducto
29	68	14.7	720	2	JC5131	glycosyltransferas

30	67	14.5	507	2	C81063	fumarate hydratase
31	67	14.5	546	2	A81807	fumarate hydratase
32	67	14.5	548	2	A54510	63K antigen - nema
33	67	14.5	1119	2	T18491	hypothetical prote
34	66.5	14.4	152	2	B70423	transcription regu
35	66.5	14.4	265	2	T46013	hypothetical prote
36	66	14.3	300	2	T32681	hypothetical prote
37	66	14.3	358	2	T34382	hypothetical prote
38	66	14.3	548	2	A28209	60K filarial anti
39	66	14.3	1129	2	S00097	phytochrome 4 - oa
40	65.5	14.2	228	2	C26599	clathrin light cha
41	65.5	14.2	346	2	B31775	hypothetical prote
42	65.5	14.2	229	2	B31775	hypothetical prote
43	65.5	14.2	1206	2	B36507	hypothetical prote
44	65	14.1	258	2	S58159	hypothetical prote
45	65	14.1	604	2	F64081	isomerase fuci (BC
46	65	14.1	796	2	T43782	hypothetical prote
47	64.5	14.0	91	2	H90521	hypothetical prote
48	64.5	14.0	472	2	S74886	phytoene dehydroge
49	64.5	14.0	853	2	S74609	hypothetical prote
50	64	13.9	179	2	H82921	conserved hypotet
51	64	13.9	423	2	T45030	hypothetical prote
52	64	13.9	501	2	A84784	hypothetical prote
53	64	13.9	583	2	T48365	hypothetical prote
54	64	13.9	847	2	G95843	conserved hypotet
55	64	13.9	895	2	A86410	protein F3M18.22 l
56	64	13.9	1129	2	A29631	phytochrome 3 - oa
57	63.5	13.7	166	2	F70562	hypothetical prote
58	63.5	13.7	324	2	T05429	hypothetical prote
59	63.5	13.7	497	2	F90471	hypothetical prote
60	63.5	13.7	577	1	A41289	moesin - human
61	63.5	13.7	1613	2	G64488	reverse gyrase (in
62	63	13.6	183	2	B33355	ferritin light cha
63	63	13.6	511	2	B90600	hypothetical prote
64	63	13.6	635	2	C71021	hypothetical prote
65	63	13.6	959	1	P2XR13	outer capsid prote
66	63	13.6	1079	2	A86220	protein F22013.29
67	63	13.6	1113	2	T00736	hypothetical prote
68	63	13.6	2101	2	A42184	nuclear mitotic ap
69	62.5	13.5	93	2	T17906	hypothetical prote
70	62.5	13.5	165	2	A81382	shikimate kinase (
71	62.5	13.5	165	2	C81915	hypothetical prote
72	62.5	13.5	379	2	S70709	type II site-speci
73	62.5	13.5	394	2	B70206	hypothetical prote
74	62.5	13.5	577	1	S39804	moesin - pig
75	62.5	13.5	610	2	S63667	phragmoplastin 12

ALIGNMENTS

RESULT 1

C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weldman, J.; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:q15

C/Superfamily: fe(II) trafficking protein YggX

Query Match 94.2%; Score 435; DB 2; Length 90;
Best Local Similarity 92.0%; Pred. No. 2e-37;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-6
Perfect score: 462
Sequence: 1 MARTVFCBYLKQSEGLDFQ.....QEMVNFLEKGVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	90	1	FETP_PASMU
2	437	94.6	91	1	FETP_MANSU
3	435	94.2	90	1	FETP_HABIN
4	435	94.2	90	2	Q4QMD9_HAB18
5	416	90.0	94	1	FETP_HABDU
6	381	82.5	90	1	FETP_VIBPA
7	375	81.2	90	1	FETP_PHOPR
8	375	81.2	90	1	FETP_VIBCH
9	374	81.0	90	1	FETP_ECO57
10	374	81.0	90	1	FETP_ECOLI
11	374	81.0	90	1	FETP_SHIFL
12	372	80.5	90	1	FETP_SALCH
13	372	80.5	90	1	FETP_SALPA
14	372	80.5	90	1	FETP_SALTI
15	372	80.5	90	1	FETP_SALTY
16	370	80.1	90	1	FETP_ECOL6
17	369	79.9	90	1	FETP_VIBVU
18	369	79.9	90	1	FETP_VIBVY
19	354	76.6	90	1	FETP_YERPS
20	352	76.2	90	1	FETP_ERWCT
21	349	75.5	90	1	FETP_YERPE
22	346	74.9	90	1	FETP_YERPE
23	345	74.7	92	1	FETP_SHEON
24	343	74.2	90	1	FETP_VIBF1
25	327	70.8	90	1	FETP_IDILO
26	251	54.3	90	1	FETP_BORBR
27	251	54.3	90	1	FETP_BORPA
28	251	54.3	90	1	FETP_BORBE
29	248	53.7	77	1	FETP_BUCAI
30	243	52.6	91	1	FETP_XANAC
31	241	52.2	90	1	FETP_XYLFT

32	238.5	51.6	89	1	FETP_LEGPL	Q5WVC4 legionella
33	238	51.5	91	1	FETP_BURMA	Q62IUG burkholderi
34	238	51.5	91	1	FETP_BURPS	Q63S94 burkholderi
35	238	51.5	92	1	FETP_XANCP	Q8P829 xanthomonas
36	238	51.5	92	1	FETP_XANOR	Q5GY22 xanthomonas
37	237	51.3	90	1	FETP_XYLFA	Q4UW14 xanthomonas
38	237	50.8	89	1	FETP_LEGPA	Q9PC73 xylella fas
39	234.5	50.8	89	1	FETP_LEGPH	Q5X3X9 legionella
40	234.5	50.8	89	1	FETP_WIGBR	Q83CS wiggleswort
41	230	49.8	90	1	FETP_PSEAB	Q9HU36 pseudomonas
42	230	49.8	90	2	Q4J228_AZOVI	Q4J228 azotobacter
43	230	49.8	90	1	FETP_NITEU	Q82XF2 nitrosomona
44	229	49.6	90	1	FETP_PSEBM	Q88749 pseudomonas
45	228	49.4	91	2	Q4US19_9BURK	Q8Y010 ralstonia s
46	225	48.7	90	1	FETP_PSEPK	Q87UF5 pseudomonas
47	225	48.7	90	1	FETP_RALSO	Q42IP3 pseudomonas
48	224	48.5	90	1	FETP_PSESM	Q83D06 coxiella bu
49	224	48.5	90	2	Q6T7F6_PSEFL	Q60AJ7 methylococc
50	224	48.5	90	2	Q4ZLP3_PSESY	Q5F553 neisseria g
51	223	48.3	90	1	FETP_COXBU	P67615 neisseria m
52	222	48.1	90	2	Q4KJT2_PSEF5	P67616 neisseria m
53	219	47.4	88	1	FETP_METCA	Q89A44 buchnera ap
54	217	47.0	88	1	FETP_NEIMA	Q7NSR4 chromobacte
55	217	47.0	88	1	FETP_NEIMA	Q6FIB3 acinetobact
56	215	46.5	78	1	FETP_BUCAP	Q89A44 buchnera ap
57	215	46.5	78	1	FETP_BUCVO	Q7NSR4 chromobacte
58	214	46.3	90	1	FETP_AC1AD	Q6FIB3 acinetobact
59	210.5	45.6	87	1	FETP_BUCBP	Q89A44 buchnera ap
60	206	44.6	87	1	FETP_BUCBP	Q7NSR4 chromobacte
61	204	44.2	79	1	FETP_CANBF	Q5NHJ8 francisella
62	198	42.9	87	1	FETP_FRATF	Q5NHJ8 francisella
63	156	33.8	92	2	Q4NWQ4_9DELT	Q4NWQ4 anaeromyxob
64	154	33.3	96	2	Q4FVU7_9GAMM	Q4FVJ7 psychrobact
65	78	16.9	599	2	Q7VPM8_HABDU	Q7VPM8 haemophilus
66	75	16.2	565	2	Q5GT78_WOLTR	Q5GT78 wolbachia s
67	75	16.2	1024	2	Q74889_SCHPO	Q74889 schizosacch
68	74.5	16.1	187	2	Q9HBF7_HUMAN	Q9HBF7 homo sapien
69	74.5	16.1	218	2	Q7SPV9_9BETR	Q7SPV9 human betar
70	74.5	16.1	281	2	Q6PG71_MOUSE	Q6PG71 mus musculu
71	74.5	16.1	372	2	Q85648_9BETR	Q85648 mouse mamma
72	74.5	16.1	452	2	Q7SPV8_9BETR	Q7SPV8 human betar
73	74.5	16.1	590	1	GAG_MMTVB	P10258 mouse mamma
74	74.5	16.1	590	1	GAG_MMTVC	P11284 mouse mamma
75	74.5	16.1	591	2	Q83391_9BETR	Q83391 mouse mamma

ALIGNMENTS

RESULT 1			
FETP_PASMU			
ID	FETP_PASMU	STANDARD;	PRT; 90 AA.
AC	Q9CLB9;		
DT	10-OCT-2003 (Rel. 42, Created)		
DT	10-OCT-2003 (Rel. 42, Last sequence update)		
DT	13-SEP-2005 (Rel. 48, Last annotation update)		
DE	Probable Fe(2+) trafficking protein.		
GN	OrderedLocustNames=PM1320;		
OS	Pasteurella multocida.		
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;		
OC	Pasteurellaceae; Pasteurella.		
OX	NCBI_TaxID=747;		
RN	[1]		
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].		
RC	STRAIN=Pm70;		
RX	MEDLINE=21145866; PubMed=11248100; DOI=10.1073/pnas.051634598;		
RA	May B.J., Zhang Q., Li L.L., Paustian M.L., Whitlam T.S., Kapur V.;		
RT	"Complete genomic sequence of Pasteurella multocida Pm70.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 98:3460-3465(2001).		
CC	-I- FUNCTION: Could be a mediator in iron transactions between iron		
CC	acquisition and iron-requiring processes, such as synthesis and/or		
CC	repair of Fe-S clusters in biosynthetic enzymes (By similarity).		
CC	-I- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.		


```
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE006170; AAK03404.1; -; Genomic_DNA.
DR SMR; Q9CLB9; 1-87.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10744 MW; B583448BA4E0DFD7 CRC64;

Query Match 100.0%; Score 462; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 5.8e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCGYLKQESGLDFQLYPGELGKRIFDSISKQAWREWMKKQTMVNEKLNMMNA 60
Db 1 MARTVFCGYLKQESGLDFQLYPGELGKRIFDSISKQAWREWMKKQTMVNEKLNMMNA 60
61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 2
FETP_MANSNM
ID FETP_MANSNM STANDARD; PRT; 91 AA.
AC Q65VT7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=MS0316;
OS Mannheimia succiniciproducens (strain MBE155E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
RT succiniciproducens.";
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC -----
DR EMBL; AE016827; AAU36923.1; -; Genomic_DNA.
DR SMR; Q65VT7; 1-88.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AACC CRC64;

Query Match 94.6%; Score 437; DB 1; Length 91;
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Best Local Similarity 92.0%; Pred. No. 2.3e-37;
Matches 80; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 1 MARTVFCGYLKQESGLDFQLYPGELGKRIFDSISKQAWREWMKKQTMVNEKLNMMNA 60
Db 1 MSRTVFCGYLKQESGLDFQLYPGELGKRIFDSISKQAWREWMKKQTMVNEKLNMMNA 60
61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87
61 DHRQLLEQEMVNFLEFGKDVHIEGYVP 87

RESULT 3
FETP_HABIN
ID FETP_HABIN STANDARD; PRT; 90 AA.
AC P44048;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=HI0760;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom B., Cotton M.D.,
RA Usterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; U32760; AAC22419.1; -; Genomic_DNA.
DR PIR; C64013; C64013.
DR SMR; P44048; 1-87.
DR TIGR; HI0760; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
DR Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10582 MW; EB34CBFF7737B93B CRC64;

Query Match 94.2%; Score 435; DB 1; Length 90;
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-6
Perfect score: 462
Sequence: 1 MARTVFCBYLKQSEGLDFQ.....QEMVNFLEKGVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued_Patents_AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	364	78.8	107	2	US-09-489-039A-11962
2	361	78.1	93	2	US-09-543-681A-5443
3	230	49.8	122	2	US-09-252-991A-23355
4	205.5	44.5	92	2	US-09-328-352-5456
5	142	30.7	110	2	US-09-540-236-2859
6	74.5	16.1	591	2	US-09-370-368-8
7	69.5	15.0	683	2	US-09-270-767-46792
8	69	14.9	474	2	US-09-252-991A-24473
9	68	14.7	680	2	US-09-298-924-4
10	68	14.7	720	1	US-08-840-236-1
11	68	14.7	720	1	US-08-505-448A-1
12	67	14.5	548	2	US-09-167-299-3
13	66.5	14.4	623	2	US-10-104-047-2547
14	65	14.1	319	2	US-09-710-279-2760
15	65	14.1	443	2	US-09-134-001C-3183
16	64.5	14.0	342	2	US-09-270-767-45174
17	64	13.9	298	2	US-09-248-796A-20683
18	64	13.9	411	2	US-09-902-540-9815
19	64	13.9	1129	2	US-08-904-871-11
20	64	13.9	1129	2	US-10-134-500-2
21	63.5	13.7	496	2	US-09-092-770-6
22	63	13.6	359	1	US-09-800-170-20
23	63	13.6	359	2	US-09-222-851-6
24	63	13.6	359	2	US-10-265-062-6
25	63	13.6	404	1	US-09-092-770-3
26	63	13.6	404	2	US-09-222-851-3
27	63	13.6	404	2	US-10-265-062-3

28	63	13.6	407	2	US-09-949-016-11184	Sequence 11184, A
29	63	13.6	2101	1	US-08-466-390-4	Sequence 4, Appli
30	63	13.6	2101	1	US-08-470-950-4	Sequence 4, Appli
31	63	13.6	2101	1	US-08-467-781-4	Sequence 4, Appli
32	63	13.6	2101	1	US-08-195-487-4	Sequence 4, Appli
33	63	13.6	2101	1	US-08-483-924-4	Sequence 4, Appli
34	63	13.6	2101	2	US-09-452-294-1	Sequence 1, Appli
35	63	13.6	2101	2	US-09-296-662-32	Sequence 32, Appli
36	63	13.6	2101	4	PCT-US93-06160-4	Sequence 4, Appli
37	63	13.6	2107	2	US-09-949-016-7646	Sequence 7646, Ap
38	63	13.6	2107	2	US-09-296-662-33	Sequence 7647, Ap
39	63	13.6	2115	2	US-08-799-138-4	Sequence 33, Appli
40	62.5	13.5	610	1	US-08-799-138-6	Sequence 4, Appli
41	62.5	13.5	610	1	US-09-392-362-4	Sequence 4, Appli
42	62.5	13.5	610	2	US-09-392-362-4	Sequence 6, Appli
43	62.5	13.5	610	2	US-09-392-362-6	Sequence 6, Appli
44	62	13.4	57	2	US-09-562-737-124	Sequence 124, App
45	62	13.4	116	2	US-09-562-737-125	Sequence 125, App
46	62	13.4	381	2	US-09-949-016-9788	Sequence 9788, Ap
47	62	13.4	381	2	US-09-964-899-13	Sequence 13, Appl
48	62	13.4	485	2	US-09-248-796A-17800	Sequence 45790, A
49	62	13.4	482	2	US-09-270-767-45790	Sequence 17800, A
50	62	13.4	556	2	US-09-800-960-4	Sequence 4, Appli
51	62	13.4	556	2	US-10-096-960-4	Sequence 4, Appli
52	62	13.4	565	2	US-09-800-960-2	Sequence 2, Appli
53	62	13.4	565	2	US-10-096-960-2	Sequence 2, Appli
54	62	13.4	1401	2	US-09-750-590A-2	Sequence 2, Appli
55	62	13.4	2388	2	US-09-695-795A-2	Sequence 32538, A
56	61.5	13.3	239	2	US-09-270-767-32538	Sequence 47755, A
57	61.5	13.3	239	2	US-09-071-035-44	Sequence 44, Appl
58	61.5	13.3	528	2	US-09-071-035-44	Sequence 44, Appl
59	61.5	13.3	528	2	US-10-206-576-44	Sequence 42, Appl
60	61.5	13.3	547	2	US-09-071-035-42	Sequence 42, Appl
61	61.5	13.3	547	2	US-10-206-576-42	Sequence 4, Appli
62	61.5	13.3	734	2	US-09-442-055-4	Sequence 2, Appli
63	61	13.2	179	2	US-09-870-574-2	Sequence 2, Appli
64	61	13.2	179	2	US-10-090-365-15	Sequence 15, Appl
65	61	13.2	179	2	US-09-728-911-15	Sequence 15, Appl
66	61	13.2	179	2	US-10-084-298-2	Sequence 2, Appli
67	61	13.2	202	2	US-09-949-016-11314	Sequence 11314, A
68	60.5	13.1	139	2	US-08-559-896B-4	Sequence 4, Appli
69	60.5	13.1	139	2	US-09-351-794A-4	Sequence 4, Appli
70	60.5	13.1	415	1	US-08-602-010A-10	Sequence 10, Appl
71	60.5	13.1	415	1	US-08-680-726A-10	Sequence 10, Appl
72	60.5	13.1	415	1	US-09-092-409-10	Sequence 10, Appl
73	60.5	13.1	642	2	US-09-902-540-16286	Sequence 16286, A
74	60.5	13.1	652	2	US-08-559-896B-2	Sequence 2, Appli
75	60.5	13.1	652	2	US-09-351-794A-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Bretton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	78.8%	Score 364;	DB 2;	Length 107;
Best Local Similarity	72.4%	Pred. No. 1e-39;		
Matches	63;	Conservative	15;	Mismatches
			9;	Indels
				Gaps
				0;

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QY      1 MARTVFC EYLKQBSEGLDPOLYPGELGKRIFDSISKAWREWMKKQTMLVNKKLNNMNA    60
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Db     17 MSRTI FCTFLQREADGDGPOLYPGBLGKRIYN EISKA MAWQH KQTMLINEKLSMNPNP   76
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QY 61 DHRQLLEQEMVNFLLFEKGKDVHIEGYTP 87
 :|::||| | ||| | ||| | ||| | ||| |
Db 77 EHKLLIQEMVQFLFEGKDVHIEGYTP 103

RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A

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1  APPLICANT: GARY BRETON
2  TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
3  TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
4  FILE REFERENCE: 2709.1002-001
5  CURRENT APPLICATION NUMBER: US/09/543,681A
6  CURRENT FILING DATE: 2000-04-05
7  PRIOR APPLICATION NUMBER: US 60/128,706
8  PRIOR FILING DATE: 1999-04-09
9  NUMBER OF SEQ ID NOS: 8344
10 SEQ ID NO 5443
11
12 LENGTH: 93
13
14 TYPE: PRT
15
16 ORGANISM: Proteus mirabilis
17
18 US-09-543-681A-5443

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Query Match	78.1%	Score 361;	DB 2;	Length 93;
Best Local Similarity	73.6%	Pred. No. 2.1e-39;		
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Dy

1 MARTVPEYLLKQSEGLDPOLYPGEIGKRIFDSISKQAWRENNKKQTMLVNEKLNMNNA 600
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Db 4 MSRTFCTPLNKADGDLFPOLYPEIGAKRIPNEISKEA WGOMNA KQTMLINEKCLNTMNP 63

QY	61	DHRQLLEQEMVNFLFEGKDVIHIEGYVP	87
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RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A

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: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 23355
: LENGTH: 122
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Query Match	49.8%;	Score 230;	DB 2;	Length 122;
Best Local Similarity	51.1%;	Pred. No. 3.7e-22;		
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Db 33 MSRTVMCRKYYHEELPGIDRRPYPGAAGEDITYNNVSRKAMDWQKHQTMLINERLNMNNA 92

Qy 61 DHRQLLEQEMVNFLEFGKD-VHIEGYVP 87

Db 93 EDRKFTLQDEMDFL-SGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958

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: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 5456
: LENGTH: 92
: TYPE: PRT
: ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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QY 61 DHRQLLEQEMVNFLEFGKDVH-IEGYVP 87
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RESULT 5
US-09-540-236-2859

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; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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Query Match	30.7%;	Score 142;	DB 2;	Length 110;
Best Local Similarity	36.1%;	Pred. No. 9.7e-11;		
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Db     25 VFCRKYYOONPKLPNPPFPNAKGQEIQDTISAKAMNAMLBJEQTMLINEKHLSMIDPQAKK   84
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QY 65 LLEQEMVNFLEFGKDVHIEGYVP 87
| :: | | |
Db 85 YLNEQREKFLDNGDYEKYPAGYKP 107

RESULT 6
US-09-370-368-8
; Sequence 8, Application US/09370368

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-6
Perfect score: 462
Sequence: 1 MARTVPCRYLKQESGLDFQ.....QEMVNFLEKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	416	90.0	87	3	US-09-955-502-8
5	379	82.0	91	3	US-09-955-502-11
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7	379	82.0	91	3	US-09-955-502-13
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9	377	81.6	91	3	US-09-955-502-14
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11	377	81.6	91	3	US-09-955-502-17
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13	370	80.1	91	3	US-09-955-502-18
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22	237	51.3	89	3	US-09-955-502-22
23	233.5	50.5	86	3	US-09-955-502-4
24	230	49.8	87	3	US-09-955-502-25
25	225	48.7	87	3	US-09-955-502-24
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27	223	48.3	88	3	US-09-955-502-33

28	219	47.4	87	3	US-09-955-502-32	Sequence 32, Appli
29	217	47.0	88	3	US-09-955-502-26	Sequence 26, Appli
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32	200	43.3	87	3	US-09-955-502-31	Sequence 31, Appli
33	75	16.2	1144	4	US-10-369-493-22774	Sequence 22774, A
34	74.5	16.1	591	3	US-09-827-822-8	Sequence 8, Appli
35	73.5	15.9	593	5	US-10-450-763-50306	Sequence 50306, A
36	70	15.2	1261	4	US-10-437-963-189166	Sequence 189166,
37	69.5	15.0	449	4	US-10-437-963-171997	Sequence 171997,
38	69.5	15.0	1286	4	US-10-424-599-151734	Sequence 151734,
39	69.5	15.0	1292	4	US-10-424-599-151745	Sequence 151745,
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41	69	14.9	169	5	US-10-732-923-12560	Sequence 12560, A
42	69	14.9	171	5	US-10-732-923-12562	Sequence 12562, A
43	68.5	14.8	322	4	US-10-437-963-171999	Sequence 171999,
44	68.5	14.8	1809	4	US-10-437-963-195972	Sequence 195972,
45	68	14.7	330	3	US-09-815-242-11319	Sequence 11319, A
46	68	14.7	330	4	US-10-282-122A-58687	Sequence 58687, A
47	68	14.7	680	4	US-10-688-276-4	Sequence 4, Appli
48	68	14.7	720	3	US-09-419-305-1	Sequence 1, Appli
49	67	14.5	507	4	US-10-282-122A-68134	Sequence 68134, A
50	67	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
51	66.5	14.4	623	4	US-10-104-047-2547	Sequence 2547, Ap
52	66.5	14.4	723	4	US-10-205-194-25	Sequence 25, Appli
53	66.5	14.4	723	4	US-10-231-913-139	Sequence 139, App
54	66.5	14.4	723	4	US-10-231-913-140	Sequence 140, Appl
55	66.5	14.4	723	4	US-10-342-844-22	Sequence 22, Appli
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57	66	14.3	1129	5	US-10-732-923-12553	Sequence 12553, A
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61	65.5	14.2	823	6	US-11-097-143-23151	Sequence 23151, A
62	65.5	14.2	966	4	US-10-424-599-169693	Sequence 169693,
63	65.5	14.2	2724	5	US-10-756-149-5518	Sequence 5518, Ap
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66	65	14.1	645	4	US-10-425-115-368990	Sequence 368990,
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68	65	14.1	671	5	US-10-631-467-1461	Sequence 1461, Ap
69	64.5	14.0	327	6	US-11-097-143-36495	Sequence 36495, A
70	64.5	14.0	634	6	US-11-097-143-6804	Sequence 6804, Ap
71	64	13.9	179	4	US-10-282-122A-76744	Sequence 76744, A
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73	64	13.9	325	4	US-10-425-114-45894	Sequence 45894, A
74	64	13.9	389	4	US-10-049-187-3	Sequence 3, Appli
75	64	13.9	389	5	US-10-732-923-10522	Sequence 10522, A

ALIGNMENTS

RESULT 1
US-09-955-502-6
; Sequence 6, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pasteurella multocida

GenCore Version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	72	15.6	593	US-11-194-246-317	Sequence 317, App
3	66.5	14.4	623	US-11-072-512-2547	Sequence 2547, App
4	65.5	14.2	285	US-10-467-657-222	Sequence 222, App
5	65.5	14.2	285	US-10-467-657-8230	Sequence 8230, App
6	65	14.1	319	US-10-793-626-2760	Sequence 2760, App
7	64	13.9	296	US-11-087-227-10	Sequence 10, Appl
8	63.5	13.7	496	US-11-069-642-20	Sequence 20, Appl
9	63.5	13.7	577	US-11-072-175-187	Sequence 187, App
10	63	13.6	140	US-11-098-686-10643	Sequence 10643, A
11	63	13.6	359	US-11-087-227-8	Sequence 8, Appl
12	63	13.6	359	US-11-192-450-6	Sequence 6, Appl
13	63	13.6	404	US-11-087-227-6	Sequence 6, Appl
14	63	13.6	404	US-11-192-450-3	Sequence 3, Appl
15	63	13.6	834	US-10-453-372-658	Sequence 658, App
16	63	13.6	2101	US-10-857-780-23	Sequence 23, Appl
17	61	13.2	179	US-10-063-703-154	Sequence 154, App
18	61	13.2	179	US-11-102-240-154	Sequence 154, App
19	61	13.2	179	US-11-177-987-43	Sequence 43, Appl
20	61	13.2	336	US-10-453-372-640	Sequence 640, Appl
21	61	13.2	342	US-11-156-084-25	Sequence 25, Appl
22	61	13.2	342	US-11-156-084-44	Sequence 44, Appl
23	61	13.2	369	US-11-156-084-45	Sequence 45, Appl
24	61	13.2	619	US-11-156-084-24	Sequence 24, Appl
25	61	13.2	695	US-10-453-372-648	Sequence 648, App

26	61	13.2	700	US-10-995-561-922	Sequence 922, App
27	61	13.2	700	US-10-995-561-924	Sequence 924, App
28	61	13.2	775	US-10-453-372-656	Sequence 656, App
29	61	13.2	793	US-10-995-561-925	Sequence 925, App
30	61	13.2	804	US-10-453-372-650	Sequence 650, App
31	61	13.2	847	US-10-453-372-654	Sequence 654, App
32	61	13.2	857	US-10-453-372-652	Sequence 652, App
33	61	13.2	905	US-10-453-372-638	Sequence 638, App
34	61	13.2	905	US-10-453-372-662	Sequence 662, App
35	61	13.2	905	US-10-453-372-664	Sequence 664, App
36	61	13.2	963	US-10-995-561-923	Sequence 923, App
37	61	13.2	963	US-10-453-372-660	Sequence 660, App
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40	59.5	12.9	765	US-11-120-308-84	Sequence 84, Appl
41	59.5	12.9	818	US-11-120-308-94	Sequence 94, Appl
42	59	12.8	139	US-10-793-626-1310	Sequence 1310, App
43	58	12.6	635	US-11-098-686-10433	Sequence 10433, A
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45	58	12.6	750	US-11-155-288-4	Sequence 4, Appl
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51	57	12.3	254	US-11-072-512-3198	Sequence 3198, App
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53	56.5	12.2	109	US-11-053-076-196	Sequence 196, App
54	56.5	12.2	782	US-10-793-626-2352	Sequence 2352, App
55	56.5	12.2	1089	US-11-148-770-32	Sequence 32, Appl
56	56.5	12.2	1089	US-11-076-427A-14	Sequence 14, Appl
57	56.5	12.2	1089	US-11-075-047A-117	Sequence 117, App
58	56.5	12.2	1451	US-10-995-561-829	Sequence 829, App
59	56	12.1	443	US-10-793-626-1200	Sequence 1200, App
60	56	12.1	668	US-11-098-686-11201	Sequence 11201, A
61	55.5	12.0	253	US-10-724-598-28	Sequence 28, Appl
62	55	11.9	266	US-09-995-493-6	Sequence 6, Appl
63	55	11.9	279	US-11-098-686-10812	Sequence 10812, A
64	55	11.9	674	US-11-000-463-471	Sequence 471, App
65	55	11.9	734	US-10-995-561-770	Sequence 770, App
66	55	11.9	739	US-10-131-826A-478	Sequence 478, App
67	54.5	11.8	229	US-10-793-626-2818	Sequence 2818, App
68	54.5	11.8	305	US-11-156-084-178	Sequence 178, App
69	54.5	11.8	349	US-10-821-234-1387	Sequence 1387, App
70	54.5	11.8	497	US-11-010-239-85	Sequence 85, Appl
71	54.5	11.8	729	US-10-511-538-101	Sequence 101, Appl
72	54.5	11.8	1151	US-10-793-626-2448	Sequence 2448, App
73	54	11.7	158	US-11-072-512-3221	Sequence 3221, App
74	54	11.7	352	US-11-098-686-10448	Sequence 10448, A
75	54	11.7	4374	US-11-128-572-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

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; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968
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Query Match          47.0%; Score 217; DB 6; Length 88;
Best Local Similarity 46.6%; Pred. No. 2.3e-18;
Matches 41; Conservative 20; Mismatches 25; Indels 2; Gaps 2;
```

```
OY      1 MARTVFCEYLKQSEGLDPQLYPGELGKRIFDSISKQAWREWMKKQTMLVNEKKLNMNNA 60
          ||| ||| | :|:|:| | | ||||| | :|:|:| | :|:|:| :
Db      1 MARVFCVKLNKEABGAKPPPLPNELGKRIFENVSGEAWAATRHQTMLINENRISLADP 60
```

```
OY      61 DHRQLLEQEMVNFLE-EGKDVHIEGYVP 87
          | :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      61 RAREVYLAQQOMEQYFFGDGADA-VQGYVP 87
```

RESULT 2

```
US-11-194-246-317
; Sequence 317, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (MAR 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
; TYPE: PRT
; ORGANISM: HAEMOPHILUS INFLUENZAE
US-11-194-246-317
```

```
Query Match          15.6%; Score 72; DB 7; Length 593;
Best Local Similarity 46.7%; Pred. No. 1.1;
Matches 14; Conservative 5; Mismatches 11; Indels 0; Gaps 0;
```

```
OY      32 DSIKQAWREWMKKQTMLVNEKKLNMNNA 61
          :| ||| ||| | | :| :| ||| :| :| :
Db      293 ESKSKQEWRYWEAKQDILKNTKLTALSK 322
```

RESULT 3

```
US-11-072-512-2547
; Sequence 2547, Application US/11072512
; Publication No. US20060029945A1
; GENERAL INFORMATION:
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: OTSUKI, TETSUJI
; APPLICANT: WAKAMATSU, AI
; APPLICANT: SATO, HIROYUKI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: YAMAMOTO, JUN-ICHI
; APPLICANT: ISONO, YUUKO
; APPLICANT: HIO, YURI
; APPLICANT: OTSUKA, KAORU
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: IRIE, RYOTARO
; APPLICANT: TAMECHIKA, ICHIRO
; APPLICANT: SEKI, NAOHIKO
; APPLICANT: YOSHIKAWA, TSUTOMU
```

```
; APPLICANT: OTSUKA, MOTOYUKI
; APPLICANT: NAGAHARI, KENJI
; APPLICANT: MASUHO, YASUHIKO
; TITLE OF INVENTION: Novel full length cDNA
; FILE REFERENCE: 084335-0191
; CURRENT APPLICATION NUMBER: US/11/072,512
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: US 60/350,978
; PRIOR FILING DATE: 2002-01-25
; PRIOR APPLICATION NUMBER: JP 2001-379298
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 4096
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2547
; LENGTH: 623
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-072-512-2547
```

```
Query Match          14.4%; Score 66.5; DB 7; Length 623;
Best Local Similarity 30.8%; Pred. No. 5.2;
Matches 24; Conservative 13; Mismatches 32; Indels 9; Gaps 3;
```

```
OY      10 LKQSEGLDPQLY-----PGEL--GKRIFDSISKQAWREWMKKQTMLVNEKKLNMNNA 61
          :| :| :| :| ||| | :| :| :| :| :| :| :| :| :| :|
Db      232 MKRLBEIKFNLYVTEKPKLELNKKELHPLQKVSEPAHGSHDLLESKINEINTE 291
```

```
OY      62 HRQLLEQEMV-NFLPEGK 78
          ||| :| :| :| :| |||
Db      292 INQLIEKKMRNEPIEGK 309
```

RESULT 4

```
US-10-467-657-222
; Sequence 222, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWIn99, version 1.04
; SEQ ID NO 222
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-222
```

```
Query Match          14.2%; Score 65.5; DB 6; Length 285;
Best Local Similarity 29.4%; Pred. No. 2.6;
Matches 20; Conservative 14; Mismatches 21; Indels 13; Gaps 4;
```

```
OY      8 EYLKQSEGLDPQLYPGELGKRIFDSISKQAWREW--MKQTMLVNEKKLNMNNAADHRQL 65
          :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      227 KYISFDDEGNMVK-----SKRLSDV---WRRWCDVKLDNNLNDKRKSYL-AVHREL 275
```

```
OY      66 LEQEMVNF 73
          :| ||| |
Db      276 MLQEDQEF 283
```

RESULT 5

```
US-10-467-657-8230
; Sequence 8230, Application US/10467657
; Publication No. US20050260581A1
```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-7
Perfect score: 461
Sequence: 1 MARTVFCEYLKKRAGLDFQ.....QEMVNFLEKGVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21: *
1: Geneseqp1980s: *
2: Geneseqp1990s: *
3: Geneseqp2000s: *
4: Geneseqp2001s: *
5: Geneseqp2002s: *
6: Geneseqp2003as: *
7: Geneseqp2003bs: *
8: Geneseqp2004s: *
9: Geneseqp2005s: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	5	ABB78152 Amino aci
2	435	94.4	87	5	ABB78151 Amino aci
3	434	94.1	91	5	ABB78150 Amino aci
4	425	92.2	87	5	ABB78153 Amino aci
5	387	83.9	91	5	ABB78158 Amino aci
6	387	83.9	91	5	ABB78157 Amino aci
7	387	83.9	91	5	ABB78156 Amino aci
8	386	83.7	90	5	ABB78155 Amino aci
9	385	83.5	88	5	ABB78160 Amino aci
10	385	83.5	91	5	ABB78161 Amino aci
11	385	83.5	91	5	ABB78159 Amino aci
12	385	83.5	91	5	ABB78162 Amino aci
13	378	82.0	91	5	ABB78163 Amino aci
14	372	80.7	107	7	ABO65445 Amino aci
15	371	80.5	93	7	ADF05158 Bacterial
16	363	78.7	90	5	ABB78165 Amino aci
17	356	77.2	88	5	ABB78154 Amino aci
18	325	70.5	78	5	ABB78164 Amino aci
19	256	55.5	76	5	ABB78166 Amino aci
20	256	55.5	87	5	ABB78148 Amino aci
21	256	55.5	87	5	ABB78147 Amino aci
22	241	52.3	87	5	ABB78175 Amino aci
23	238.5	51.7	86	5	ABB78149 Amino aci
24	236	51.2	87	5	ABB78170 Amino aci

25	236	51.2	122	7	ABO74609	AbO74609 Pseudomon
26	235.5	51.1	89	9	ABE41576	Aeb41576 L. pneumo
27	235.5	51.1	95	5	ABE38294	Aeb38294 L. pneumo
28	235	51.0	87	5	ABB78174	Abb78174 Amino aci
29	230	49.9	90	5	ABB78168	Abb78168 Amino aci
30	229	49.7	87	5	ABB78169	Abb78169 Amino aci
31	227.5	49.3	90	5	ABB78167	Abb78167 Amino aci
32	227	49.2	88	5	ABB78171	Abb78171 Amino aci
33	227	49.2	88	5	ABB78172	Abb78172 Amino aci
34	227	49.2	88	5	ABB78173	Abb78173 Amino aci
35	227	49.2	88	6	ABP77219	Abp77219 N. gonorr
36	224	48.6	87	5	ABB78177	Abb78177 Amino aci
37	224	48.6	88	5	ABB78178	Abb78178 Amino aci
38	214.5	46.5	92	6	ADA34169	Ada34169 Acinetoba
39	202	43.8	87	5	ABB78176	Abb78176 Amino aci
40	144	31.2	110	8	ADL05173	Adl05173 M. catarr
41	76.5	16.6	591	2	AAV41141	Aay41141 Mouse mam
42	76.5	16.6	860	2	AAV41140	Aay41140 Mouse mam
43	76.5	16.6	1755	2	AAV41139	Aay41139 Mouse mam
44	73	15.8	975	5	ABP66068	Abp66068 Bifidobac
45	73	15.8	1144	8	ADS44344	Ads44344 Bacterial
46	72	15.6	506	3	AAV74371	Aay74371 Neisseria
47	71	15.4	503	4	ABG16577	Abg16577 Novel hum
48	71	15.4	883	8	ADN47233	Adn47233 Thermococ
49	70.5	15.3	723	7	ADB85144	Adb85144 Rat calci
50	70.5	15.3	723	8	ADI81552	Adi81552 Rat epith
51	70.5	15.3	723	8	ADI81556	Adi81556 Rat calci
52	70.5	15.3	949	6	ABU40639	Abu40639 Protein e
53	70.5	15.3	959	7	ADF06594	Adf06594 Bacterial
54	69.5	15.1	227	3	AAG38052	Aag38052 Arabidops
55	69.5	15.1	593	4	ABG19947	Abg19947 Novel hum
56	69	15.0	484	8	ADM90985	Adm90985 Human pha
57	69	15.0	507	6	ABU40210	Abu40210 Protein e
58	68.5	14.9	218	3	AAG45909	Aag45909 Arabidops
59	68.5	14.9	234	3	AAG45908	Aag45908 Arabidops
60	68	14.8	257	3	AAG31203	Aag31203 Arabidops
61	68	14.8	297	3	AAG31202	Aag31202 Arabidops
62	68	14.8	324	3	AAG31201	Aag31201 Arabidops
63	67.5	14.6	283	8	ADY12704	Ady12704 Plant ful
64	67	14.5	474	7	ABO75727	AbO75727 Pseudomon
65	67	14.5	507	3	AAV74372	Aay74372 Neisseria
66	67	14.5	507	3	AAV74373	Aay74373 Neisseria
67	67	14.5	546	6	ABU38097	Abu38097 Protein e
68	67	14.5	1399	8	ADR75314	Adr75314 Bovine ac
69	67	14.5	1401	8	ADR75290	Adr75290 Bovine ac
70	66.5	14.4	330	4	AAU35726	Aau35726 Helicobac
71	66.5	14.4	330	6	ABU30763	Abu30763 Protein e
72	66.5	14.4	487	8	ADN01595	Adn01595 Enterobac
73	66.5	14.4	730	8	ADI81550	Adi81550 Rabbit ep
74	66.5	14.4	765	6	ADA20715	Ada20715 Artichoke
75	66.5	14.4	818	6	ADA20725	Ada20725 Artichoke

ALIGNMENTS

RESULT 1	
ABB78152	standard; protein; 87 AA.
ID	ABB78152
XX	
AC	ABB78152;
XX	
DT	05-NOV-2002 (first entry)
XX	
DE	Amino acid sequence of a Yggx homologue.
XX	
KW	Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
XX	
OS	hydroxyl radical; DNA damage; Yggx homologue.
XX	
PN	Haemophilus influenzae.
XX	
XX	US2002072118-A1.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-7
Perfect score: 461
Sequence: 1 MARTVFCEYLKKBAGLDFQ.....QEMVNFLPEGKDVHIBGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	90	2	C64013 hypothetical prote
2	387	83.9	91	2	A85954 hypothetical prote
3	387	83.9	91	2	A65082 hypothetical prote
4	387	83.9	91	2	P91108 hypothetical prote
5	386	83.7	90	2	C82320 conserved hypot
6	385	83.5	91	2	AH0879 conserved hypot
7	363	78.7	90	2	AI0116 conserved hypot
8	256	55.5	93	2	E84994 conserved hypot
9	237	51.4	105	2	C82624 conserved hypot
10	236	51.2	90	2	H83003 conserved hypot
11	227	49.2	88	2	H81014 conserved hypot
12	76.5	15.6	591	1	FOVMVM gag polypeptid
13	73	15.8	1024	2	T41415 gag polypeptid
14	72.5	15.7	353	1	FOVMGR gag polypeptid
15	68.5	14.9	1206	2	E96507 hypothetical prote
16	68	14.8	324	2	T05429 hypothetical prote
17	68	14.8	555	2	C96667 unknown prote
18	68	14.8	583	2	T48365 hypothetical prote
19	68	14.8	593	2	C64097 probable soluble
20	67.5	14.6	1119	2	T18491 hypothetical prote
21	67	14.5	328	2	T28363 ORF MSV202 hypo
22	67	14.5	485	2	A84043 chromosome repli
23	67	14.5	507	2	A83105 probable fumarate
24	67	14.5	507	2	C81063 fumarate hydratase
25	67	14.5	546	2	A81807 fumarate hydratase
26	66.5	14.4	330	1	B64561 ketol-acid reducto
27	66.5	14.4	394	2	B70206 hypothetical prote
28	66.5	14.4	487	1	IOBP34 DNA ligase (ATP)
29	66	14.3	258	2	S58159 hypothetical prote

30	66	14.3	548	2	A54510 63K antigen - nema
31	65.5	14.2	152	2	B70423 transcription regu
32	65.5	14.2	300	2	F84178 hypothetical prote
33	65.5	14.2	348	2	H70337 conserved hypot
34	65.5	14.2	723	2	UC7795 epithelial calcium
35	65.5	14.2	1787	2	G97222 hypothetical prote
36	65	14.1	166	2	C95944 probable acetyltra
37	65	14.1	182	2	C69416 hypothetical prote
38	65	14.1	330	2	G91204 hypothetical prote
39	65	14.1	367	2	A86051 hypothetical prote
40	65	14.1	392	2	H90174 hypothetical prote
41	65	14.1	548	2	A28209 probable Fe-S oxid
42	65	14.1	558	2	B97026 hypothetical prote
43	65	14.1	558	2	A85296 hypothetical prote
44	65	14.1	559	2	T05786 hypothetical prote
45	65	14.1	604	2	F64081 isomerase fuci (BC
46	64.5	14.0	165	2	A81382 shikimate kinase
47	64.5	14.0	480	2	S38134 GLG1 protein - yea
48	64.5	14.0	1526	2	AC2239 WD-40 repeat prote
49	64.5	14.0	1645	2	A37792 spectrin beta-H ch
50	64.5	14.0	1939	2	T18372 repeat organellar
51	64	13.9	342	2	T13113 probable scpb prot
52	64	13.9	553	2	G70115 ribosomal protein
53	64	13.9	641	2	T38659 methylenetetrahydr
54	64	13.9	720	2	JC5131 glycosyltransferas
55	64	13.9	742	1	S58691 kinesin-related pr
56	64	13.9	946	2	T31488 tetrahydrolipicoll
57	63.5	13.8	236	2	F69866 hypothetical prote
58	63.5	13.8	996	2	A71080 conserved hypot
59	63.5	13.8	1008	2	H72310 mucin MUC5B, trach
60	63.5	13.8	1321	2	JB0352 protein C05E4.8 [l
61	63	13.7	225	2	C88939 hypothetical prote
62	63	13.7	241	2	T27636 hypothetical prote
63	63	13.7	271	2	A84643 probable WRKY-type
64	63	13.7	274	2	S04610 gene 2 protein - p
65	63	13.7	372	2	E81350 hypothetical RNA nucle
66	63	13.7	501	2	A84784 hypothetical prote
67	63	13.7	1209	2	T46027 hypothetical prote
68	63	13.7	1262	2	T33074 translation activa
69	63	13.7	2672	2	A48126 hypothetical prote
70	62.5	13.6	91	2	H90521 probable proteinas
71	62.5	13.6	308	2	E71697 moesin - human
72	62.5	13.6	577	1	A41289 hypothetical prote
73	62.5	13.6	853	2	S74609 probable ATP-depen
74	62.5	13.6	1101	2	G70951 pyruvate carboxyla
75	62.5	13.6	1150	2	G89881

ALIGNMENTS

RESULT 1

C64013 hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800

A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Residues: 1-90 <TIGR>

A/Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C/Superfamily: fe(II) trafficking protein YggX

Query Match 100.0%; Score 461; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-39;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

Db 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

RESULT 2

A85954

hypothetical protein yggx [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004

C/Accession: A85954

R./Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: A85954

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <STO>

A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: yggx

C/Superfamily: fe(II) trafficking protein Yggx

Query Match 83.9%; Score 387; DB 2; Length 91;

Best Local Similarity 78.2%; Pred. No. 4.6e-32;

Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

Db 1 MSRTIFCTFLQREABEGDQFQLYPGELGKRIFYNEISKEAWAQWQHKTMLINEKCLNMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87

RESULT 3

A65082

hypothetical protein b2962 - Escherichia coli (strain K-12)
C/Species: Escherichia coli

C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004

C/Accession: A65082

R./Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.

A/Title: The complete genome sequence of Escherichia coli K-12.

A/Reference number: A64720; MUID:97426617; PMID:9278503

A/Accession: A65082

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-91 <BLAT>

A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9

A/Experimental source: strain K-12, substrain MG1655

C/Superfamily: fe(II) trafficking protein Yggx

Query Match 83.9%; Score 387; DB 2; Length 91;

Best Local Similarity 78.2%; Pred. No. 4.6e-32;

Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

Db 1 MSRTIFCTFLQREABEGDQFQLYPGELGKRIFYNEISKEAWAQWQHKTMLINEKCLNMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87

RESULT 4

F91108

hypothetical protein ECS3838 [imported] - Escherichia coli (strain O157:H7, substrain RI,
C/Species: Escherichia coli

C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004

C/Accession: F91108

R./Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.

DNA Res. 8, 11-22, 2001

A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno

A/Reference number: A99629; MUID:21156231; PMID:11258796

A/Accession: F91108

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-91 <HAY>

A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1;

A/Experimental source: strain O157:H7, substrain RIMD 0509952

C/Genetics:

A/Gene: ECS3838

C/Superfamily: fe(II) trafficking protein Yggx

Query Match 83.9%; Score 387; DB 2; Length 91;

Best Local Similarity 78.2%; Pred. No. 4.6e-32;

Matches 68; Conservative 12; Mismatches 7; Indels 0; Gaps 0;

QY 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

Db 1 MSRTIFCTFLQREABEGDQFQLYPGELGKRIFYNEISKEAWAQWQHKTMLINEKCLNMNNA 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87

RESULT 5

C82320

conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogr
C/Species: Vibrio cholerae

C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004

C/Accession: C82320

R./Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P

l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A/Reference number: A82035; MUID:20406833; PMID:10952301

A/Accession: C82320

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-90 <HEID>

A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:g9654871; PIDN:

A/Experimental source: serogroup O1, strain N16961; biotype El Tor

C/Genetics:

A/Gene: VC0451

A/Map position: 1

C/Superfamily: fe(II) trafficking protein Yggx

Query Match 83.7%; Score 386; DB 2; Length 90;

Best Local Similarity 80.5%; Pred. No. 5.7e-32;

Matches 70; Conservative 9; Mismatches 8; Indels 0; Gaps 0;

QY 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNNA 60

Db 1 MARTVFCBYLKKEAEGLDPOLYPGELGKRIFDNICKEAWAQWQTKQTMLINEKCLNMNDP 60

QY 61 EHRKLLBQEMVNFLEFGKDVHIEGYVP 87

Db 61 EHRKLLBQEMVNFLEFGKDVHIEGYTP 87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 : Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-7
Perfect score: 461
Sequence: 1 MARTVFCVYLKKBAGLDFQ.....QEMVNFLEKGVHIGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	461	100.0	90	1	FETP_HAEIN	P44048 haemophilus
2	461	100.0	90	2	Q4QMD9_HAE18	Q4qmd9 haemophilus
3	439	95.2	91	1	FETP_MANSN	Q65vt7 mannheimia
4	435	94.4	90	1	FETP_PASMU	Q9cib9 pasteurella
5	425	92.2	94	1	FETP_HABDU	Q7vkb6 haemophilus
6	389	84.4	90	1	FETP_VIBPA	Q87li5 vibrio para
7	387	83.9	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
8	387	83.9	90	1	FETP_VIBVY	Q87h14 vibrio vuln
9	386	83.7	90	1	FETP_VIBCH	Q9kur4 vibrio chol
10	382	82.9	90	1	FETP_ECO57	Q0a8p4 escherichia
11	382	82.9	90	1	FETP_ECOLI	Q0a8p3 escherichia
12	380	82.4	90	1	FETP_SHIFL	Q57k04 shigella fl
13	380	82.4	90	1	FETP_SALCH	Q5pmu1 salmonella
14	380	82.4	90	1	FETP_SALPA	Q5pmu1 salmonella
15	380	82.4	90	1	FETP_SALTI	P67617 salmonella
16	380	82.4	90	1	FETP_SALTY	P67617 salmonella
17	379	82.2	90	1	FETP_PHOPR	Q6lmk7 photobacter
18	378	82.0	90	1	FETP_ECOL6	Q8fel9 escherichia
19	371	80.5	90	1	FETP_YERPS	Q66m3 yersinia ps
20	363	78.7	90	1	FETP_YERPS	Q8zhe7 yersinia ps
21	361	78.3	90	1	FETP_YIBF1	Q5e7c0 vibrio fisc
22	356	77.2	92	1	FETP_SHEON	Q8ebx6 shewanella
23	353	76.6	90	1	FETP_ERWCT	Q6d8j9 erwinia car
24	348	75.5	90	1	FETP_PHOOL	Q5n7i1 photorhabdu
25	330	71.6	90	1	FETP_IDILO	Q5gy58 bidimarinia
26	256	55.5	77	1	FETP_BUCAL	P57618 buchnera ap
27	256	55.5	90	1	FETP_BORBR	Q7wh06 bordetella
28	256	55.5	90	1	FETP_BORPA	Q7w9q2 bordetella
29	256	55.5	90	1	FETP_BORPE	Q7wvc4 bordetella
30	244	52.9	91	1	FETP_XANAC	Q8pjh7 xanthomonas
31	243	52.7	90	1	FETP_NITEU	Q82xf2 nitrosomona

32	241	52.3	90	1	FETP_XYLFT	Q87d06 xylella fas
33	241	52.3	91	1	FETP_BURMA	Q62i19 burkholderi
34	241	52.3	91	1	FETP_BURPS	Q63sj4 burkholderi
35	239.5	52.0	89	1	FETP_LEGPL	Q5wvc4 legionella
36	239	51.8	92	1	FETP_XANOR	Q5gy22 xanthomonas
37	237	51.4	90	1	FETP_XYLPA	Q9pc73 xylella fas
38	236	51.2	90	1	FETP_PSEAB	Q9hu36 pseudomonas
39	236	51.2	90	2	Q4J228_AZOV1	Q4j228 azotobacter
40	235.5	51.1	89	1	FETP_LEGPA	Q5x3x9 legionella
41	235.5	51.1	89	1	FETP_LEGPH	Q5zu80 legionella
42	235	51.0	92	1	FETP_XANCP	Q8p829 xanthomonas
43	235	51.0	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
44	232	50.3	91	1	FETP_RALSO	Q8y010 ralstonia s
45	231	50.1	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
46	230	49.9	78	1	FETP_WIGBR	Q8d3c5 wigglewort
47	230	49.9	90	1	FETP_PSESM	Q87uf5 pseudomonas
48	230	49.9	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
49	230	49.9	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
50	229	49.7	90	1	FETP_PSEPK	Q88r49 pseudomonas
51	227	49.2	88	1	FETP_NEIG1	Q5f553 neisseria g
52	227	49.2	88	1	FETP_NEIMA	P67615 neisseria m
53	227	49.2	88	1	FETP_NEIMB	P67616 neisseria m
54	224	48.6	90	1	FETP_COXBU	Q83d06 coxiella bu
55	224	48.6	90	1	FETP_METCA	Q60aj7 methylococc
56	221	47.9	90	2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
57	214	46.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
58	214	46.4	90	1	FETP_CHRVO	Q7nsr4 chromobacte
59	212	46.0	78	1	FETP_BUCAP	Q8k925 buchnera ap
60	211.5	45.9	90	1	FETP_AC1AD	Q6ffb3 acinetobact
61	209	45.3	79	1	FETP_CANBF	Q7vr99 candidatus
62	192	41.6	87	1	FETP_FRATT	Q5nhj8 francisella
63	154	33.4	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
64	146	31.7	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	77.5	16.8	416	2	Q89KZ1_BRAJA	Q89kz1 bradyrhizob
66	76.5	16.6	187	2	Q9HBF7_HUMAN	Q9hbf7 homo sapien
67	76.5	16.6	218	2	Q7SPV9_9BETR	Q7spv9 human betar
68	76.5	16.6	281	2	Q6PG71_MOUSE	Q6pg71 mus musculu
69	76.5	16.6	372	2	Q85648_9BETR	Q85648 mouse mamma
70	76.5	16.6	452	2	Q7SPV8_9BETR	Q7spv8 human betar
71	76.5	16.6	590	1	GAG_MMTVC	P10258 mouse mamma
72	76.5	16.6	590	1	GAG_MMTVC	P11284 mouse mamma
73	76.5	16.6	591	2	Q83391_9BETR	Q83391 mouse mamma
74	76.5	16.6	591	2	Q91ZT6_9BETR	Q91zt6 exogenous m
75	76.5	16.6	591	2	Q91ZU1_9BETR	Q91zui endogenous m

ALIGNMENTS

RESULT 1
FETP_HAEIN
ID FETP_HAEIN STANDARD; PRT; 90 AA.
AC P44048;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=HI0760;
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellales; Haemophilus.
OX NCBI_TaxID=727;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G.G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Uitterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,


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RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RN [2]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=20137488; PubMed=10675023;
RX DOI=10.1002/(SICI)1522-2683(20000101)21:2<411::AID-ELPS411>3.3.CO;2-W;
RA Langen H., Takacs B., Evers S., Berndt P., Lahm H.W., Wipf B.,
RA Gray C., Fountoulakis M.;
RT "Two-dimensional map of the proteome of Haemophilus influenzae.";
RL Electrophoresis 21:411-429(2000).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC EMBL, U32760; AAC22419.1; -; Genomic_DNA.
DR PIR, C64013; C64013.
DR SMR, P44048; 1-87.
DR TIGR, H10760; -.
DR HAMAP, MF_00686; -; 1.
DR InterPro, IPR007457; YggX.
DR Pfam, PF04362; DUF495; 1.
DR PIRSF, PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom, PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCYLLKKEAEGDLFQLYPGLGKRIFDSVSKQAWGEWIKQTMLVNEKQLNMWNA 60
Db 1 MARTVFCYLLKKEAEGDLFQLYPGLGKRIFDSVSKQAWGEWIKQTMLVNEKQLNMWNA 60
QY 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87
Db 61 EHRKLLQEMVNFLEFGKDVHIEGYVP 87

RESULT 2
Q4QMD9_HAE18
ID Q4QMD9_HAE18 PRELIMINARY; PRT; 90 AA.
AC Q4QMD9;
DT 13-SEP-2005 (TReMBLrel. 31, Created)
DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
DE Hypothetical protein.
OS OrderedLocustNames=NTHI0920;
ON Haemophilus influenzae (strain 86-028NP).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=281310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15968074; DOI=10.1128/JB.187.13.4627-4636.2005;
RA Harrison A., Dyer D.W., Gillaspay A., Ray W.C., Mungur R., Carson M.B.,
RA Zhong H., Gipson J., Gipson M., Johnson L.S., Lewis L., Bakaletz L.O.,
RA Munson R.S. Jr.;
RT "Genomic sequence of an otitis media isolate of nontypeable
RT Haemophilus influenzae: comparative study with H. influenzae serotype
RT J. Bacteriol. 187:4627-4636(2005).
RL EMBL, CP000057; AAX87808.1; -; Genomic DNA.

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DR InterPro;IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 90 AA; 10582 MW; EB34CEFF7737B93B CRC64;

Query Match 100.0%; Score 461; DB 2; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.8e-39;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCEYLKKEAGLDLQLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKLLNMNA 60
   |||||
Db 1 MARTVFCEYLKKEAGLDLQLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKLLNMNA 60
   |||||

61 EHRKLLQEWMVNFLEGGKDVHIEGYVP 87
   |||||
61 EHRKLLQEWMVNFLEGGKDVHIEGYVP 87
   |||||

RESULT 3
FETP_MANSM STANDARD; PRT; 91 AA.
ID FETP_MANSM
AC Q65VT7;
DT 13-SEP-2005 (Rel. 48, Created)
DT 13-SEP-2005 (Rel. 48, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=MS0316;
OS Mannheimia succiniciproducens (strain MBE155E).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Mannheimia.
OX NCBI_TaxID=221988;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=15378067; DOI=10.1038/nbt1010;
RA Hong S.H., Kim J.S., Lee S.Y., In Y.H., Choi S.S., Rih J.-K.,
RA Kim C.H., Jeong H., Hur C.G., Kim J.J.;
RT "The genome sequence of the capnophilic rumen bacterium Mannheimia
succiniciproducens.";
RL Nat. Biotechnol. 22:1275-1281(2004).
CC -|- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -|- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AB016827; AAU36923.1; -; Genomic_DNA.
DR SMR; Q65VT7; 1-88.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 91 AA; 10801 MW; 8190E2DA0B35AACC CRC64;

Query Match 95.2%; Score 439; DB 1; Length 91;
Best Local Similarity 90.8%; Pred. No. 3.3e-37;
Matches 79; Conservative 8; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCEYLKKEAGLDLQLYPGELGKRIFDSVSKQAWGEWIKQTMLVNEKLLNMNA 60
   |||||
Db 1 MSRTVFCEYLKKEAGLDLQLYPGELGKRIFDNISKXAWGEWIKQTMLVNEKLLNMNA 60
   |||||

61 EHRKLLQEWMVNFLEGGKDVHIEGYVP 87
   |||||
61 EHRKLLQEWMVNFLEGGKDVHIEGYVP 87
   |||||

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-7
Perfect score: 461
Sequence: 1 MARTVFCBYLKKEAGLDFO.....QEMVNFLRSGKDVHIREYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/iaa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/iaa/H_COMB.pep:*
- 4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
- 6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	372	80.7	107	2	US-09-489-039A-11962
2	371	80.5	93	2	US-09-543-681A-5443
3	236	51.2	122	2	US-09-252-991A-23355
4	214.5	46.5	92	2	US-09-328-352-5456
5	144	31.2	110	2	US-09-540-236-2859
6	76.5	16.6	591	2	US-09-370-368-8
7	70.5	15.3	959	2	US-09-543-681A-6879
8	67.5	14.6	271	2	US-09-248-796A-19265
9	67	14.5	474	2	US-09-252-991A-24473
10	67	14.5	1401	2	US-09-750-590A-2
11	66	14.3	548	2	US-09-167-299-3
12	65.5	14.2	623	2	US-10-104-047-2547
13	65	14.1	292	2	US-09-328-352-5836
14	65	14.1	482	2	US-09-248-796A-17800
15	64.5	14.0	415	1	US-08-602-010A-10
16	64.5	14.0	415	1	US-08-680-726A-10
17	64.5	14.0	415	2	US-09-092-409-10
18	64.5	14.0	683	2	US-09-270-767-46792
19	64	13.9	217	2	US-09-543-681A-7862
20	64	13.9	633	2	US-09-328-352-6519
21	64	13.9	680	2	US-09-298-924-4
22	64	13.9	720	1	US-08-840-236-1
23	64	13.9	720	1	US-08-505-448A-1
24	63.5	13.8	586	2	US-09-270-767-44373
25	62.5	13.6	177	1	US-08-647-960-6
26	62.5	13.6	2285	2	US-09-308-375-2
27	62.5	13.6	2285	2	US-09-932-183A-2

28	62	13.4	337	2	US-09-270-767-41746	Sequence 41746, A
29	62	13.4	455	2	US-09-270-767-45790	Sequence 45790, A
30	62	13.4	550	2	US-09-107-532A-7201	Sequence 7201, Ap
31	62	13.4	674	2	US-08-961-083-200	Sequence 200, App
32	62	13.4	674	2	US-09-536-784-200	Sequence 200, App
33	62	13.4	674	2	US-09-765-271-200	Sequence 200, App
34	62	13.4	674	2	US-09-765-272A-200	Sequence 200, App
35	62	13.4	817	1	US-08-381-931B-2	Sequence 2, Appli
36	61.5	13.3	734	2	US-09-442-055-2	Sequence 2, Appli
37	61	13.2	191	1	US-08-468-576B-13	Sequence 13, Appl
38	61	13.2	191	1	US-08-468-579B-13	Sequence 13, Appl
39	61	13.2	191	1	US-08-468-577B-13	Sequence 13, Appl
40	61	13.2	359	1	US-09-092-770-6	Sequence 6, Appli
41	61	13.2	359	2	US-09-222-851-6	Sequence 6, Appli
42	61	13.2	359	2	US-10-265-062-6	Sequence 6, Appli
43	61	13.2	404	1	US-09-092-770-3	Sequence 3, Appli
44	61	13.2	404	2	US-09-222-851-3	Sequence 3, Appli
45	61	13.2	404	2	US-10-265-062-3	Sequence 3, Appli
46	61	13.2	407	2	US-09-949-016-11184	Sequence 11184, A
47	61	13.2	625	2	US-09-949-016-8485	Sequence 8485, Ap
48	61	13.2	625	2	US-09-949-016-8810	Sequence 8810, Ap
49	60.5	13.1	279	2	US-09-198-452A-221	Sequence 221, App
50	60.5	13.1	279	2	US-09-438-185A-205	Sequence 205, App
51	60.5	13.1	438	2	US-09-198-452A-985	Sequence 985, App
52	60.5	13.1	496	2	US-09-800-170-20	Sequence 20, Appl
53	60.5	13.1	547	2	US-09-438-185A-914	Sequence 914, App
54	60.5	13.1	720	2	US-09-583-110-2940	Sequence 2940, Ap
55	60.5	13.1	720	2	US-09-107-433-4193	Sequence 4193, Ap
56	60.5	13.1	782	2	US-09-710-279-2352	Sequence 2352, Ap
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62	60	13.0	443	2	US-09-134-001C-3183	Sequence 3183, Ap
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66	60	13.0	1315	2	US-08-899-595-3	Sequence 3, Appli
67	60	13.0	2101	1	US-08-466-390-4	Sequence 4, Appli
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70	60	13.0	2101	1	US-08-195-487-4	Sequence 4, Appli
71	60	13.0	2101	1	US-08-483-924-4	Sequence 4, Appli
72	60	13.0	2101	2	US-09-452-294-1	Sequence 1, Appli
73	60	13.0	2101	2	US-09-296-662-32	Sequence 32, Appl
74	60	13.0	2101	4	PCT-US93-06160-4	Sequence 4, Appli
75	60	13.0	2107	2	US-09-949-016-7646	Sequence 7646, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT FILING DATE: 2000-01-27
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR APPLICATION NUMBER: US 60/117, 747
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-7
Perfect score: 461
Sequence: 1 MARTVFCERYLKKEAGLDFQ.....QEMVNPFLFEGKDVHIEGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_Main:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	435	94.4	87	3	US-09-955-502-6 Sequence 6, Appli
3	434	94.1	91	3	US-09-955-502-5 Sequence 5, Appli
4	425	92.2	87	3	US-09-955-502-8 Sequence 8, Appli
5	387	83.9	91	3	US-09-955-502-11 Sequence 11, Appli
6	387	83.9	91	3	US-09-955-502-12 Sequence 12, Appli
7	387	83.9	91	3	US-09-955-502-13 Sequence 13, Appli
8	386	83.7	90	3	US-09-955-502-10 Sequence 10, Appli
9	385	83.5	88	3	US-09-955-502-15 Sequence 15, Appli
10	385	83.5	91	3	US-09-955-502-14 Sequence 14, Appli
11	385	83.5	91	3	US-09-955-502-16 Sequence 16, Appli
12	385	83.5	91	3	US-09-955-502-17 Sequence 17, Appli
13	378	82.0	91	3	US-09-955-502-18 Sequence 18, Appli
14	363	78.7	90	3	US-09-955-502-20 Sequence 20, Appli
15	356	77.2	88	3	US-09-955-502-9 Sequence 9, Appli
16	325	70.5	78	3	US-09-955-502-19 Sequence 19, Appli
17	256	55.5	76	3	US-09-955-502-21 Sequence 21, Appli
18	256	55.5	87	3	US-09-955-502-2 Sequence 2, Appli
19	256	55.5	87	3	US-09-955-502-3 Sequence 3, Appli
20	241	52.3	87	3	US-09-955-502-29 Sequence 29, Appli
21	241	52.3	86	3	US-09-955-502-30 Sequence 30, Appli
22	238.5	51.7	89	3	US-09-955-502-4 Sequence 4, Appli
23	237	51.4	89	3	US-09-955-502-22 Sequence 22, Appli
24	236	51.2	87	3	US-09-955-502-25 Sequence 25, Appli
25	230	49.9	90	3	US-09-955-502-23 Sequence 23, Appli
26	229	49.7	87	3	US-09-955-502-24 Sequence 24, Appli
27	227	49.2	88	3	US-09-955-502-26 Sequence 26, Appli

28	227	49.2	88	3	US-09-955-502-27	Sequence 27, Appli
29	227	49.2	88	3	US-09-955-502-28	Sequence 28, Appli
30	224	48.6	87	3	US-09-955-502-32	Sequence 32, Appli
31	224	48.6	88	3	US-09-955-502-33	Sequence 33, Appli
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35	71	15.4	503	5	US-10-450-763-46936	Sequence 46936, A
36	70.5	15.3	723	4	US-10-205-194-25	Sequence 25, Appli
37	70.5	15.3	723	4	US-10-231-913-139	Sequence 139, App
38	70.5	15.3	723	4	US-10-231-913-140	Sequence 140, App
39	70.5	15.3	723	4	US-10-342-844-22	Sequence 22, Appli
40	70.5	15.3	723	4	US-10-342-844-26	Sequence 26, Appli
41	70.5	15.3	949	4	US-10-282-122A-68563	Sequence 68563, A
42	70	15.2	226	4	US-10-424-599-246645	Sequence 246645,
43	70	15.2	1261	4	US-10-437-963-189166	Sequence 189166,
44	69.5	15.1	593	5	US-10-450-763-50306	Sequence 50306, A
45	69	15.0	507	5	US-10-282-122A-68134	Sequence 68134, A
46	68.5	14.9	2724	5	US-10-756-149-5518	Sequence 5518, Ap
47	67.5	14.6	283	4	US-10-425-114-68519	Sequence 68519, A
48	67.5	14.6	284	4	US-10-425-115-278111	Sequence 278111,
49	67	14.5	546	4	US-10-282-122A-66021	Sequence 66021, A
50	67	14.5	853	4	US-10-437-963-168426	Sequence 168426,
51	66.5	14.4	330	3	US-09-815-242-11319	Sequence 11319, A
52	66.5	14.4	730	4	US-10-282-122A-58687	Sequence 58687, A
53	66.5	14.4	730	4	US-10-231-913-141	Sequence 141, App
54	66.5	14.4	730	4	US-10-342-844-20	Sequence 20, Appli
55	66.5	14.4	765	4	US-10-078-770-84	Sequence 84, Appli
56	66.5	14.4	818	4	US-10-078-770-94	Sequence 94, Appli
57	66.5	14.4	1809	4	US-10-437-963-195972	Sequence 195972, A
58	65.5	14.2	463	4	US-10-156-761-12981	Sequence 12981, A
59	65.5	14.2	623	4	US-10-104-047-2547	Sequence 2547, Ap
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66	64.5	14.0	497	5	US-10-917-602A-57	Sequence 57, Appli
67	64.5	14.0	507	4	US-10-282-122A-69897	Sequence 69897, A
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69	64.5	14.0	527	5	US-10-917-602A-47	Sequence 47, Appli
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72	64.5	14.0	1939	5	US-10-732-923-3340	Sequence 3340, Ap
73	64.5	14.0	4097	6	US-11-097-143-237	Sequence 237, App
74	64	13.9	553	4	US-10-282-122A-47026	Sequence 47026, A
75	64	13.9	553	5	US-10-732-923-18350	Sequence 18350, A

ALIGNMENTS

RESULT 1
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; Sequence 7, Application US/099555502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus influenzae

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Title: US-09-955-502A-7
Perfect score: 461
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and is derived by analysis of the total score distribution.

SUMMARIES

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3	66.5	14.4	765	US-11-120-308-84	Sequence 84, Appl
4	66.5	14.4	818	US-11-120-308-94	Sequence 94, Appl
5	65.5	14.2	623	US-11-072-512-2547	Sequence 2547, App
6	62.5	13.6	577	US-11-072-175-187	Sequence 187, App
7	61	13.2	342	US-11-156-084-25	Sequence 25, Appl
8	61	13.2	342	US-11-156-084-44	Sequence 44, Appl
9	61	13.2	359	US-11-087-227-8	Sequence 8, Appl
10	61	13.2	359	US-11-192-450-6	Sequence 6, Appl
11	61	13.2	369	US-11-156-084-45	Sequence 45, Appl
12	61	13.2	404	US-11-087-227-6	Sequence 6, Appl
13	61	13.2	404	US-11-192-450-3	Sequence 3, Appl
14	61	13.2	619	US-11-156-084-24	Sequence 24, Appl
15	60.5	13.1	285	US-10-467-657-222	Sequence 222, App
16	60.5	13.1	285	US-10-467-657-8230	Sequence 8230, App
17	60.5	13.1	496	US-11-069-642-20	Sequence 20, Appl
18	60.5	13.1	782	US-10-793-626-2352	Sequence 2352, App
19	60	13.0	319	US-10-793-626-2760	Sequence 2760, App
20	60	13.0	465	US-10-873-528-164	Sequence 164, App
21	60	13.0	2101	US-10-857-780-23	Sequence 23, Appl
22	59	12.8	834	US-10-453-372-658	Sequence 658, App
23	59	12.8	1734	US-11-192-967-6	Sequence 6, Appl
24	59	12.8	1734	US-11-193-715-6	Sequence 6, Appl
25	58.5	12.7	253	US-10-724-598-28	Sequence 28, Appl

26	58.5	12.7	466	US-10-524-647-114	Sequence 114, App
27	58.5	12.7	466	US-10-524-972-102	Sequence 102, App
28	58.5	12.7	729	US-10-511-538-101	Sequence 101, App
29	58.5	12.7	774	US-11-070-627-7	Sequence 7, Appl
30	58	12.6	296	US-11-087-227-10	Sequence 10, Appl
31	58	12.6	452	US-10-467-9628-14	Sequence 14, Appl
32	57.5	12.5	305	US-11-156-084-178	Sequence 178, App
33	57.5	12.5	635	US-11-098-686-10433	Sequence 10433, A
34	57.5	12.5	650	US-10-467-657-1948	Sequence 1948, App
35	57	12.4	336	US-10-453-372-640	Sequence 640, App
36	57	12.4	391	US-11-207-626A-16	Sequence 16, Appl
37	57	12.4	391	US-11-207-626A-27	Sequence 27, Appl
38	57	12.4	695	US-10-453-372-648	Sequence 648, App
39	57	12.4	700	US-10-995-561-922	Sequence 922, App
40	57	12.4	700	US-10-995-561-924	Sequence 924, App
41	57	12.4	775	US-10-453-372-656	Sequence 656, App
42	57	12.4	793	US-10-995-561-925	Sequence 925, App
43	57	12.4	804	US-10-453-372-650	Sequence 650, App
44	57	12.4	847	US-10-453-372-654	Sequence 654, App
45	57	12.4	857	US-10-453-372-652	Sequence 652, App
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50	57	12.4	963	US-10-453-372-660	Sequence 660, App
51	57	12.4	1012	US-10-453-372-646	Sequence 646, App
52	56.5	12.3	349	US-10-821-234-1387	Sequence 1387, App
53	56.5	12.3	411	US-11-072-512-3452	Sequence 3452, App
54	56.5	12.3	1766	US-11-075-185-10	Sequence 10, Appl
55	55.5	12.0	250	US-11-098-686-11014	Sequence 11014, A
56	55.5	12.0	268	US-10-995-561-718	Sequence 718, App
57	55.5	12.0	299	US-11-156-084-288	Sequence 288, App
58	55.5	12.0	301	US-11-055-822-1062	Sequence 1062, App
59	55.5	12.0	355	US-10-995-561-720	Sequence 720, App
60	55.5	12.0	739	US-10-131-826A-478	Sequence 478, App
61	55	11.9	266	US-09-995-493-6	Sequence 6, Appl
62	55	11.9	279	US-11-098-686-10812	Sequence 10812, A
63	55	11.9	504	US-11-072-512-3467	Sequence 3467, App
64	55	11.9	560	US-11-131-479-16	Sequence 16, Appl
65	54.5	11.8	242	US-11-022-562-220	Sequence 220, App
66	54.5	11.8	1299	US-10-821-234-1145	Sequence 1145, App
67	54	11.7	139	US-10-793-626-1310	Sequence 1310, App
68	54	11.7	175	US-09-978-360A-762	Sequence 762, App
69	54	11.7	175	US-10-821-234-1522	Sequence 1522, App
70	54	11.7	175	US-10-821-175-206	Sequence 206, App
71	54	11.7	177	US-10-467-657-1658	Sequence 1658, App
72	54	11.7	254	US-11-072-512-3198	Sequence 3198, App
73	54	11.7	403	US-11-192-450-4	Sequence 4, Appl
74	54	11.7	603	US-10-770-726-75	Sequence 75, Appl
75	54	11.7	1122	US-10-467-657-6112	Sequence 6112, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match 49.2%; Score 227; DB 6; Length 88;
Best Local Similarity 50.0%; Pred. No. 1.9e-19;
Matches 44; Conservative 17; Mismatches 25; Indels 2; Gaps 2;

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QY 61 EHRKLLQEMVNFLLF-EGKDVHIEGYVP 87
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RESULT 2
US-11-194-246-317

; Sequence 317, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John

; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Staffan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND MET
; TITLE OF INVENTION: USE
; FILE REFERENCE: 00592.US1 (M&R 268, 05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; PRIOR FILING DATE: 2005-08-01
; PRIOR APPLICATION NUMBER: US/10/274,586
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 60/345,438
; PRIOR FILING DATE: 2001-10-19
; NUMBER OF SEQ ID NOS: 621
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 317
; LENGTH: 593
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; ORGANISM: HAEMOPHILUS INFLUENZAE
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Db 293 ESKSKQEWRYWEAKQDILKNTKLTALSKS 322

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; Sequence 84, Application US/11120308
; Publication No. US20060005277A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13

; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 84
; LENGTH: 765
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-11-120-308-84

Query Match 14.4%; Score 66.5; DB 7; Length 765;
Best Local Similarity 25.0%; Pred. No. 7.4;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

QY 7 CEVLKKAEGLDPLYP-----PGLGK-----RIFDSVSKQAW--GEW-----I 43
Db 43 CHYTKATVDGISFDLYDAYVKAEEGKPDYARIVEMFETVDKELYPGSAQWFFRAEDTVI 102

QY 44 KKQTMLVNEKKL 55
Db 103 KSOAHLIDKRRV 114

RESULT 4
US-11-120-308-94

; Sequence 94, Application US/11120308
; Publication No. US20060005277A1
; GENERAL INFORMATION:
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Forge, Charlie
; APPLICANT: Miao, Guo-Hua
; TITLE OF INVENTION: CDNAS Encoding Polypeptides
; FILE REFERENCE: BB-1365 US NA
; CURRENT APPLICATION NUMBER: US/11/120,308
; CURRENT FILING DATE: 2005-05-02
; PRIOR APPLICATION NUMBER: US/10/078,770
; PRIOR FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/614,188
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: 60/143,400
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/153,534
; PRIOR FILING DATE: 1999-09-13
; PRIOR APPLICATION NUMBER: 60/161,223
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/159,878
; PRIOR FILING DATE: 1999-10-15
; PRIOR APPLICATION NUMBER: 60/157,401
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/143,419
; PRIOR FILING DATE: 1999-07-12
; PRIOR APPLICATION NUMBER: 60/143,409
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 196
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 94
; LENGTH: 818
; TYPE: PRT
; ORGANISM: Helianthus tuberosus
US-11-120-308-94

Query Match 14.4%; Score 66.5; DB 7; Length 818;
Best Local Similarity 25.0%; Pred. No. 8;
Matches 18; Conservative 14; Mismatches 17; Indels 23; Gaps 4;

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 : Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARMVFCEYLKKEAEGLDFO.....AEMVNFLPEGKVDHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	87	5	ABB78153 Amino aci
2	425	92.0	87	5	ABB78152 Amino aci
3	416	90.0	87	5	ABB78151 Amino aci
4	412	89.2	91	5	ABB78150 Amino aci
5	375	81.2	90	5	ABB78155 Amino aci
6	373	80.7	91	5	ABB78158 Amino aci
7	373	80.7	91	5	ABB78157 Amino aci
8	373	80.7	91	5	ABB78156 Amino aci
9	371	80.3	88	5	ABB78160 Amino aci
10	371	80.3	91	5	ABB78161 Amino aci
11	371	80.3	91	5	ABB78159 Amino aci
12	371	80.3	91	5	ABB78162 Amino aci
13	371	80.3	107	7	ABO65445 Klebsiell
14	367	79.4	93	7	ADF05158 Bacteri
15	364	78.8	91	5	ABB78163 Amino aci
16	351	76.0	90	5	ABB78165 Amino aci
17	336	72.7	88	5	ABB78154 Amino aci
18	327	70.8	78	5	ABB78164 Amino aci
19	255	55.2	87	5	ABB78175 Amino aci
20	249	53.9	87	5	ABB78174 Amino aci
21	247	53.5	76	5	ABB78166 Amino aci
22	243	52.6	87	5	ABB78148 Amino aci
23	243	52.6	87	5	ABB78147 Amino aci
24	237	51.3	88	5	ABB78178 Amino aci

25	235.5	51.0	90	5	ABB78167 Amino aci	Abb78167 Amino aci
26	235	50.9	88	5	ABB78171 Amino aci	Abb78171 Amino aci
27	235	50.9	88	5	ABB78172 Amino aci	Abb78172 Amino aci
28	235	50.9	88	5	ABB78173 Amino aci	Abb78173 Amino aci
29	235	50.9	88	6	ABP77219 Amino aci	Abp77219 N. gonorr
30	225.5	48.8	86	5	ABB78149 Amino aci	Abb78149 Amino aci
31	224.5	48.6	89	9	ABB41576 Amino aci	Aeb41576 L. pneumo
32	224.5	48.1	95	9	ABB38294 Amino aci	Aeb38294 L. pneumo
33	222	48.1	87	5	ABB78170 Amino aci	Abb78170 Amino aci
34	222	48.1	122	7	ABO74609 Pseudomon	AbO74609 Pseudomon
35	221	47.8	90	5	ABB78168 Amino aci	Abb78168 Amino aci
36	219	47.4	87	5	ABB78169 Amino aci	Abb78169 Amino aci
37	211.5	45.8	92	6	ADA34169 Acinetoba	Ada34169 Acinetoba
38	211	45.7	87	5	ABB78176 Amino aci	Abb78176 Amino aci
39	205	44.4	87	5	ABB78177 Amino aci	Abb78177 Amino aci
40	143	31.0	110	8	ADL05173 Bacteri	Adl05173 M. catarr
41	76	16.5	217	7	ADF07577 Bacteri	Adf07577 Bacteri
42	74	16.0	1144	8	ADS44344 Bacteri	Ada44344 Bacteri
43	71	15.4	292	6	ADA34549 Acinetoba	Ada34549 Acinetoba
44	70	15.2	506	3	AAV74371 Neisseria	Aay74371 Neisseria
45	70	15.2	975	5	ABP66068 Bifidobac	Abp66068 Bifidobac
46	68.5	14.8	476	3	AAV54039 Amino aci	Aay54039 Amino aci
47	68.5	14.8	476	5	ABG92539 Platelet	Abg92539 Platelet
48	68.5	14.8	476	7	ADG34449 Platelet	Adg34449 Platelet
49	68.5	14.8	503	2	AAR22667 50 kd sub	Aar22667 50 kd sub
50	68	14.7	2206	3	AAB18254 Plasmodi	Ab18254 Plasmodi
51	67.5	14.6	507	6	ABU19863 Protein e	Abu19863 Protein e
52	67.5	14.6	765	6	ADA20715 Artichoke	Ada20715 Artichoke
53	67.5	14.6	818	6	ADA20725 Artichoke	Ada20725 Artichoke
54	67.5	14.6	1233	6	ADA36587 Acinetoba	Ada36587 Acinetoba
55	67	14.5	507	6	ABU40210 Protein e	Abu40210 Protein e
56	66.5	14.4	226	9	AEB40601 L. pneumo	Aeb40601 L. pneumo
57	66.5	14.4	234	9	AEB37277 L. pneumo	Aeb37277 L. pneumo
58	66.5	14.4	415	2	AAW22982 Canine he	Aaw22982 Canine he
59	66.5	14.4	415	2	AAW72649 Canine he	Aaw72649 Canine he
60	66.5	14.4	415	4	AAW51306 Canine he	Aaw51306 Canine he
61	66.5	14.4	415	7	AAE39123 CHV PCyG	Aae39123 CHV PCyG
62	66.5	14.4	1232	6	ABU17270 Protein e	Abu17270 Protein e
63	66	14.3	149	6	ABU25552 Protein e	Abu25552 Protein e
64	66	14.3	150	6	ABU29530 Protein e	Abu29530 Protein e
65	66	14.3	154	7	ADC94984 E. faeciu	Adc94984 E. faeciu
66	66	14.3	167	2	AAR14362 E.histoly	Aar14362 E.histoly
67	65.5	14.2	511	6	ABU22540 Protein e	Abu22540 Protein e
68	65.5	14.2	567	4	AAW00976 Human bon	Aam00976 Human bon
69	65.5	14.2	591	2	AAV41141 Mouse mam	Aay41141 Mouse mam
70	65.5	14.2	860	2	AAV41140 Mouse mam	Aay41140 Mouse mam
71	65.5	14.2	1755	2	AAV41139 Mouse mam	Aay41139 Mouse mam
72	65	14.1	217	7	ADF07364 Bacteri	Adf07364 Bacteri
73	65	14.1	330	4	ABB57984 Drosophil	Abb57984 Drosophil
74	65	14.1	471	7	ADE62425 Human Pro	Ade62425 Human Pro
75	65	14.1	471	7	ADE62433 Human Pro	Ade62433 Human Pro

ALIGNMENTS

RESULT 1
ABB78153 standard; protein; 87 AA.
XX ABB78153;
DT 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent Yggx homologues
XX
SQ Sequence 87 AA;

Query Match 100.0%; Score 462; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 1.1e-46;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MARWVFCEYLKKEAEGLDFOLYPGLGKRIFNSISKQAWAEWIKQTMLVNEKCLNMNP 60
|||
Db 1 MARWVFCEYLKKEAEGLDFOLYPGLGKRIFNSISKQAWAEWIKQTMLVNEKCLNMNP 60
61 EHRQLLEAEMVNFLFEGKDVHIDGYVP 87
|||
61 EHRQLLEAEMVNFLFEGKDVHIDGYVP 87

RESULT 2
ABB78152
ID ABB78152 standard; protein; 87 AA.
XX
AC ABB78152;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a Yggx homologue.
XX
KW Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; Yggx homologue.
XX
OS Haemophilus influenzae.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. Yggx reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent Yggx homologues
XX
SQ Sequence 87 AA;

Query Match 92.0%; Score 425; DB 5; Length 87;
Best Local Similarity 90.8%; Pred. No. 2.6e-42;
Matches 79; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 1 MARWVFCEYLKKEAEGLDFOLYPGLGKRIFNSISKQAWAEWIKQTMLVNEKCLNMNP 60
|||
Db 1 MARWVFCEYLKKEAEGLDFOLYPGLGKRIFDSVSKQAWGEWIKQTMLVNEKCLNMNA 60
61 EHRQLLEAEMVNFLFEGKDVHIDGYVP 87
|||
61 EHRQLLEQEMVNFLFEGKDVHIEGYVP 87

RESULT 3
ABB78151
ID ABB78151 standard; protein; 87 AA.
XX
AC ABB78151;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a Yggx homologue.
XX
KW Superoxide damage; cell; Yggx; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; Yggx homologue.
XX
OS Pasteurella multocida.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more Yggx protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of Yggx protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARWVPCGYLKKEAGLDPO.....AEMVNFLEGGKVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	425	92.0	90	2	C64013	hypothetical prote
2	375	81.2	90	2	C82320	conserved hypotet
3	373	80.7	91	2	A85954	hypothetical prote
4	373	80.7	91	2	A65082	hypothetical prote
5	373	80.7	91	2	F91108	hypothetical prote
6	371	80.3	91	2	AH0879	conserved hypotet
7	351	76.0	90	2	AI0116	conserved hypotet
8	247	53.5	93	2	E84994	hypothetical prote
9	246	53.2	105	2	C82624	conserved hypotet
10	235	50.9	88	2	H81014	conserved hypotet
11	222	48.1	90	2	H83003	conserved hypotet
12	74	16.0	1024	2	T41415	probable leucine p
13	71	15.4	1111	2	T23047	hypothetical prote
14	70	15.2	946	2	T31488	hypothetical prote
15	69	14.9	241	2	T27636	hypothetical prote
16	69	14.9	317	1	A31797	Spec-related prote
17	69	14.9	593	2	C64097	probable soluble l
18	69	14.9	629	2	T28217	hypothetical prote
19	68.5	14.8	394	2	B70206	hypothetical prote
20	68.5	14.8	1526	2	AC2239	WD-40 repeat prote
21	68	14.7	225	2	C88939	protein C05E4.8 (l
22	68	14.7	2206	2	G71611	hypothetical prote
23	67	14.5	1119	2	T18491	hypothetical prote
24	66.5	14.4	1206	2	E96507	hypothetical prote
25	66	14.3	300	2	T32681	hypothetical prote
26	66	14.3	358	2	T34382	hypothetical prote
27	66	14.3	472	2	S74886	phytoene dehydrog
28	65.5	14.2	399	2	T31789	hypothetical prote
29	65.5	14.2	591	1	FOVMVM	gag polypotein -

30	65	14.1	394	2	T22868	hypothetical prote
31	65	14.1	507	2	C81063	fumurate hydratase
32	65	14.1	546	2	A81807	hypothetical prote
33	65	14.1	796	2	T43782	hypothetical prote
34	64.5	14.0	94	2	S17449	probable ligand-bi
35	64.5	14.0	416	2	S19896	plasmidogen activa
36	64.5	14.0	996	2	A71080	hypothetical prote
37	64.5	14.0	1008	2	H72310	conserved hypotet
38	64.5	14.0	1150	2	G89881	pyruvate carboxyla
39	64	13.9	258	2	S58159	hypothetical prote
40	64	13.9	274	2	S04610	gene 2 protein - p
41	64	13.9	696	2	D95206	hypothetical prote
42	63.5	13.7	348	2	H70337	conserved hypotet
43	63.5	13.7	363	2	S73661	hypothetical prote
44	63.5	13.7	713	2	D71631	hypothetical prote
45	63.5	13.7	1121	2	T25715	hypothetical prote
46	63.5	13.7	1613	2	G64488	reverse gyrase (in
47	63	13.6	251	2	B90428	hypothetical prote
48	63	13.6	253	2	F85060	hypothetical prote
49	63	13.6	474	2	S16250	phytoene dehydrog
50	63	13.6	577	2	A64131	arginine-tRNA liga
51	63	13.6	961	2	T01167	hypothetical prote
52	63	13.6	2672	2	A48126	translation activa
53	62.5	13.5	236	2	F69866	tetrahydridipicoli
54	62.5	13.5	330	1	B64561	ketol-acid reducto
55	62.5	13.5	383	2	A49562	cartilage glycopro
56	62.5	13.5	476	2	A28439	endonuclease SceI
57	62.5	13.5	1114	2	T30299	dynein heavy chain
58	62.5	13.5	3390	1	GNWVD3	genome polypotein
59	62	13.4	501	2	A84784	hypothetical prote
60	62	13.4	507	2	A83105	probable fumarate
61	62	13.4	720	2	JC5131	glycosyltransferas
62	62	13.4	749	2	E86774	hypothetical prote
63	62	13.4	959	1	B60017	outer capsid prote
64	62	13.4	1129	2	S00097	phytochrome 4 - oa
65	61.5	13.3	330	2	S74456	regulatory protein
66	61.5	13.3	353	1	FOVGR	gag polypotein -
67	61.5	13.3	652	2	B59102	hypothetical prote
68	61.5	13.3	785	2	C64305	ansr 5'-region hyp
69	61.5	13.3	1320	2	E59092	hypothetical prote
70	61.5	13.3	1451	2	S42167	190K protein - hum
71	61	13.2	169	2	PN0560	phytochrome - long
72	61	13.2	171	2	PN0558	phytochrome - wild
73	61	13.2	220	2	S62410	hypothetical prote
74	61	13.2	326	2	AC0832	pseudouridylate sy
75	61	13.2	386	2	AG0081	conserved hypotet

ALIGNMENTS

RESULT 1

C64013 hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C:Species: Haemophilus influenzae

C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004

C:Accession: C64013

R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J.

; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.

; D.M.; Brandon, R.C.; Pine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.

Science 269, 496-512, 1995

A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,

A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.

A:Reference number: A64000; MUID:95350630; PMID:7542800

A:Accession: C64013

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-90 <TIGR>

A:Cross-references: UNIPROT:P44048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:glf

C:Superfamily: fe(ii) trafficking protein Yggx

Query Match 92.0%; Score 425; DB 2; Length 90;
Best local Similarity 90.8%; Pred. No. 9.6e-37;

Matches	79;	Conservative	4;	Mismatches	4;	Indels	0;	Gaps	0;
QY	1	MARMVFCEYLLKKKAEGLD	FQLYP	GLGKRI	FN	SISKQAWAEWIKKQ	TMLVNE	KKLNMNP	60
					:				
DB	1	MARTVFCEYLLKKKAEGLD	FQLYP	GLGKRI	FDS	SVSKQAWGEWIKKQ	TMLVNE	KKLNMNNA	60
QY	61	EHRQLLEAEMVNFLEFGK	DVHI	DGYVP					87
					:				
DB	61	EHRKLLLEQEMVNFLEFGK	DVHI	EGYVP					87

RESULT 2

conserved hypothetical protein VC0451 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)

C;Species: *Vibrio cholerae*
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C;Accession: C82320
R;Heidelberg, J.F.; Bisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, B. L., R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: C82320
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-90 <HEI>
A;Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:99654871; PIDN A;Experimental source: serogroup O1, strain N16961, biotype El Tor
C;Genetics:
A;Gene: VC0451
A;Map position: 1
C;Superfamily: fe(II) trafficking protein YggX

Query Match	81.2%;	Score 375;	DB 2;	Length 90;
Best Local Similarity	78.2%;	Pred. No. 1.3e-31;		
Matches	68;	Conservative	11;	Mismatches 8;
			Indels	0;
			Gaps	0;

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QY      1 MARWVFCEYLKKEAGLDLQLYPBGELGRIFNSISIQAWAEWIKQTMVLVNEKKLNMMNP    600
        ||| ||| :|||:|||::|||:||||:||||:|
Db      1 MARTVFCTRLOKEADGLDQLYPGELGRIFDNCIWEAQAOWTQTOMLVINEKKLNMMNDP    600
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QY	61	EHKQLLEAEWVNFLPFEGKDVHIDGYVP	87
		: :	
Db	61	EHKRLLEQEMVNFLEFGKSVHIEGYTP	87

RESULT 3

A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93)
C/Species: Escherichia coli
C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C/Accession: A85954
R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A/Reference number: A85480; MUID:21074935; PMID:11206551
A/Accession: A85954
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <STO>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; E
A/Experimental source: strain O157:H7, substrain EDL933
C/Genetics:
A/Gene: yggX
C/Superfamily: fe(II) trafficking protein YggX

Query Match	80.7%	Score 373;	DB 2;	Length 91;
Best Local Similarity	75.9%	Pred. No. 2.1e-31;		
Matches	66;	Conservative	12;	Mismatches 9;
			Indels	0;
			Gaps	0;

1 MARWVCEYLKKEAEGLDQLYPGELGRI FNSISKQAWAEWIKKQTMLVNEKKLNMNP 60

Db 1 MSRTIFCTFLQREAEQGDQFLYPGELSKRIYNISKEAWAQWQHKKQTMILNEKLMNNA 60

QY 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87

Db 61 EHRKLLEQEMVNFLEFGKEVHIIEGYTP 87

RESULT 4

hypothetical protein b2962 - *Escherichia coli* (strain K-12)
C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R./Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co.
.A./Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A./Title: The complete genome sequence of *Escherichia coli* K-12.
A./Reference number: A64720; MUID:97426617; PMID:9278503
A./Accession: A65082
A./Status: preliminary; nucleic acid sequence not shown; translation not shown
A./Molecule type: DNA
A./Residues: 1-91 <BIAT>
A./Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
A./Experimental source: Strain K-12, substrain M61655
C./Superfamily: fe(II) trafficking protein Y9gx

Query Match	80.7%;	Score 373;	DB 2;	Length 91;
Best Local Similarity	75.9%;	Pred. No. 2.1e-31;		
Matches	66;	Conservative	12;	Mismatches 9;
				Indels 0;
				Gaps 0;

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Db     1 MSRTIETCTLOREAEGODFOLYPGELGRILYEISKEAWAQWHKHOTMLINEKKLNMNNA   60
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QY	61	EHRQLLEAEWVNFLEFGKDVHIDGYVP	87
		:	
Db	61	EHRKLLEQEWVNFLEFGKEVHIEGYTP	87

RESULT 5

F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genc
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: F91108
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-91 <HAY>
A/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:BA000007; PIDN:BAB37261.1.
A/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
A/Gene: ECs3838
C/Superfamily: fe(II) trafficking protein YggX

Query Match	80.7%;	Score 373;	DB 2;	Length 91;
Best Local Similarity	75.9%;	Pred. NO. 2.1e-31;		
Matches 66;	Conservative 12;	Mismatches 9;	Indels 0;	Gaps 0;

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       ||::||::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MSRTIFCTFLQREAGGDFOLYPBGELGR IYNEISKEAQAQWQHKTMLINEKKLNMNA 60
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QY	61	EHKQLLEAMVNFLEFGKDVHIDGYVP	87
		: :	
Db	61	EHKRLLEQEMVNFLEFGKGVHIEGYTP	87

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARVFCBYLKKGAAGLDFQ.....AEMVNFLREGKDVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	462	100.0	94	1	FETP_HAEDU	O7Vkb6 haemophilus
2	425	92.0	90	1	FETP_HAEDU	P44048 haemophilus
3	425	92.0	90	2	O4QMD9_HAE18	O4qmd9 haemophilus
4	416	90.0	90	1	FETP_PASMT	O9cib9 pasteurella
5	405	87.7	91	1	FETP_MANSN	O65vt7 manheimia
6	385	83.3	90	1	FETP_VIBPA	O87115 vibrio para
7	375	81.2	90	1	FETP_VIBCH	O9kur4 vibrio chol
8	373	80.7	90	1	FETP_VIBVU	O8dcs5 vibrio vuln
9	373	80.7	90	1	FETP_VIBVY	O7mhi4 vibrio vuln
10	368	79.7	90	1	FETP_ECO57	P0a8p4 escherichia
11	368	79.7	90	1	FETP_ECOLI	P0a8p3 escherichia
12	368	79.7	90	1	FETP_SHIFL	P0a8p5 shigella fl
13	366	79.2	90	1	FETP_SALCH	O5pmn1 salmonella
14	366	79.2	90	1	FETP_SALPA	O57k04 salmonella
15	366	79.2	90	1	FETP_SALTI	P67618 salmonella
16	366	79.2	90	1	FETP_SALTY	P67617 salmonella
17	365	79.0	90	1	FETP_PHODR	O6lmk7 photobacter
18	364	78.8	90	1	FETP_ECOL6	O8fe19 escherichia
19	359	77.7	90	1	FETP_YERPS	O66m3 yersinia ps
20	354	76.6	90	1	FETP_VIBF1	O5e7t0 vibrio fisc
21	351	76.0	90	1	FETP_VIBOL	O7n711 photorhabd
22	351	76.0	90	1	FETP_YERPE	O8zhe7 yersinia pe
23	342	74.0	90	1	FETP_ERWCT	O6d8j9 erwinia car
24	338	72.7	90	1	FETP_IDILO	O5qy58 idiomarina
25	336	72.7	92	1	FETP_SHEON	O8ebx6 shewanella
26	255	55.2	91	1	FETP_BURMA	O62iu9 burkholderi
27	255	55.2	91	1	FETP_BURPS	O63sj4 burkholderi
28	250	54.1	90	1	FETP_XYLFT	O87d06 xylella fas
29	250	54.1	91	1	FETP_XANAC	O8bjh7 xanthomonas
30	248	53.7	92	1	FETP_XANOR	O5gy22 xanthomonas
31	247	53.5	77	1	FETP_BUCAI	P57618 buchnera ap

32	246	53.2	90	1	FETP_XYLPA	O9pc73 xylella fas
33	245	53.0	91	2	O41s19_9BURK	O41s19 burkholderi
34	243	52.6	90	1	FETP_BORBR	O7wh06 bordetella
35	243	52.6	90	1	FETP_BORPA	O7w9q2 bordetella
36	243	52.6	90	1	FETP_BORPE	O7wvc4 bordetella
37	241	52.2	91	1	FETP_RALSO	O8y010 ralstonia s
38	241	52.2	92	1	FETP_XANCP	O8p829 xanthomonas
39	241	52.2	92	2	O4UWI4_XANCP	O4uw14 xanthomonas
40	237	51.3	90	1	FETP_COXBU	O83d06 coxiella bu
41	235	50.9	88	1	FETP_NEIG1	O5f553 neisseria g
42	235	50.9	88	1	FETP_NEIMA	P67615 neisseria m
43	235	50.9	88	1	FETP_NEIMB	P67616 neisseria m
44	230	49.8	90	1	FETP_NITBU	O82xf2 nltrosomona
45	229	49.6	78	1	FETP_WIGBR	O8d3c5 wiggleswort
46	228.5	49.5	89	1	FETP_LEGPL	O4j228 azotobacter
47	226	48.9	90	2	O4J228_AZOVI	O5x3x9 legionella
48	224.5	48.6	89	1	FETP_LEGPA	O5zu80 pseudomonas
49	224.5	48.6	89	1	FETP_LEGPH	O87u15 pseudomonas
50	222	48.1	90	1	FETP_PSEAB	O421p3 pseudomonas
51	221	47.8	90	1	FETP_PSESM	O88r49 pseudomonas
52	221	47.8	90	2	O4ZLP3_PSESY	O8x25 buchnera ap
53	219	47.4	90	1	FETP_PSEPK	O89a44 buchnera ap
54	215	46.5	78	1	FETP_BUCBP	O6c7f6 pseudomonas
55	212	45.9	87	1	FETP_BUCBP	O4kt12 pseudomonas
56	212	45.9	90	2	O6T7F6_PSEFL	O6f1b3 acinetobact
57	210	45.5	90	2	O4KJ22_PSEBS	O7nsr4 chromobact
58	207.5	44.9	90	1	FETP_ACTAD	O5nhj8 francisella
59	206	44.6	90	1	FETP_CHRVO	O60aj7 methylococc
60	205	44.4	87	1	FETP_FRATT	O7vr99 candidatus
61	205	44.4	90	1	FETP_METCA	O4nwq4 anaeromyxob
62	204	44.2	79	1	FETP_CANBF	O4fvj7 psychrobact
63	160	34.6	92	2	O4NMQ4_9DELT	O81609 arabidopsis
64	145	31.4	96	2	O4FVJ7_9GAMM	O9rah0 nostoc sp.
65	80.5	17.4	1208	2	O8L609_ARATH	O868d5 dugesia ryu
66	80	17.3	265	2	O9RAH0_9NOSO	O74ft8 lactobacill
67	79.5	17.2	416	2	O89KZ1_BRAJA	O4u8t5 theileria a
68	76.5	16.6	655	2	O868D5_9TURB	O74889 schizosacch
69	75.5	16.3	422	2	O74UT8_LACJO	O60k14 caenorhabdi
70	74	16.0	469	2	O4U8T5_THEAN	O81jz7 plasmodium
71	74	16.0	1024	2	O74889_SCHPO	O81110 plasmodium
72	73.5	15.9	386	2	O60K14_CABBR	
73	73	15.8	175	2	O4UEM3_THEAN	
74	73	15.8	202	2	O81JZ7_PLAF7	
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ALIGNMENTS

RESULT 1
FETP_HAEDU
ID FETP_HAEDU STANDARD; PRT; 94 AA.
AC O7VKB6;
DT 05-JUL-2004 (Rel. 44, Created)
DT 13-SBP-2005 (Rel. 48, Last sequence update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=HD2003;
OS Haemophilus ducreyi.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=730;
[1]
NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=35000HP / ATCC 700724;
RA Munson R.S. Jr., Ray W.C., Mahairas G., Sabo P., Mungur R.,
RA Johnson L., Nguyen D., Wang J., Forst C., Hood L.,
RT "The complete genome sequence of Haemophilus ducreyi.",
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-regulating processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARNVFCEYLKKEAEGLDFO.....AEMVNFLEKGVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
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5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	371	80.3	107	2	US-09-489-039A-11962 Sequence 11962, A
2	367	79.4	93	2	US-09-543-681A-5443 Sequence 5443, Ap
3	222	48.1	122	2	US-09-252-991A-23355 Sequence 23355, A
4	211.5	45.8	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	143	31.0	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	76	16.5	217	2	US-09-543-681A-7862 Sequence 7862, Ap
7	71	15.4	292	2	US-09-328-352-5836 Sequence 5836, Ap
8	68.5	14.8	476	2	US-09-316-083-3 Sequence 3, Appli
9	68.5	14.8	476	2	US-09-933-700-3 Sequence 3, Appli
10	67.5	14.6	1233	2	US-09-328-352-7874 Sequence 7874, Ap
11	66.5	14.4	415	1	US-08-602-010A-10 Sequence 10, Appl
12	66.5	14.4	415	1	US-08-680-726A-10 Sequence 10, Appl
13	66.5	14.4	415	2	US-09-092-409-10 Sequence 10, Appl
14	66	14.3	154	2	US-09-107-532A-4611 Sequence 4611, Ap
15	65.5	14.2	591	2	US-09-370-368-8 Sequence 8, Appli
16	65.5	14.2	683	2	US-09-270-767-46792 Sequence 46792, A
17	65	14.1	191	2	US-09-270-767-33624 Sequence 33624, A
18	65	14.1	191	2	US-09-270-767-48841 Sequence 48841, A
19	65	14.1	217	2	US-09-543-681A-7649 Sequence 7649, Ap
20	65	14.1	754	1	US-08-941-262-1 Sequence 1, Appli
21	64	13.9	360	2	US-10-037-417-67 Sequence 67, Appl
22	64	13.9	674	2	US-08-961-083-200 Sequence 200, App
23	64	13.9	674	2	US-09-536-784-200 Sequence 200, App
24	64	13.9	674	2	US-09-765-271-200 Sequence 200, App
25	64	13.9	674	2	US-09-765-272A-200 Sequence 200, App
26	63.5	13.7	496	2	US-09-800-170-20 Sequence 20, Appl
27	63.5	13.7	623	2	US-10-104-047-2547 Sequence 2547, Ap

28	63	13.6	359	1	US-09-092-770-6	Sequence 6, Appli
29	63	13.6	359	2	US-09-222-851-6	Sequence 6, Appli
30	63	13.6	359	2	US-10-265-062-6	Sequence 6, Appli
31	63	13.6	404	1	US-09-092-770-3	Sequence 3, Appli
32	63	13.6	404	2	US-09-222-851-3	Sequence 3, Appli
33	63	13.6	404	2	US-10-265-062-3	Sequence 3, Appli
34	63	13.6	407	2	US-09-949-016-11184	Sequence 11184, A
35	62.5	13.5	365	2	US-09-949-016-7947	Sequence 7947, Ap
36	62.5	13.5	383	2	US-09-949-016-6053	Sequence 6053, Ap
37	62.5	13.5	959	2	US-09-543-681A-6879	Sequence 6879, Ap
38	62	13.4	474	2	US-09-328-352-4659	Sequence 4659, Ap
39	62	13.4	680	2	US-09-252-991A-24473	Sequence 24473, A
40	62	13.4	720	1	US-08-840-236-1	Sequence 4, Appli
41	62	13.4	720	1	US-08-505-448A-1	Sequence 1, Appli
42	62	13.4	1120	1	US-09-147-404-1	Sequence 1, Appli
43	61.5	13.3	239	2	US-09-270-767-32538	Sequence 32538, A
44	61.5	13.3	239	2	US-09-270-767-47755	Sequence 47755, A
45	61.5	13.3	337	2	US-09-270-767-41746	Sequence 41746, A
46	61	13.2	369	2	US-09-819-607-2	Sequence 2, Appli
47	61	13.2	384	2	US-09-801-876B-6	Sequence 6, Appli
48	61	13.2	384	2	US-10-254-869-6	Sequence 6, Appli
49	61	13.2	384	2	US-10-667-442-6	Sequence 6, Appli
50	61	13.2	399	2	US-09-819-607-4	Sequence 4, Appli
51	61	13.2	419	2	US-09-799-875-14	Sequence 14, Appl
52	61	13.2	482	2	US-09-248-796A-17800	Sequence 17800, A
53	61	13.2	1724	2	US-09-607-510-2	Sequence 2, Appli
54	61	13.2	1935	2	US-09-538-092-916	Sequence 916, App
55	61	13.2	1944	2	US-09-949-016-10929	Sequence 10929, A
56	61	13.2	57	2	US-09-562-737-124	Sequence 124, App
57	60.5	13.1	116	2	US-09-562-737-125	Sequence 125, App
58	60.5	13.1	205	2	US-09-080-983-19	Sequence 19, Appl
59	60.5	13.1	205	2	US-09-613-486-19	Sequence 19, Appl
60	60.5	13.1	858	2	US-09-248-796A-19082	Sequence 19082, A
61	60.5	13.1	402	2	US-09-489-039A-9252	Sequence 9252, Ap
62	60	13.0	528	2	US-10-206-576-44	Sequence 44, Appl
63	60	13.0	528	2	US-09-071-035-42	Sequence 42, Appl
64	60	13.0	547	2	US-10-206-576-42	Sequence 42, Appl
65	60	13.0	713	2	US-09-949-016-6674	Sequence 6674, Ap
66	60	13.0	737	2	US-09-949-016-7675	Sequence 7675, Ap
67	60	13.0	1003	2	US-09-991-181-33	Sequence 33, Appl
68	60	13.0	1003	2	US-09-990-444-33	Sequence 33, Appl
69	60	13.0	1003	2	US-09-997-333-33	Sequence 33, Appl
70	60	13.0	1003	2	US-09-992-598-33	Sequence 33, Appl
71	60	13.0	236	2	US-09-492-709A-342	Sequence 342, App
72	60	13.0	390	2	US-09-711-164-405	Sequence 405, App
73	59.5	12.9	396	2	US-09-328-352-5040	Sequence 5040, Ap
74	59.5	12.9				
75	59.5	12.9				

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; FILE REFERENCE: 2709.2004001
; PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match	80.3%;	Score 371;	DB 2;	Length 107;
Best Local Similarity	74.7%;	Pred. No. 1.6e-40;		
Matches 65;	Conservative 13;	Mismatches 9;	Indels 0;	Gaps 0;

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Qy      1 MARVFCBYLKKAEGLDFOLYPGELGKRIFNSISKQAAEWIKQOTMLVNEKCLNNMNP 600
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Db      17 MSRTIFCTFLQREADGDGFOLYPGELGKRINYBISKAAWAQWQHOKTMLINEKCLSMNP 760

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Qy 61 EHRQLLAEAMVNFLEFGKDVHIDGYTP 87
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Db 77 EHRKLLIQEMNQFLFEFGKDVHIEGYTP 103

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RESULT 2
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
;
; LENGTH: 93
;
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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Query Match	79.4%	Score 367;	DB 2;	Length 93;
Best Local Similarity	74.7%	Pred. No. 4.5e-40;		
Matches 65;	Conservative 10;	Mismatches 12;	Indels 0;	Gaps 0;

[illegible]

QY 61 EHRQLRAEMVNFLEGGKDVHIDGYVP 87
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Db 64 DDRKLLLEQEMVRFLFEGSHVDHIDGYTP 90

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RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-991A-23355

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Query Match	48.1%;	Score 222;	DB 2;	Length 122;
Best Local Similarity	51.1%;	Pred. No. 4.8e-21;		
Matches 45;	Conservative 14;	Mismatches 27;	Indels 2;	Gaps 2;

QY 1 MARVFCBYLKKEAGLDFQLYPGBLGKRIFNISISKQAWAEWIKKQTMVNEKKLNMMNP 60

Db 33 MSRTVMCRKYHEELPGLDRPPYPGAKGEDIYNNVSRKAWEQKHQTMLINERRLNWNA 922

Qy 61 EHRQLLEAMVNFLEFGKD-VHIDGYVP 87

Db 93 EDRKFLQEQEMDKFL-SGEDYAKADGYVP 119

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RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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Query Match	45.8%	Score 211.5;	DB 2;	Length 92;
Best Local Similarity	44.3%;	Pred. No. 7.7e-20;		
Matches 39;	Conservative 17;	Mismatches 31;	Indels 1;	Gaps 1;

QY	Db
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4	MSRQVFCRKYQKEMEGDLPAFDPGAKGQGFENNVSQKQWQEWLQHOTTLINERKRLNVFEP 63

QY	61	EHRQLLEAEMVNFLEFGKDVH-IDGYVP	87
		:: : : : : : :	
Dbo	64	EAKKFLBQREKFFNNDESVEKAGWKPF	91

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RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATARRHALIS
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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Query Match	31.0%;	Score 143;	DB 2;	Length 110;
Best Local Similarity	35.7%;	Pred. No. 8.1e-11;		
Matches 30;	Conservative 17;	Mismatches 37;	Indels 0;	Gaps 0;

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QY      4 MWFCEYLKKEABGLDFQLYPBGJGRI FNSISKQAWAEWIKQTM LVNEKKLNMNPNRHR 63
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DB     24 MWFCRYQQNLPKLPNPFPAKGGQEI QDTISAKAMNANBELQTML INEKLHLSMIDPQAK 83
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QY 64 QLLAEAMVNFLEEGKDVHIDGYVP 87
: | : | | | | | |
Db 84 KYLNEQREKFLDNGDYEKYPAGYKP 107

RESULT 6
US-09-543-681A-7862
; Sequence 7862, Application US/09543681A

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
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549.414 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARWVCEYLKKEAGLDFQ.....AEMVNFLFEGKVHIDGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA_Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	462	100.0	87	3	US-09-955-502-8
2	425	92.0	87	3	US-09-955-502-7
3	416	90.0	87	3	US-09-955-502-6
4	412	89.2	91	3	US-09-955-502-5
5	375	81.2	90	3	US-09-955-502-10
6	373	80.7	91	3	US-09-955-502-11
7	373	80.7	91	3	US-09-955-502-12
8	371	80.3	91	3	US-09-955-502-13
9	371	80.3	88	3	US-09-955-502-15
10	371	80.3	91	3	US-09-955-502-14
11	371	80.3	91	3	US-09-955-502-16
12	371	80.3	91	3	US-09-955-502-17
13	364	78.8	91	3	US-09-955-502-18
14	351	76.0	90	3	US-09-955-502-20
15	336	72.7	88	3	US-09-955-502-9
16	327	70.8	78	3	US-09-955-502-19
17	255	55.2	87	3	US-09-955-502-29
18	255	55.2	87	3	US-09-955-502-30
19	247	53.5	76	3	US-09-955-502-21
20	246	53.2	89	3	US-09-955-502-22
21	243	52.6	87	3	US-09-955-502-2
22	243	52.6	87	3	US-09-955-502-3
23	237	51.3	88	3	US-09-955-502-33
24	235	50.9	88	3	US-09-955-502-26
25	235	50.9	88	3	US-09-955-502-27
26	235	50.9	88	3	US-09-955-502-28
27	225.5	48.8	86	3	US-09-955-502-4

28	222	48.1	87	3	US-09-955-502-25	Sequence 25, Appl
29	221	47.8	90	3	US-09-955-502-23	Sequence 23, Appl
30	219	47.4	87	3	US-09-955-502-24	Sequence 24, Appl
31	211	45.7	87	3	US-09-955-502-31	Sequence 31, Appl
32	205	44.4	87	3	US-09-955-502-32	Sequence 32, Appl
33	74	16.0	1144	4	US-10-369-493-22774	Sequence 22774, A
34	68.5	14.8	476	3	US-09-774-414-3	Sequence 3, Appl
35	68.5	14.8	476	4	US-10-373-639-3	Sequence 3, Appl
36	67.5	14.6	507	4	US-10-282-122A-47787	Sequence 47787, A
37	67.5	14.6	765	4	US-10-078-770-84	Sequence 84, Appl
38	67.5	14.6	818	4	US-10-078-770-94	Sequence 94, Appl
39	67.5	14.6	1809	4	US-10-437-963-195972	Sequence 195972, A
40	67.5	14.6	2478	4	US-10-437-963-131742	Sequence 131742, A
41	67	14.5	507	4	US-10-282-122A-68134	Sequence 68134, A
42	66.5	14.4	160	4	US-10-425-115-355492	Sequence 355492, A
43	66.5	14.4	415	4	US-10-156-275-10	Sequence 10, Appl
44	66.5	14.4	1232	4	US-10-282-122A-45194	Sequence 45194, A
45	66	14.3	149	4	US-10-282-122A-53476	Sequence 53476, A
46	66	14.3	150	4	US-10-282-122A-57454	Sequence 57454, A
47	65.5	14.2	511	4	US-10-282-122A-50464	Sequence 50464, A
48	65.5	14.2	591	3	US-09-827-822-8	Sequence 8, Appl
49	65	14.1	330	6	US-11-097-143-744	Sequence 744, App
50	65	14.1	449	4	US-10-231-913-110	Sequence 110, App
51	65	14.1	471	4	US-10-231-913-109	Sequence 109, App
52	65	14.1	546	4	US-10-282-122A-66021	Sequence 66021, A
53	65	14.1	745	3	US-09-881-852-1	Sequence 1, Appl
54	65	14.1	856	4	US-10-408-765A-2006	Sequence 2006, Ap
55	64.5	14.0	206	5	US-10-510-812-76	Sequence 76, Appl
56	64.5	14.0	500	4	US-10-437-963-170681	Sequence 170681, A
57	64.5	14.0	631	4	US-10-425-115-317990	Sequence 317990, A
58	64.5	14.0	711	4	US-10-424-599-178578	Sequence 178578, A
59	64.5	14.0	1073	3	US-09-815-242-5468	Sequence 5468, Ap
60	64.5	14.0	1147	3	US-09-815-242-5468	Sequence 44391, A
61	64.5	14.0	1150	4	US-10-282-122A-44391	Sequence 35066, A
62	64	13.9	235	4	US-10-767-701-35066	Sequence 7, Appl
63	64	13.9	307	3	US-09-911-826A-7	Sequence 88, Appl
64	64	13.9	360	4	US-10-023-634-88	Sequence 67, Appl
65	64	13.9	360	4	US-10-037-417-67	Sequence 200, App
66	64	13.9	674	3	US-09-765-272-200	Sequence 200, App
67	64	13.9	674	6	US-11-106-649-200	Sequence 3656, App
68	64	13.9	696	5	US-10-472-928-3656	Sequence 45127, A
69	64	13.9	1111	5	US-10-450-763-45127	Sequence 42869, A
70	64	13.9	1183	5	US-10-450-763-42869	Sequence 46162, A
71	64	13.9	1183	5	US-10-450-763-46162	Sequence 53544, A
72	64	13.9	1183	5	US-10-437-963-189166	Sequence 189166, A
73	64	13.9	1261	4	US-10-739-930-9367	Sequence 9367, Ap
74	63.5	13.7	115	5	US-10-282-122A-46765	Sequence 46765, A
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ALIGNMENTS

RESULT 1
US-09-955-502-8
Sequence 8, Application US/099555502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downs, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 87
TYPE: PRT
ORGANISM: Haemophilus ducreyi

US-09-955-502-8

Query Match 100.0%; Score 462; DB 3; Length 87;
Best Local Similarity 100.0%; Pred. No. 4.8e-44;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARMVFCEYLKKEAEGLDFOLYPGELGKRIFNSISKQAWAEWIKQTMLVNEKKLNMNP 60
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DB 1 MARMVFCEYLKKEAEGLDFOLYPGELGKRIFNSISKQAWAEWIKQTMLVNEKKLNMNP 60

QY 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87
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DB 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87

RESULT 2

US-09-955-502-7

; Sequence 7, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 7

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Haemophilus influenzae

US-09-955-502-7

Query Match 92.0%; Score 425; DB 3; Length 87;
Best Local Similarity 90.8%; Pred. No. 6.9e-40;
Matches 79; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

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QY 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87
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DB 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87

RESULT 3

US-09-955-502-6

; Sequence 6, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 6

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Pasteurella multocida

US-09-955-502-6

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Best Local Similarity 88.5%; Pred. No. 7.1e-39;
Matches 77; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

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QY 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87
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DB 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87

RESULT 4

US-09-955-502-5

; Sequence 5, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 5

; LENGTH: 91

; TYPE: PRT

; ORGANISM: Actinobacillus actinomycetemcomitans

US-09-955-502-5

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Best Local Similarity 88.5%; Pred. No. 2.1e-38;
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QY 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87
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DB 61 EHRQLLEAMVNFLEFGKDVHIDGYVP 87

RESULT 5

US-09-955-502-10

; Sequence 10, Application US/09955502
; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnick, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: Patentin Ver. 2.1

; SEQ ID NO 10

; LENGTH: 90

; TYPE: PRT

; ORGANISM: Vibrio cholerae

US-09-955-502-10

Query Match 81.2%; Score 375; DB 3; Length 90;
Best Local Similarity 78.2%; Pred. No. 3e-34;
Matches 68; Conservative 11; Mismatches 8; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 seconds
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218.595 Million cell updates/sec

Title: US-09-955-502A-8
Perfect score: 462
Sequence: 1 MARWVFCBYLKKEAGLDFQ.....AEMVNFLEGGKDVHIDGYVP 87

Scoring table: BLOSUM62
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Searched: 117670 seqs, 14887254 residues

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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	235	50.9	88	6	US-10-467-657-968 Sequence 968, App
2	69	14.9	593	7	US-11-194-246-317 Sequence 317, App
3	67.5	14.6	765	7	US-11-120-308-84 Sequence 84, Appl
4	67.5	14.6	818	7	US-11-120-308-94 Sequence 94, Appl
5	64	13.9	360	7	US-11-019-711-67 Sequence 67, Appl
6	63.5	13.7	496	7	US-11-069-642-20 Sequence 20, Appl
7	63.5	13.7	623	7	US-11-072-512-2547 Sequence 2547, Ap
8	63	13.6	359	7	US-11-087-227-8 Sequence 8, Appli
9	63	13.6	359	7	US-11-192-450-6 Sequence 6, Appli
10	63	13.6	404	7	US-11-087-227-6 Sequence 6, Appli
11	63	13.6	404	7	US-11-192-450-3 Sequence 3, Appli
12	61.5	13.3	834	6	US-10-453-372-658 Sequence 658, App
13	60	13.0	140	7	US-11-098-686-10643 Sequence 10643, A
14	60	13.0	296	7	US-11-087-227-10 Sequence 10, Appl
15	59.5	12.9	336	6	US-10-453-372-640 Sequence 640, App
16	59.5	12.9	372	7	US-11-143-980-37 Sequence 37, Appl
17	59.5	12.9	423	6	US-10-821-234-900 Sequence 900, App
18	59.5	12.9	695	6	US-10-453-372-648 Sequence 648, App
19	59.5	12.9	700	6	US-10-995-561-922 Sequence 922, App
20	59.5	12.9	700	6	US-10-995-561-924 Sequence 924, App
21	59.5	12.9	775	6	US-10-453-372-656 Sequence 656, App
22	59.5	12.9	793	6	US-10-995-561-925 Sequence 925, App
23	59.5	12.9	804	6	US-10-453-372-650 Sequence 650, App
24	59.5	12.9	847	6	US-10-453-372-654 Sequence 654, App
25	59.5	12.9	857	6	US-10-453-372-652 Sequence 652, App

26	59.5	12.9	905	6	US-10-453-372-638 Sequence 638, App
27	59.5	12.9	905	6	US-10-453-372-662 Sequence 662, App
28	59.5	12.9	905	6	US-10-453-372-664 Sequence 664, App
29	59.5	12.9	963	6	US-10-995-561-923 Sequence 923, App
30	59.5	12.9	963	6	US-10-453-372-660 Sequence 660, App
31	59.5	12.9	1012	6	US-10-453-372-646 Sequence 646, App
32	58.5	12.7	253	6	US-10-517-939-16 Sequence 28, Appl
33	58.5	12.7	369	6	US-10-517-939-16 Sequence 16, Appl
34	57.5	12.4	508	7	US-11-072-512-2186 Sequence 2186, Ap
35	57.5	12.4	760	7	US-11-186-284-55 Sequence 55, Appl
36	57.5	12.4	774	7	US-11-070-627-7 Sequence 7, Appli
37	57	12.3	650	6	US-10-467-657-1948 Sequence 1948, Ap
38	56.5	12.2	349	6	US-10-821-234-1387 Sequence 1387, Ap
39	56.5	12.2	1734	7	US-11-192-967-6 Sequence 6, Appli
40	56.5	12.2	1734	7	US-11-193-715-6 Sequence 6, Appli
41	56.5	12.2	1822	7	US-11-169-041-193 Sequence 94, App
42	56	12.1	209	5	US-09-995-493-94 Sequence 25, Appl
43	56	12.1	342	7	US-11-156-084-25 Sequence 44, Appl
44	56	12.1	342	7	US-11-156-084-44 Sequence 44, Appl
45	56	12.1	369	7	US-11-156-084-45 Sequence 45, Appl
46	56	12.1	619	7	US-11-156-084-24 Sequence 24, Appl
47	55.5	12.0	301	7	US-11-055-822-1062 Sequence 1062, Ap
48	55.5	12.0	382	6	US-10-995-561-926 Sequence 926, App
49	55.5	12.0	415	6	US-10-995-561-927 Sequence 927, App
50	55.5	12.0	415	7	US-11-219-282-10 Sequence 10, Appl
51	55.5	12.0	1613	7	US-11-108-528-84 Sequence 84, Appl
52	55.5	12.0	1613	7	US-11-108-528-86 Sequence 86, Appl
53	55	11.9	236	7	US-11-156-084-284 Sequence 284, App
54	55	11.9	319	6	US-10-793-626-2760 Sequence 2760, Ap
55	55	11.9	443	6	US-10-793-626-1200 Sequence 1200, Ap
56	54.5	11.8	311	6	US-10-873-528-117 Sequence 117, App
57	54.5	11.8	445	7	US-11-074-176-182 Sequence 182, App
58	54.5	11.8	674	7	US-11-000-463-471 Sequence 471, App
59	54.5	11.8	782	6	US-10-793-626-2352 Sequence 2352, Ap
60	54.5	11.8	864	7	US-11-077-550-102 Sequence 102, App
61	54	11.7	175	6	US-10-821-234-1522 Sequence 1522, Ap
62	54	11.7	254	7	US-11-072-512-3198 Sequence 3198, Ap
63	54	11.7	403	7	US-11-192-450-4 Sequence 4, Appli
64	54	11.7	510	7	US-11-087-100-26 Sequence 26, Appl
65	54	11.7	510	7	US-11-087-084-26 Sequence 26, Appl
66	54	11.7	510	7	US-11-087-085-26 Sequence 26, Appl
67	54	11.7	739	6	US-10-131-826A-478 Sequence 478, App
68	54	11.7	783	7	US-11-192-219-7 Sequence 7, Appli
69	54	11.7	894	7	US-11-202-330-2 Sequence 2, Appli
70	54	11.7	1047	7	US-11-072-512-2408 Sequence 2408, Ap
71	54	11.7	1162	7	US-11-202-330-43 Sequence 43, Appl
72	54	11.7	2059	7	US-11-087-100-4 Sequence 4, Appli
73	54	11.7	2059	7	US-11-087-084-4 Sequence 4, Appli
74	54	11.7	2059	7	US-11-087-085-4 Sequence 4, Appli
75	54	11.7	2335	6	US-10-821-234-1610 Sequence 1610, Ap

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZAZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 83.9047 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFEKDVIEGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1:	geneseqp1980s:*
2:	geneseqp1990s:*
3:	geneseqp2000s:*
4:	geneseqp2001s:*
5:	geneseqp2002s:*
6:	geneseqp2003as:*
7:	geneseqp2003bs:*
8:	geneseqp2004s:*
9:	geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	100.0	88	5	ABB78154 Amino aci
2	356	76.4	87	5	ABB78152 Amino aci
3	347	74.5	90	5	ABB78155 Amino aci
4	346	74.2	93	7	ADP05158 Bacterial
5	345	74.0	87	5	ABB78151 Amino aci
6	344	73.8	91	5	ABB78150 Amino aci
7	336	72.1	87	5	ABB78153 Amino aci
8	336	72.1	88	5	ABB78160 Amino aci
9	336	72.1	91	5	ABB78161 Amino aci
10	336	72.1	91	5	ABB78159 Amino aci
11	336	72.1	91	5	ABB78162 Amino aci
12	332	71.2	91	5	ABB78158 Amino aci
13	332	71.2	91	5	ABB78157 Amino aci
14	332	71.2	91	5	ABB78156 Amino aci
15	327	70.2	107	7	ABO65445 KLebsiell
16	326	70.0	91	5	ABB78163 Amino aci
17	308	66.1	90	5	ABB78165 Amino aci
18	292	62.7	78	5	ABB78164 Amino aci
19	256	54.9	87	5	ABB78148 Amino aci
20	256	54.9	87	5	ABB78147 Amino aci
21	242.5	52.0	86	5	ABB78149 Amino aci
22	237	50.9	87	5	ABB78169 Amino aci
23	235	50.4	87	5	ABB78170 Amino aci
24	235	50.4	122	7	ABO74609 Pseudomon

25	230	49.4	88	5	ABB78171 Amino aci
26	230	49.4	88	5	ABB78172 Amino aci
27	230	49.4	88	5	ABB78173 Amino aci
28	230	49.4	88	6	ABP77219 N. gonorr
29	228	48.9	90	5	ABB78168 Amino aci
30	226	48.5	87	5	ABB78175 Amino aci
31	220	47.2	87	5	ABB78174 Amino aci
32	216	46.4	76	5	ABB78166 Amino aci
33	215	46.1	87	5	ABB78177 Amino aci
34	213	45.7	87	5	ABB78176 Amino aci
35	211.5	45.4	89	9	ABE41576 L. pneumo
36	211.5	45.4	95	9	ABE38294 L. pneumo
37	205	44.0	88	5	ABB78178 Amino aci
38	200.5	43.0	92	6	ADA34169 Acinetoba
39	186.5	40.0	90	5	ABB78167 Amino aci
40	130	27.9	110	8	ADL05173 M. catarr
41	77.5	16.6	2364	5	ABP65068 Hypoxia-i
42	77.5	16.6	2364	8	ABM80299 Tumour-as
43	77.5	16.6	2364	9	ADZ70337 Human pro
44	75.5	16.2	1120	2	AAW81642 Mouse elf
45	75.5	16.2	1630	2	AAW81639 Mouse elf
46	75.5	16.2	2154	2	AAW81639 Mouse elf
47	75.5	16.2	2154	7	ADP74491 Murine el
48	75.5	16.2	2154	8	ADQ88363 Mouse elf
49	75.5	16.2	2154	9	ADZ85101 Full-leng
50	68.5	14.7	352	7	ADB80553 Ovarian c
51	68	14.6	315	7	ADF83528 C. reinha
52	68	14.6	315	7	ADF83527 C. reinha
53	68	14.6	344	8	ADT71540 Human CGD
54	68	14.6	359	2	AAW43175 Human cyc
55	68	14.6	359	4	AAW72464 Human cyc
56	68	14.6	359	7	ADP48690 Human cyc
57	68	14.6	359	8	ADR14323 Human NF-
58	68	14.6	404	2	AAW43173 Human cyc
59	68	14.6	404	3	AAW77483 Human cyc
60	68	14.6	404	4	AAW72462 Human cyc
61	68	14.6	404	7	ADB67893 Human lun
62	68	14.6	404	7	ADF48687 Human cyc
63	68	14.6	404	8	ADI82506 Human mod
64	68	14.6	404	8	ADN05983 Antipsori
65	68	14.6	404	8	ADO19484 Human PRO
66	68	14.6	404	8	ADU06662 Novel bro
67	68	14.6	404	9	ADY15468 PRO polyp
68	68	14.6	737	7	ADF83524 C. reinha
69	68	14.6	737	7	ADF83526 C. reinha
70	66.5	14.3	689	8	ADS28247 Bacterial
71	66.5	14.3	1176	6	ABR53186 Protein s
72	66.5	14.3	1176	7	ADK63224 Disease t
73	66	14.2	261	8	ADP81257 Protein o
74	66	14.2	269	8	ADP81258 Protein o
75	66	14.2	307	5	ABB90271 Human pol

ALIGNMENTS

RESULT 1
ID ABB78154 standard, protein; 88 AA.
AC ABB78154;
XX 05-NOV-2002 (first entry)
XX Amino acid sequence of a YggX homologue.
DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX Unidentified.
OS US2002072118-A1.
XX PN
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 88 AA;

Query Match	100.0%;	Score 466;	DB 5;	Length 88;
Best Local Similarity	100.0%;	Pred. No. 4.8e-49;		
Matches 88;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

OY 1 MARTVNCVHLNKEADGLDLPQLYPGDLGKRI FDNISKEAWGLWQKQTMLINEKNMNV 60
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MARTVNCVHLNKEADGLDLPQLYPGDLGKRI FDNISKEAWGLWQKQTMLINEKNMNV 60

QY	61	DDRKFLAQMSTFLFEKQVELEGVPR	88
Db	61	DDRKFLAQMSTFLFEKQVELEGVPR	88

RESULT 2
ABB78152
ID ABB78152 standard; protein; 87 AA.

AC ABB78152;
XX
DT 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

OS Haemophilus influenzae.

PN US2002072118-A1.

PD 13-JUN-2002.

18-SEP-2001; 2001US-00955502.

22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.

31/10/2019 14:00

XX : 3000

DR WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.

Example; Rig 1A; 16pp; English.

xx The specification describes a method for reducing superoxide damage to a cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from *Salmonella enterica* serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from clusters. The resulting decrease in free-iron levels generates fewer hydroxyl radicals and thus reduced DNA damage. The method is useful for reducing superoxide damage in a bacterial, yeast, mammalian or plant cell. ABB78147-78 represent YggX homologues

Sequence 87 AA;

Query Match	76.4%	Score 356;	DB 5;	Length 87;
Best Local Similarity	74.7%	Pred. No. 1.4e-35;		
Matches 65; Conservative	11;	Mismatches 11;	Indels 0;	Gaps 0;

```

OY      1 MARTVNCVHLNKEADGLDLPYBDLGKRI PDNISKEAWGLMOKQOTML INEKKLMNNV 60
        ||||| : |||||:|||||||:|||||||:|||||||:|||||||:|||||||:|||||||
DB      1 MARTVFCEYLKKEAEGLDLPQLYPBGLGKRI FDSVSKQAMGEWIKQOTML VNEKKLMNNNA 60

```

```

QY      61 DDRKFLDAQNTSFLPEGQDYIEGVP 87
      : ||| : : ||||| ||| : ||
Db      61 EHRKLEQEMVNFLPEGQDYIEGVP 87

```

RESULT 3
ABB78155
ID ABB78155 standard; protein; 90 AA

ABB78155;

DT 05-NOV-2002 (first entry)

Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.

Vibrio cholerae.

AA US2002072118-A1.
PN

PD 13-JUN-2002.

18-SEP-2001; 2001US-00955502.

22-SEP-2000; 2000US-0234588P.

AA (DOWN/) DOWNS D.
PA

XX 10/25/10 09:44:30

PI Downs D, Gralnick JA;

DR WPI: 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT

PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.5846 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLPEGKDVIEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	356	76.4	90	2 C64013	hypothetical prote
2	347	74.5	90	2 C82320	conserved hypothet
3	336	72.1	91	2 AH0879	conserved hypothet
4	332	71.2	91	2 A85954	hypothetical prote
5	332	71.2	91	2 A65082	hypothetical prote
6	332	71.2	91	2 F91108	hypothetical prote
7	308	66.1	90	2 A10116	conserved hypothet
8	235	50.4	90	2 H83003	conserved hypothet
9	230	49.4	88	2 H81014	conserved hypothet
10	216	46.4	93	2 E84994	hypothetical prote
11	196	42.1	105	2 C82624	conserved hypothet
12	77.5	16.6	2364	1 A44159	spectrin beta-G ch
13	75.5	16.2	2	A47213	beta-fodrin - huma
14	70	15.0	936	2 H71728	2-oxoglutarate deh
15	68.5	14.7	412	2 S62538	hypothetical colle
16	67.5	14.5	568	2 T25859	hypothetical prote
17	67.5	14.5	1111	2 T23047	hypothetical prote
18	67	14.4	928	2 C97728	hypothetical prote
19	66.5	14.3	260	2 H82925	hypothetical prote
20	66.5	14.3	689	2 F83902	beta-galactosidase
21	66.5	14.3	1123	2 T30880	dynein heavy chain
22	66.5	14.3	1176	2 S40899	VPS8 protein - Yea
23	66	14.2	384	2 F64438	hypothetical prote
24	65.5	14.1	1021	2 AC2202	hypothetical prote
25	65	13.9	300	2 T15690	hypothetical prote
26	65	13.9	380	2 T18509	hypothetical prote
27	65	13.9	651	2 G69177	methionine-CRNA 11
28	64.5	13.8	577	1 S39804	moesin - pig
29	64.5	13.8	1119	2 T18491	hypothetical prote

30	64	13.7	365	2 C83885	hypothetical prote
31	64	13.7	578	2 T11659	hypothetical prote
32	64	13.7	964	2 T32482	hypothetical prote
33	63.5	13.6	310	2 C64370	modification methy
34	63.5	13.6	1333	2 S65812	RNA-directed DNA p
35	63.5	13.6	1492	2 T14652	protein J - Yersin
36	63.5	13.6	1545	2 T14966	phage lambda-relat
37	63	13.5	151	2 S72243	dynein heavy chain
38	63	13.5	151	2 S72245	hypothetical prote
39	63	13.5	408	2 H64513	fumarate hydratase
40	63	13.5	507	2 C81063	fumarate hydratase
41	63	13.5	546	2 A81807	DNA mismatch repair
42	63	13.5	793	2 C72219	protein unc-73b [1
43	63	13.5	1638	2 D87749	guanine nucleotide
44	63	13.5	2488	2 T42739	hypothetical prote
45	62.5	13.4	368	2 G71961	sugar-binding peri
46	62.5	13.4	432	2 C97258	hypothetical prote
47	62.5	13.4	481	2 T14300	probable threonine
48	62.5	13.4	516	2 A96753	dynein heavy chain
49	62	13.3	150	2 S72244	phytochrome - long
50	62	13.3	169	2 PNO560	phytochrome - wild
51	62	13.3	171	2 PNO558	probable translati
52	62	13.3	179	2 B71274	helper component p
53	62	13.3	486	2 B46341	probable soluble 1
54	62	13.3	593	2 C64097	hypothetical prote
55	62	13.3	679	2 E90560	DNA topoisomerase
56	62	13.3	972	2 S35521	hypothetical prote
57	62	13.3	1006	2 T00050	hypothetical prote
58	61.5	13.2	118	2 I55515	dynein-like protei
59	61.5	13.2	237	2 A71082	hypothetical prote
60	61.5	13.2	265	2 T46013	hypothetical prote
61	61.5	13.2	423	2 H84566	probable RING zinc
62	61.5	13.2	504	2 C64398	hypothetical prote
63	61.5	13.2	583	1 A41129	radixin - mouse
64	61.5	13.2	583	1 A46127	radixin - human
65	61.5	13.2	583	1 S39805	hypothetical prote
66	61.5	13.2	813	2 D64527	nucleotide diphosp
67	61.5	13.2	905	1 A27410	vsaa-like (mycopla
68	61.5	13.2	1017	2 D90550	hypothetical prote
69	61.5	13.2	1922	2 T00637	dynein heavy chain
70	61	13.1	151	2 S72239	dynein-like protei
71	61	13.1	188	2 I70176	beta-glucosidase h
72	61	13.1	477	2 G69760	helper component p
73	61	13.1	486	2 T48341	hypothetical prote
74	61	13.1	583	2 T48365	conserved hypothet
75	61	13.1	847	2 G95843	

ALIGNMENTS

RESULT 1
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kervatage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A./Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A/Reference number: A64000; MUID:95350630; PMID:7542800
A/Accession: C64013
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-90 <TIGR>
A/Cross-references: UNIPROT:P44048; UNIPARC:UP1000013B0A4; GB:U32760; GB:L42023; NID:g15.
C/Superfamily: fe(II) trafficking protein YggX

Query Match 76.4%; Score 356; DB 2; Length 90;
Best Local Similarity 74.7%; Pred. No. 1.9e-30;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 80.9081 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKEADGLDFQ.....QMTSFLFGKDVIRIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	466	100.0	92	1	PETP_SHEON
2	362	77.7	90	1	PETP_VIBVU
3	362	77.7	90	1	PETP_VIBVY
4	361	77.5	91	1	PETP_MANSM
5	360	77.3	90	1	PETP_VIBF1
6	359	77.0	90	1	PETP_PHOPR
7	356	76.4	90	1	PETP_HABIN
8	356	76.4	90	2	O4QMD9_HAB18
9	347	74.5	90	1	PETP_VIBCH
10	346	74.2	90	1	PETP_VIBPA
11	345	74.0	90	1	PETP_PASMU
12	341	73.2	90	1	PETP_IDILO
13	338	72.5	90	1	PETP_ERWCT
14	336	72.1	94	1	PETP_HABDU
15	331	71.0	90	1	PETP_SALCH
16	331	71.0	90	1	PETP_SALPA
17	331	71.0	90	1	PETP_SALTI
18	331	71.0	90	1	PETP_SALTY
19	330	70.8	90	1	PETP_ECOL6
20	327	70.2	90	1	PETP_ECOL7
21	327	70.2	90	1	PETP_ECOLI
22	327	70.2	90	1	PETP_SHIFL
23	322	69.1	90	1	PETP_PHOUL
24	316	67.8	90	1	PETP_YERPS
25	308	66.1	90	1	PETP_YERPS
26	257	55.2	90	1	PETP_NITBU
27	256	54.9	90	1	PETP_BORBR
28	256	54.9	90	1	PETP_BORPA
29	240	51.5	90	1	PETP_BORPE
30	237	50.9	90	2	Q4J228_AZOVI
31			90	1	PETP_PSEPK

32	236	50.6	91	1	PETP_RALSO	Q8Y010 ralstonia s
33	235	50.4	90	1	PETP_PSEAB	Q9hu36 pseudomonas
34	230	49.4	88	1	PETP_NEIG1	Q5f553 neisseria g
35	230	49.4	88	1	PETP_NEIMA	P67615 neisseria m
36	230	49.4	88	1	PETP_NEIMB	P67616 neisseria m
37	229	49.1	90	2	Q4KJ2_PSEPS	Q4kjt2 pseudomonas
38	228	48.9	90	1	PETP_PSESM	Q87uf5 pseudomonas
39	228	48.9	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
40	227	48.7	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
41	226	48.5	91	1	PETP_BURMA	Q62iug burkholderi
42	226	48.5	91	1	PETP_BURPS	Q63sj4 burkholderi
43	224	48.1	90	1	PETP_CHRVO	Q7nsr4 chromobacte
44	224	48.1	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
45	216	46.4	89	1	PETP_BUCAI	P57618 buchnera ap
46	215.5	46.2	89	1	PETP_LEGPL	Q5wvc4 legionella
47	215	46.1	78	1	PETP_WIGBR	Q8d3c5 wigglewort
48	215	46.1	90	1	PETP_METCA	Q60aj7 methylococc
49	213	45.7	91	1	PETP_XANAC	Q8pjh7 xanthomonas
50	211.5	45.4	89	1	PETP_LEGPA	Q5x3x9 legionella
51	211.5	45.4	89	1	PETP_LEGPH	Q5zu80 legionella
52	208	44.6	79	1	PETP_CANBF	Q7vr9g candidatus
53	206	44.2	92	1	PETP_XANOR	Q5gy22 xanthomonas
54	205	44.0	90	1	PETP_COXBU	Q83d06 coxiella bu
55	203	43.6	92	1	PETP_XANCP	Q8p829 xanthomonas
56	203	43.6	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
57	199	42.7	78	1	PETP_BUCAP	Q8k925 buchnera ap
58	197.5	42.4	90	1	PETP_AC1AD	Q6efb3 acinetobact
59	196	42.1	90	1	PETP_XYLFA	Q9pc73 xyella fas
60	196	42.1	90	1	PETP_XYLFT	Q87d06 xyella fas
61	185	39.7	87	1	PETP_FRATT	Q5nhj8 francisella
62	181	38.8	87	1	PETP_BUCBP	Q89a44 buchnera ap
63	148.5	31.9	92	2	Q4NMQ4_9DELT	Q4nwq4 anaeromyxob
64	131	28.1	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	92	19.7	507	2	Q4YI97_PLABR	Q4yi97 plasmodium
66	92	19.7	1132	2	Q4Z7L5_PLABR	Q4z7l5 plasmodium
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71	75.5	16.2	2154	2	Q9QWJ7_MOUSE	Q9qwj7 mus musculu
72	75.5	16.2	2154	2	Q5SQL7_MOUSE	Q5sql7 mus musculu
73	75.5	16.2	2314	2	Q53R99_HUMAN	Q53r99 homo sapien
74	75.5	16.2	2363	2	Q5SQL8_MOUSE	Q5sql8 mus musculu
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ALIGNMENTS

RESULT 1
PETP_SHEON
ID PETP_SHEON STANDARD; PRT; 92 AA.
AC Q8EBX6;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=SO3369;
OS Shewanella oneidensis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;
OC Shewanellaceae; Shewanella.
OX NCBI_TaxID=70863;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RP STRAIN=MR-1;
RC MEDLINE=22297686; PubMed=12368813; DOI=10.1038/nbt749;
RX Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,
Read T.D., Eissen J.A., Seshadri R., Ward N.L., Methe B.A.,
Clayton R.A., Meyer T., Tsaplin A., Scott J., Beanan M.J.,
Brinkac L.M., Daugherty S.C., DeBoy R.T., Dodson R.J., Durkin A.S.,
Hart D.H., Kolonay J.F., Madupu R., Peterson J.D., Umayam L.A.,
White O., Wolf A.M., Vamathevan J.J., Weidman J.F., Impraim M.,
Lee K., Berry K.J., Lee C., Mueller J., Khouri H.M., Gill J.,


```
RA Utterback T.R., McDonald L.A., Feldblyum T.V., Smith H.O.,
RA Venter J.C., Nealson K.H., Fraser C.M.;
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium
RT Shewanella oneidensis.";
RL Nat. Biotechnol. 20:1118-1123(2002).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE015774; AAN56367.1; -; Genomic_DNA.
DR TIGR; SO3369; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 92 AA; 10742 MW; 3116B2E995289B86 CRC64;

Query Match 100.0%; Score 466; DB 1; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.1e-42;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MARTVNCVHLNKADGLDPQLYPGDLGKRIPDNISKEAWGLMOKQTMLINEKLANMNV 60

OY 61 DDRKFLAQMTSFLFEGKDVIEGFVE 88
DB 61 DDRKFLAQMTSFLFEGKDVIEGFVE 88

RESULT 2
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DCC5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV11514;
OS Vibrio vulnificus.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of Vibrio vulnificus CMCP6.";
RT Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
RL -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; AE016801; AAC09940.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
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DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 77.7%; Score 362; DB 1; Length 90;
Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 1 MARTVNCVHLNKADGLDPQLYPGDLGKRIPDNISKEAWGLMOKQTMLINEKLANMNV 60
DB 1 MSRTVFCARLNKADGLDPQLYPGDLGKRIPDNISKEAWGOMHKQTMLINEKLANMNDP 60

OY 61 DDRKFLAQMTSFLFEGKDVIEGFVP 87
DB 61 EHRKLETEMVNFLEFGKEVHIEGYTP 87

RESULT 3
FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q7MH14;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV2885;
OS Vibrio vulnificus (Strain YJ016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chang H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-P.;
RT "Comparative genome analysis of Vibrio vulnificus, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587(2003).
RL -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; YggX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_YggX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 77.7%; Score 362; DB 1; Length 90;
Best Local Similarity 77.0%; Pred. No. 2.1e-31;
Matches 67; Conservative 8; Mismatches 12; Indels 0; Gaps 0;

OY 1 MARTVNCVHLNKADGLDPQLYPGDLGKRIPDNISKEAWGLMOKQTMLINEKLANMNV 60
DB 1 MSRTVFCARLNKADGLDPQLYPGDLGKRIPDNISKEAWGOMHKQTMLINEKLANMNDP 60

OY 61 DDRKFLAQMTSFLFEGKDVIEGFVP 87
DB 61 EHRKLETEMVNFLEFGKEVHIEGYTP 87
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.5766 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFEKDVRIEGLVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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3: /cgn2_6/ptodata/1/1aa/H_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	346	74.2	93	2	US-09-543-681A-5443 Sequence 5443, Ap
2	327	70.2	107	2	US-09-489-039A-11962 Sequence 11962, A
3	235	50.4	122	2	US-09-252-991A-23355 Sequence 23355, A
4	200.5	43.0	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	130	27.9	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	77.5	16.6	2364	2	US-09-538-092-1243 Sequence 1243, Ap
7	75.5	16.2	2154	1	US-08-841-349-4 Sequence 4, Appli
8	75.5	16.2	2154	2	US-09-431-184A-4 Sequence 4, Appli
9	68	14.6	359	1	US-09-092-770-6 Sequence 6, Appli
10	68	14.6	359	2	US-09-222-851-6 Sequence 6, Appli
11	68	14.6	359	2	US-10-265-062-6 Sequence 6, Appli
12	68	14.6	404	1	US-09-092-770-3 Sequence 3, Appli
13	68	14.6	404	2	US-09-222-851-3 Sequence 3, Appli
14	68	14.6	404	2	US-10-265-062-3 Sequence 3, Appli
15	68	14.6	407	2	US-09-949-016-11184 Sequence 11184, A
16	64	13.7	373	2	US-09-071-035-116 Sequence 116, App
17	64	13.7	373	2	US-10-206-576-116 Sequence 116, App
18	64	13.7	406	2	US-09-071-035-114 Sequence 114, App
19	64	13.7	406	2	US-10-206-576-114 Sequence 114, App
20	64	13.7	557	2	US-09-134-000C-4354 Sequence 4354, Ap
21	63	13.5	369	2	US-09-906-779-5 Sequence 5, Appli
22	62.5	13.4	182	2	US-09-248-796A-17806 Sequence 17806, A
23	62.5	13.4	278	2	US-09-567-003C-23 Sequence 23, Appli
24	62	13.3	309	2	US-09-248-796A-14939 Sequence 14939, A
25	62	13.3	525	2	US-09-540-236-2250 Sequence 2250, Ap
26	62	13.3	911	2	US-09-949-002-425 Sequence 425, Appl
27	62	13.3	1006	2	US-09-023-905A-12 Sequence 12, Appli

28	62	13.3	1006	2	US-09-949-002-361	Sequence 361, App
29	61.5	13.2	583	2	US-09-538-092-1071	Sequence 1071, Ap
30	61.5	13.2	688	2	US-09-113-750A-3	Sequence 3, Appli
31	61.5	13.2	1143	2	US-09-949-016-6137	Sequence 6137, Ap
32	61.5	13.2	3878	2	US-09-914-259-11	Sequence 11, Appli
33	61	13.1	139	2	US-09-710-279-1310	Sequence 1310, Ap
34	61	13.1	168	2	US-09-134-001C-5599	Sequence 5599, Ap
35	61	13.1	184	2	US-09-325-932A-66	Sequence 66, Appli
36	61	13.1	403	1	US-09-092-770-4	Sequence 4, Appli
37	61	13.1	403	2	US-09-222-851-4	Sequence 4, Appli
38	61	13.1	403	2	US-10-265-062-4	Sequence 4, Appli
39	61	13.1	901	2	US-09-134-001C-5351	Sequence 5351, Ap
40	61	13.1	1078	2	US-09-583-110-4036	Sequence 4036, Ap
41	61	13.1	1080	2	US-09-107-433-4843	Sequence 4843, Ap
42	61	13.1	1295	2	US-09-328-352-6045	Sequence 6045, Ap
43	60.5	13.0	526	2	US-09-071-035-84	Sequence 84, Appli
44	60.5	13.0	526	2	US-10-206-576-84	Sequence 84, Appli
45	60.5	13.0	546	2	US-09-071-035-82	Sequence 82, Appli
46	60.5	13.0	546	2	US-10-206-576-82	Sequence 82, Appli
47	60.5	13.0	586	2	US-09-040-725A-1	Sequence 1, Appli
48	60	12.9	301	2	US-09-107-532A-4953	Sequence 4953, Ap
49	59.5	12.8	92	2	US-09-513-999C-5393	Sequence 5393, Ap
50	59.5	12.8	191	2	US-09-270-767-33624	Sequence 33624, A
51	59.5	12.8	191	2	US-09-270-767-48841	Sequence 48841, A
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53	59.5	12.8	380	2	US-09-902-540-15247	Sequence 15247, A
54	59.5	12.8	1078	2	US-09-949-016-11185	Sequence 11185, A
55	59.5	12.8	1085	1	US-08-431-080-28	Sequence 28, Appli
56	59.5	12.8	1085	1	US-08-938-534-28	Sequence 28, Appli
57	59.5	12.8	1085	2	US-09-345-294-28	Sequence 28, Appli
58	59	12.7	66	2	US-09-107-532A-4003	Sequence 4003, Ap
59	59	12.7	336	2	US-09-252-991A-28882	Sequence 28882, A
60	59	12.7	376	2	US-09-248-796A-14887	Sequence 14887, A
61	59	12.7	579	2	US-09-949-016-10483	Sequence 10483, A
62	59	12.7	580	2	US-09-248-796A-25118	Sequence 25118, A
63	59	12.7	750	2	US-10-104-047-2432	Sequence 2432, Ap
64	59	12.7	793	1	US-08-468-558-5	Sequence 5, Appli
65	59	12.7	793	2	US-08-676-444-5	Sequence 5, Appli
66	59	12.7	982	2	US-09-023-905A-7	Sequence 7, Appli
67	58.5	12.6	301	2	US-09-543-681A-8264	Sequence 8264, Ap
68	58.5	12.6	342	2	US-09-107-532A-5496	Sequence 5496, Ap
69	58.5	12.6	548	2	US-09-167-299-3	Sequence 3, Appli
70	58.5	12.6	867	2	US-10-104-047-3052	Sequence 3052, Ap
71	58	12.4	170	2	US-10-101-464A-617	Sequence 617, App
72	58	12.4	228	2	US-09-328-352-7306	Sequence 7306, Ap
73	58	12.4	245	2	US-09-902-540-11576	Sequence 11576, A
74	58	12.4	296	2	US-09-100-804-12	Sequence 12, Appli
75	58	12.4	336	2	US-09-848-294-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-09-543-681A-5443
; Sequence 5443, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543, 681A
; PRIOR FILING DATE: 2000-04-05
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

Query Match 74.2%; Score 346; DB 2; Length 93;
Best Local Similarity 73.6%; Pred. No. 2.4e-38;
Matches 64; Conservative 7; Mismatches 16; Indels 0; Gaps 0;

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4 MSRTIFCTFLNKEADGLDFQLYPBGELGRIFNEISKEAWGQWMAKQTMLINEKLNMMNP 63
DB 61 DDRKFLAQMTSFLFEGKDVIEGFVP 87
64 DDRKLEQEMVRFLEGHVDHIDGYTP 90

RESULT 2
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

Query Match 70.2%; Score 327; DB 2; Length 107;
Best Local Similarity 69.0%; Pred. No. 1e-35;
Matches 60; Conservative 10; Mismatches 17; Indels 0; Gaps 0;

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17 MSRTIFCTFLNKEADGLDFQLYPBGELGRIFNEISKEAWGQWMAKQTMLINEKLNMMNP 76
DB 61 DDRKFLAQMTSFLFEGKDVIEGFVP 87
77 EHRKLEQEMVRFLEGHVDHIDGYTP 103

RESULT 3
US-09-252-991A-23355
; Sequence 23355, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 23355
; LENGTH: 122
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

Query Match 50.4%; Score 235; DB 2; Length 122;
Best Local Similarity 52.3%; Pred. No. 2.1e-23;
Matches 46; Conservative 18; Mismatches 22; Indels 2; Gaps 2;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60

DB 33 MSRTVMCRKXHEELPGLDRPPYPGAKGEDLYNNVSRKAWDEWQKQTMLINEKLNMMNA 92
QY 61 DDRKFLAQMTSFLFEGKD-VIEGFVP 87
93 EDRKFLQEMDKFL-SGEDYAKADGYTP 119
DB

RESULT 4
US-09-328-352-5456
; Sequence 5456, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5456
; LENGTH: 92
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

Query Match 43.0%; Score 200.5; DB 2; Length 92;
Best Local Similarity 46.1%; Pred. No. 5.7e-19;
Matches 41; Conservative 14; Mismatches 33; Indels 1; Gaps 1;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNV 60
4 MSROYFCRKYQKEMEGLDPAFPFGAKQGFENNVSQAQWQEWLQHOTTLINKEKLNVEFP 63
DB 61 DDRKFLAQMTSFLFEGKDV-IEGFVPE 88
64 EAKKFLQEMRKEFFNNDSEVERKAGWKPE 92

RESULT 5
US-09-540-236-2859
; Sequence 2859, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATA.
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarhalis
US-09-540-236-2859

Query Match 27.9%; Score 130; DB 2; Length 110;
Best Local Similarity 40.9%; Pred. No. 1.8e-09;
Matches 27; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 22 YPGDLGKRIFDNISKEAWGLWQKQTMLINEKLNMMNVDDRKFLAQMTSFLFEGKDV 81
42 FPNKAGQEIQDTISAKAWNAWLBQTMLINEKLSMIDPQAKKYLNEQREKFLDNGDYEK 101
DB 82 IEGFVP 87
102 PAGYKP 107

RESULT 6
US-09-538-092-1243
; Sequence 1243, Application US/09538092

GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: March 1, 2006, 00:01:31 ; Search time 66.924 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFECKDVEIEGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications_AA_Main:*
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4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	466	100.0	88	3	US-09-955-502-9 Sequence 9, Appli
2	356	76.4	87	3	US-09-955-502-7 Sequence 7, Appli
3	347	74.5	90	3	US-09-955-502-10 Sequence 10, Appli
4	345	74.0	87	3	US-09-955-502-6 Sequence 6, Appli
5	344	73.8	91	3	US-09-955-502-5 Sequence 5, Appli
6	336	72.1	87	3	US-09-955-502-8 Sequence 8, Appli
7	336	72.1	88	3	US-09-955-502-15 Sequence 15, Appli
8	336	72.1	91	3	US-09-955-502-14 Sequence 14, Appli
9	336	72.1	91	3	US-09-955-502-16 Sequence 16, Appli
10	336	72.1	91	3	US-09-955-502-17 Sequence 17, Appli
11	332	71.2	91	3	US-09-955-502-11 Sequence 11, Appli
12	332	71.2	91	3	US-09-955-502-12 Sequence 12, Appli
13	332	71.2	91	3	US-09-955-502-13 Sequence 13, Appli
14	326	70.0	91	3	US-09-955-502-18 Sequence 18, Appli
15	308	66.1	90	3	US-09-955-502-20 Sequence 20, Appli
16	292	62.7	78	3	US-09-955-502-19 Sequence 19, Appli
17	256	54.9	87	3	US-09-955-502-2 Sequence 2, Appli
18	256	54.9	87	3	US-09-955-502-3 Sequence 3, Appli
19	242.5	52.0	86	3	US-09-955-502-4 Sequence 4, Appli
20	237	50.9	87	3	US-09-955-502-24 Sequence 24, Appli
21	235	50.4	87	3	US-09-955-502-25 Sequence 25, Appli
22	230	49.4	88	3	US-09-955-502-26 Sequence 26, Appli
23	230	49.4	88	3	US-09-955-502-27 Sequence 27, Appli
24	230	49.4	88	3	US-09-955-502-28 Sequence 28, Appli
25	228	48.9	90	3	US-09-955-502-23 Sequence 23, Appli
26	226	48.5	87	3	US-09-955-502-29 Sequence 29, Appli
27	226	48.5	87	3	US-09-955-502-30 Sequence 30, Appli

28	216	46.4	76	3	US-09-955-502-21	Sequence 21, Appli
29	215	46.1	87	3	US-09-955-502-32	Sequence 32, Appli
30	213	45.7	87	3	US-09-955-502-31	Sequence 31, Appli
31	205	44.0	88	3	US-09-955-502-33	Sequence 33, Appli
32	196	42.1	89	3	US-09-955-502-22	Sequence 22, Appli
33	77.5	16.6	2364	4	US-10-170-385-15	Sequence 15, Appli
34	75.5	16.2	1630	4	US-10-408-765A-2431	Sequence 2431, Ap
35	75.5	16.2	2154	4	US-10-695-994-4	Sequence 4, Appli
36	75.5	16.2	2154	5	US-10-805-684-150	Sequence 150, App
37	69	14.8	921	5	US-10-732-923-3305	Sequence 3305, Ap
38	68	14.6	315	5	US-10-510-628-4	Sequence 4, Appli
39	68	14.6	359	4	US-10-265-062-6	Sequence 6, Appli
40	68	14.6	359	4	US-10-755-889-324	Sequence 324, App
41	68	14.6	374	5	US-10-732-923-2938	Sequence 2938, Ap
42	68	14.6	404	4	US-10-265-062-3	Sequence 3, Appli
43	68	14.6	404	5	US-10-732-923-2939	Sequence 2939, Ap
44	68	14.6	737	5	US-10-510-628-2	Sequence 2, Appli
45	66.5	14.3	689	4	US-10-369-493-17280	Sequence 17280, A
46	66	14.2	307	4	US-10-264-237-2647	Sequence 2647, Ap
47	66	14.2	316	4	US-10-094-749-2195	Sequence 2195, Ap
48	66	14.2	321	4	US-10-308-279-58	Sequence 58, Appli
49	66	14.2	321	4	US-10-126-103-126	Sequence 126, App
50	66	14.2	321	4	US-10-431-096-126	Sequence 126, App
51	66	14.2	321	5	US-10-719-993-655	Sequence 655, App
52	66	14.2	321	5	US-10-719-993-656	Sequence 656, App
53	66	14.2	321	5	US-10-974-440-57	Sequence 57, Appli
54	66	14.2	344	4	US-10-050-704-281	Sequence 281, App
55	66	14.2	344	4	US-10-798-512-281	Sequence 281, App
56	66	14.2	348	4	US-10-798-512-129	Sequence 129, App
57	66	14.2	348	4	US-10-424-599-264222	Sequence 264222, App
58	66	14.2	355	5	US-10-501-282-5848	Sequence 5848, Ap
59	66	14.2	395	5	US-10-425-115-325713	Sequence 325713, A
60	65.5	14.1	85	4	US-10-282-122A-63394	Sequence 63394, A
61	65.5	14.1	364	4	US-10-264-049-2841	Sequence 2841, Ap
62	65.5	14.1	806	4	US-10-296-115-1407	Sequence 1407, Ap
63	65	13.9	305	4	US-10-369-493-8852	Sequence 8852, Ap
64	65	13.9	477	4	US-10-732-923-19695	Sequence 19695, A
65	65	13.9	483	5	US-10-250-613-5	Sequence 538, App
66	65	13.9	505	4	US-10-424-599-153968	Sequence 153968, A
67	65	13.9	687	5	US-10-424-599-153969	Sequence 153969, A
68	64.5	13.8	357	4	US-10-282-122A-48667	Sequence 48667, A
69	64.5	13.8	393	4	US-10-450-763-50306	Sequence 50306, A
70	64.5	13.8	593	5	US-10-437-963-173299	Sequence 173299, A
71	64.5	13.8	946	4	US-10-050-704-278	Sequence 278, App
72	64.5	13.8	81	4	US-10-798-512-278	Sequence 278, App
73	64	13.7	81	4	US-10-363-829-442	Sequence 442, App
74	64	13.7	81	4		
75	64	13.7	311	4		

ALIGNMENTS

RESULT 1
US-09-955-502-9
Sequence 9, Application US/09955502
Patent No. US20020072118A1
GENERAL INFORMATION:
APPLICANT: Downb, Diana M.
APPLICANT: Gralnick, Jeff A.
TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
TITLE OF INVENTION: Oxygen-labile Proteins
FILE REFERENCE: 960296.97559
CURRENT APPLICATION NUMBER: US/09/955,502
PRIOR FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: 60/234,588
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 9
LENGTH: 88
TYPE: PRT
ORGANISM: Shewanella putrefaciens

Wed Mar 1 09:16:05 2006

us-09-955-502a-9.rapbm

US-09-955-502-9

Query Match 100.0%; Score 466; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 4.4e-47;
Matches 88; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 88
61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 88

RESULT 2
US-09-955-502-7

; Sequence 7, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Haemophilus influenzae
US-09-955-502-7

Query Match 76.4%; Score 356; DB 3; Length 87;
Best Local Similarity 74.7%; Pred. No. 4.2e-34;
Matches 65; Conservative 11; Mismatches 11; Indels 0; Gaps 0;

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DB 61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87
61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87

RESULT 3
US-09-955-502-10

; Sequence 10, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Vibrio cholerae
US-09-955-502-10

Query Match 74.5%; Score 347; DB 3; Length 90;

Best Local Similarity 74.7%; Pred. No. 5e-33;
Matches 65; Conservative 7; Mismatches 15; Indels 0; Gaps 0;

QY 1 MARTVNCVHLNKEADGLDFQLYPGDLGKRIFDNIISKEAWGLWQKKQTMLINEKLNMMNV 60
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DB 61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87
61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87

RESULT 4
US-09-955-502-6

; Sequence 6, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Pasteurella multocida
US-09-955-502-6

Query Match 74.0%; Score 345; DB 3; Length 87;
Best Local Similarity 72.4%; Pred. No. 8.3e-33;
Matches 63; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

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DB 61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87
61 DDRKFLAQMSTFLFEGKDVIEIGFVPE 87

RESULT 5
US-09-955-502-5

; Sequence 5, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 91
; TYPE: PRT
; ORGANISM: Actinobacillus actinomycetemcomitans
US-09-955-502-5

Query Match 73.8%; Score 344; DB 3; Length 91;
Best Local Similarity 72.4%; Pred. No. 1.2e-32;
Matches 63; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.99319 Seconds
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218.595 Million cell updates/sec

Title: US-09-955-502A-9
Perfect score: 466
Sequence: 1 MARTVNCVHLNKADGLDFQ.....QMTSFLFEKQVEIGFVPE 88

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	230	49.4	88	6	US-10-467-657-968
2	68	14.6	359	7	US-11-087-227-8
3	68	14.6	359	7	US-11-192-450-6
4	68	14.6	404	7	US-11-087-227-6
5	68	14.6	404	7	US-11-192-450-3
6	62	13.3	593	7	US-11-194-246-317
7	61	13.1	139	6	US-10-793-626-1310
8	61	13.1	403	7	US-11-192-450-4
9	60	12.9	296	7	US-11-087-227-10
10	59.5	12.8	577	7	US-11-072-175-187
11	59	12.7	750	7	US-11-072-512-2432
12	58.5	12.6	867	7	US-11-072-512-3052
13	57.5	12.3	468	7	US-11-167-273-1
14	56	12.0	539	6	US-10-793-626-888
15	55.5	11.9	312	6	US-10-793-626-1210
16	55	11.8	266	5	US-09-995-493-6
17	55	11.8	731	6	US-10-613-744-10
18	54.5	11.7	588	6	US-10-793-626-3328
19	54.5	11.7	1432	6	US-10-510-386-218
20	54	11.6	125	7	US-11-098-686-10739
21	54	11.6	205	6	US-10-498-026-83
22	54	11.6	304	7	US-11-156-084-274
23	54	11.6	354	7	US-11-019-711-198
24	54	11.6	391	6	US-10-623-155-110
25	54	11.6	391	7	US-11-019-711-63

26	54	11.6	400	6	US-10-623-155-112	Sequence 112, App
27	54	11.6	400	7	US-11-019-711-12	Sequence 12, Appl
28	54	11.6	400	7	US-11-019-711-14	Sequence 14, Appl
29	54	11.6	466	6	US-10-524-647-114	Sequence 114, App
30	54	11.6	466	6	US-10-524-972-102	Sequence 102, App
31	54	11.6	508	7	US-11-072-512-2186	Sequence 2186, Ap
32	54	11.6	648	6	US-10-467-657-2802	Sequence 2802, Ap
33	54	11.6	829	6	US-10-909-769-26	Sequence 26, Appl
34	53.5	11.5	267	7	US-11-052-554A-219	Sequence 219, App
35	53.5	11.5	326	6	US-10-485-517-306	Sequence 306, App
36	53.5	11.5	340	7	US-11-165-226-128	Sequence 128, App
37	53.5	11.5	734	6	US-10-995-561-770	Sequence 770, App
38	53.5	11.5	756	7	US-11-074-176-202	Sequence 202, App
39	53.5	11.5	765	7	US-11-120-308-84	Sequence 84, Appl
40	53.5	11.5	782	6	US-10-793-626-2352	Sequence 2352, Ap
41	53.5	11.5	818	7	US-11-120-308-94	Sequence 94, Appl
42	53	11.4	177	6	US-10-467-657-1658	Sequence 1658, Ap
43	53	11.4	259	7	US-11-180-418-4	Sequence 4, Appli
44	53	11.4	269	7	US-11-180-418-3	Sequence 3, Appli
45	53	11.4	308	7	US-11-180-418-2	Sequence 2, Appli
46	53	11.4	391	7	US-11-019-711-61	Sequence 61, Appl
47	53	11.4	400	7	US-11-019-711-10	Sequence 10, Appl
48	53	11.4	607	7	US-11-096-051-14	Sequence 14, Appl
49	53	11.4	1558	6	US-10-329-258-14	Sequence 14, Appl
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51	53	11.4	2715	7	US-11-096-051-2	Sequence 2, Appli
52	53	11.4	2715	7	US-11-113-424-51	Sequence 51, Appl
53	53	11.4	2721	7	US-11-096-051-10	Sequence 10, Appl
54	53	11.4	2725	7	US-11-096-051-8	Sequence 8, Appli
55	52.5	11.3	1122	6	US-10-467-657-6112	Sequence 6112, Ap
56	52	11.2	325	7	US-11-074-176-368	Sequence 368, App
57	52	11.2	359	6	US-10-055-877-265	Sequence 265, App
58	52	11.2	359	7	US-11-080-091-1	Sequence 1, Appli
59	52	11.2	359	7	US-11-116-939-15	Sequence 15, Appl
60	52	11.2	359	7	US-11-087-177-23	Sequence 23, Appl
61	52	11.2	359	7	US-11-087-177-25	Sequence 25, Appl
62	52	11.2	359	7	US-11-087-177-29	Sequence 29, Appl
63	52	11.2	364	7	US-11-087-177-31	Sequence 31, Appl
64	52	11.2	364	7	US-11-087-177-33	Sequence 33, Appl
65	52	11.2	365	7	US-11-087-177-27	Sequence 27, Appl
66	52	11.2	386	7	US-11-072-512-2777	Sequence 2777, Ap
67	52	11.2	405	7	US-11-072-512-3581	Sequence 3581, Ap
68	52	11.2	588	7	US-11-052-554A-339	Sequence 339, App
69	52	11.2	640	6	US-10-467-657-4930	Sequence 4930, Ap
70	52	11.2	694	6	US-11-072-512-2469	Sequence 2469, Ap
71	52	11.2	717	6	US-10-793-626-3022	Sequence 3022, Ap
72	52	11.2	842	6	US-10-909-769-22	Sequence 22, Appl
73	52	11.2	893	7	US-11-072-512-3504	Sequence 3504, Ap
74	51.5	11.1	206	7	US-11-124-367A-316	Sequence 316, App
75	51.5	11.1	319	7	US-11-055-822-334	Sequence 334, App

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqMan99, version 1.04

```

; SEQ ID NO 968
;
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

```

Query Match	49.4%;	Score 230;	DB 6;	Length 88;
Best Local Similarity	49.4%;	Pred. No. 9.2e-20;		
Matches 44; Conservative	19;	Mismatches 24;	Indels 2;	Gaps 2;

```
QY      1 MARTVNCVHLNKEADGLDFQLYPBGDLGKRI PDNI SKEAWGLWQKKQTM LINCKLNNMNV 600
        ||| | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | : | | | | | :
Db      1 MARMVFCVKLNKEAEGMKF PPLPNELGKRI FENVSQEAWAAWTRHQTML INENRSLIADP 600
```

```
QY      61 DDRKFLBAQMTSFLP-EGKDVIEIGFVPE 88
      |::|||::|::|::|:
Db      61 RAREYLAQOMEQYFFGDADA-VQGIIVPQ 88
```

RESULT 2
US-11-08

US 11087227 ; Sequence 8, Application US/11087227
US 20050260566A1 ; Publication No. US20050260566A1
; GENERAL INFORMATION:

```

: APPLICANT: Fischer, Timothy J.
: APPLICANT: Malinowski, Douglas P.
: APPLICANT: Taylor, Adrian J.
: APPLICANT: Parker, Margaret R.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
: TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
: FILE REFERENCE: 046143/287139
: CURRENT APPLICATION NUMBER: US/11/087,227
: CURRENT FILING DATE: 2005-03-23
: PRIOR APPLICATION NUMBER: 60/556,495
: PRIOR FILING DATE: 2004-03-24
: NUMBER OF SEQ ID NOS: 90
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 8
: LENGTH: 359
: TYPE: PRT
: ORGANISM: Homo sapiens
: US-11-087-227-8

```

Query Match	14.6%;	Score 68;	DB 7;	Length 359;
Best Local Similarity	27.6%;	Pred. No. 1.8;		
Matches 21; Conservative	12;	Mismatches 29;	Indels 14;	Gaps 2;

```

QY      11 NKEADGLDFQLYPGDLGKRI PDN-----ISKEAAGLWQKQUTMLINEKILNNMNV 60
      :||      :      :      :      :      :      :      :      :      :
Db      76 HKEIGTSDFSRFTNYRPNULFINPSPLDLISWGCSEKWTMLNMLKGESRYVHDKHFEVLHS 135

```

```
QY      61 DDRKFLAQM T SFLFB 76
        | | | | | :
Db      136 D---LEPQMR SILLD 147
```

RESULT 3
US-11-19

US-11-192-450-0
; Sequence 6, Application US/11192450
; Publication No. US20050282150A1
; GENERAL INFORMATION:

```

: APPLICANT: Coats, Steven R.
:
: APPLICANT: Babs, Michael B.
:
: APPLICANT: Robinson, Murray O.
:
: TITLE OF INVENTION: Novel Cyclin E Genes and Proteins
:
: FILE REFERENCE: A-524
:
: CURRENT APPLICATION NUMBER: US/11/192,450
:
: CURRENT FILING DATE: 2005-07-28
:
: PRIOR APPLICATION NUMBER: US/10/265,062
:
: PRIOR FILING DATE: 2002-10-04
:
: PRIOR APPLICATION NUMBER: US/09/442,919
:
: PRIOR FILING DATE: 1999-11-18
:
: PRIOR APPLICATION NUMBER: 09/222,851
:

```

```

; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/092,770
; PRIOR FILING DATE: 1998-06-05
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 359
; TYPE: PRT
; ORGANISM: Human
US-11-192-450-6

```

Query Match	14.6%;	Score 68;	DB 7;	Length 359;
Best Local Similarity	27.6%;	Pred. No. 1.8;		
Matches 21; Conservative	12;	Mismatches 29;	Indels 14;	Gaps 2;

```
QY      11 NKEADGLDFQLYPGDLGKRIFDN-----ISKAWGLWQKKQTMLINEKKNMNV   60
       :|||:::|||:::|||||:::
Db      76 HKGTCTSDFSRFTNYRFKNLFINSPPLPDLSWGCSKEVWLNLTKESRYVDKHFEVLHS 135
```

```

QY      61  DDRKFLAQMTSFLFE  76
          |  |||||
Db      136 D---LEPQMSILDD  147

```

RESULT 4
US-11-08

```

; Sequence 6, Application US/11087227
; Publication No. US20050260566A1
;
; GENERAL INFORMATION:
; APPLICANT: Fischer, Timothy J.
; APPLICANT: Malinowski, Douglas P.
; APPLICANT: Taylor, Adrian J.
; APPLICANT: Parker, Margaret R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
; TITLE OF INVENTION: DETECTION OF CERVICAL DISEASE
; FILE REFERENCE: 046143/287139
; CURRENT APPLICATION NUMBER: US/11/087,227
; CURRENT FILING DATE: 2005-03-23
; PRIOR APPLICATION NUMBER: 60/556,495
; PRIOR FILING DATE: 2004-03-24
; NUMBER OF SEQ ID NOS: 90
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 404
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-087-227-6

```

Query Match	14.6%;	Score 68;	DB 7;	Length 404;
Best Local Similarity	27.6%;	Pred. No. 2.1;		
Matches 21; Conservative	12;	Mismatches 29;	Indels 14;	Gaps 2;

```

QY      11 NKEADGLDFQLYPBDLGKRI.FDN-----ISKEAWGLMÖKKÖTMLINEKKLMMNV 60
      :||      :      |:||      |||      |||      :||      :||
Db      76 HKEIGTSDFSRFTNYRPFKNLFINPSPPLDLSWGCSEKVMNLMLKKESRYVHDKHFEVLHS 135

```

```
QY      61 DDRKFLAQM T S F L E E 76
      | | | | | :
Db      136 D---LEPQMR S I L D 147
```

RESULT 5
US-11-15

```

; Sequence 3, Application US/11192450
; Publication No. US20050282150A1
; GENERAL INFORMATION:
; APPLICANT: Coats, Steven R.
; APPLICANT: Bass, Michael B.
; APPLICANT: Robinson, Murray O.
; TITLE OF INVENTION: Novel Cyclin B Genes and Proteins
; FILE REFERENCE: A-524
; CURRENT APPLICATION NUMBER: US/11/192,450
; CURRENT FILING DATE: 2005-07-28

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 85.8116 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-10
Perfect score: 485
Sequence: 1 MARTVFCRLQKEADGLDFQ.....VNFLPEGKEVHIEGYTPPAK 90.

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq 21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	485	100.0	90	5 ABB78155	Abb78155 Amino aci
2	409	84.3	107	7 ABO65445	ABO65445 Klebsiell
3	402	82.9	91	5 ABB78158	Abb78158 Amino aci
4	402	82.9	91	5 ABB78157	Abb78157 Amino aci
5	399	82.3	91	5 ABB78156	Abb78156 Amino aci
6	389	80.2	91	5 ABB78150	Abb78150 Amino aci
7	389	80.2	91	5 ABB78161	Abb78161 Amino aci
8	389	80.2	91	5 ABB78159	Abb78159 Amino aci
9	387	79.8	88	5 ABB78162	Abb78162 Amino aci
10	387	79.8	88	5 ABB78160	Abb78160 Amino aci
11	387	79.8	93	7 ADF05158	Adf05158 Bacteri
12	386	79.6	87	5 ABB78152	Abb78152 Amino aci
13	375	77.3	87	5 ABB78151	Abb78151 Amino aci
14	375	77.3	87	5 ABB78153	Abb78153 Amino aci
15	375	77.3	91	5 ABB78163	Abb78163 Amino aci
16	366	75.5	90	5 ABB78165	Abb78165 Amino aci
17	350	72.2	78	5 ABB78164	Abb78164 Amino aci
18	347	71.5	88	5 ABB78154	Abb78154 Amino aci
19	249	51.3	87	5 ABB78148	Abb78148 Amino aci
20	249	51.3	87	5 ABB78147	Abb78147 Amino aci
21	241	49.7	88	5 ABB78178	Abb78178 Amino aci
22	240	49.5	88	5 ABB78171	Abb78171 Amino aci
23	240	49.5	88	5 ABB78172	Abb78172 Amino aci
24	240	49.5	88	5 ABB78173	Abb78173 Amino aci

25	240	49.5	88	6 ABP77219	Abp77219 N. gonorr
26	235	48.5	86	5 ABB78149	Abb78149 Amino aci
27	231	47.6	76	5 ABB78166	Abb78166 Amino aci
28	231	47.6	122	7 ABO74609	ABO74609 Pseudomon
29	228	47.0	87	5 ABB78169	Abb78169 Amino aci
30	228	47.0	90	5 ABB78168	Abb78168 Amino aci
31	226	46.6	87	5 ABB78175	Abb78175 Amino aci
32	224.5	46.3	89	9 ABB41576	Aeb41576 L. pneumo
33	224.5	46.3	95	9 AEB38294	Aeb38294 L. pneumo
34	223	46.0	87	5 ABB78170	Abb78170 Amino aci
35	220	45.4	87	5 ABB78174	Abb78174 Amino aci
36	218.5	45.1	92	6 ADA34169	Ada34169 Acinetoba
37	217.5	44.8	90	5 ABB78167	Abb78167 Amino aci
38	215	44.3	87	5 ABB78177	Abb78177 Amino aci
39	204	42.1	87	5 ABB78176	Abb78176 Amino aci
40	154	31.8	110	8 ADL05173	Adl05173 M. catarr
41	92	19.0	506	3 AAY74371	Aay74371 Neisseria
42	87	17.9	507	3 AAY74372	Aay74372 Neisseria
43	87	17.9	507	3 AAY74373	Aay74373 Neisseria
44	87	17.9	546	6 ABU38097	Abu38097 Protein e
45	84	17.3	507	6 ABU40210	Abu40210 Protein e
46	76.5	15.8	525	8 ADL04564	Adl04564 M. catarr
47	75.5	15.6	507	6 ABU41973	Abu41973 Protein e
48	75	15.5	474	7 ABO75727	ABO75727 Pseudomon
49	73.5	15.2	406	6 ABU35111	Abu35111 Protein e
50	72	14.8	309	8 ADN46828	Adn46828 Thermococ
51	72	14.8	311	7 ADM26256	Adm26256 Hyperther
52	71.5	14.7	3390	4 AAE07989	Aae07989 Wild-type
53	71.5	14.7	3390	4 AAE07990	Aae07990 Attenuate
54	71.5	14.7	3390	8 ADG93316	Adg93316 DEN3 (Sle
55	71	14.6	118	8 ADE28311	Ade28311 Human KPP
56	71	14.6	211	8 ADH48383	Adh48383 Human KPP
57	71	14.6	315	7 ADJ68481	Adj68481 Human hea
58	71	14.6	411	8 ADR51530	Adr51530 Human lip
59	71	14.6	488	8 ABBM83531	Abbm83531 Human dia
60	71	14.6	495	8 ADR51529	Adr51529 Human lip
61	71	14.6	504	8 ADR51531	Adr51531 Human lip
62	71	14.6	504	8 ABM83533	Abm83533 Human dia
63	71	14.6	515	7 ADC10046	Adc10046 Human NOV
64	71	14.6	518	8 ADR51528	Adr51528 Human lip
65	71	14.6	518	8 ADS92961	Ads92961 Calcium/c
66	71	14.6	518	8 ADU17989	Adu17989 Human can
67	71	14.6	518	8 ADU47349	Adu47349 Human Cam
68	71	14.6	525	4 AAM25814	Aam25814 Human pro
69	71	14.6	525	4 AAM79441	Aam79441 Human pro
70	71	14.6	527	7 ADE56673	Ade56673 Rat Prote
71	71	14.6	527	7 ADE61790	Ade61790 Rat Prote
72	71	14.6	527	7 ADE61788	Ade61788 Rat Prote
73	71	14.6	527	8 ADR51527	Adr51527 Human lip
74	71	14.6	549	8 ABM83534	Abm83534 Human dia
75	71	14.6	556	7 ADC99066	Adc99066 Human KPP

ALIGNMENTS

RESULT 1
ID ABB78155 standard; protein; 90 AA.
XX ABB78155;
AC
XX 05-NOV-2002 (first entry)
DT
XX Amino acid sequence of a YggX homologue.
DE
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Vibrio cholerae.
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
XX WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from *Salmonella*
CC *enterica* serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
XX cell. ABB78147-78 represent YggX homologues
SQ Sequence 90 AA;

Query Match	100.0%;	Score 485;	DB 5;	Length 90;
Best Local Similarity	100.0%;	Pred. No. 8.7e-52;		
Matches	90;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

[illegible]

	61	EHRKLLQEEMWNFLFEKGKEVHIEGYTPPAK	90
QY			
Db	61	EHRKLLQEEMWNFLFEKGKEVHIEGYTPPAK	90

RESULT 2	ABO65445	ABO65445	standard; protein; 107 AA.
ID	ABO65445		
XX			
AC	ABO65445;		
XX			
DT	29-JUL-2004	(first entry)	
XX			
DE	Klebsiella pneumoniae polypeptide seqid 11962.		
XX			
KW	Recombinant expression vector; transcription regulatory element;		
KW	Klebsiella pneumoniae protein; antibacterial; vaccine.		
XX			
OS	Klebsiella pneumoniae.		
XX			
PN	US6610836-B1.		
XX			
PD	26-AUG-2003.		
XX			
PF	27-JAN-2000; 2000US-00489039.		
XX			
PR	29-JAN-1999; 99US-0117747P.		
XX			
PA	(GENO-) GENOME THERAPEUTICS CORP.		
XX			
PI	Breton GL, Osborne M;		
XX			
DR	WPI; 2003-895346/82.		

DR N-PSDB; ACH988996.
XX
XX New nucleic acid encoding a *Klebsiella pneumoniae* polypeptide, useful for
PT preparing a vaccine composition against *Klebsiella pneumoniae*.
XX
XX
PS Disclosure; SEQ ID NO 11962; 932pp; English.
XX
XX The invention describes a new isolated nucleic acid encoding a *Klebsiella*
CC pneumoniae polypeptide. Also described are: a recombinant expression
CC vector comprising the nucleic acid, operably linked to a transcription
CC regulatory element; and a cell comprising the recombinant expression
CC vector. The nucleic acid is useful for preparing a vaccine composition
CC against *Klebsiella pneumoniae*. This is the amino acid sequence of a
CC *Klebsiella pneumoniae* polypeptide of the invention
XX
XX Sequence 107 AA;
SQ

Query Match	84.3%	Score 409;	DB 7;	Length 107;
Best Local Similarity	83.3%	Pred. No. 2.7e-42;		
Matches	75;	Conservative	8;	Mismatches 7;
			Indels	0;
			Gaps	0;

```
Qy      1 MARTVFCTRLQKADGLDFQLYPGELGKRIIPDNICEAWAQWOTKQMTLINEKKLNMMDP 600
      ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      17 MSRTIFCTFLQKADGQDFQLYPGELGKRIINVEISKEAWAQWQHQTMLINEKKLSMNNP 760
```

Qy 61 EHRKLTQEMTNFLFEGKEVHIIEGYTPPAK 90
|||
77 EHRKLTQEMTNFLFEGKDVHIIEGYTPPEK 106

RESULT 3
ABB78158
ID ABB78158 standard; protein; 91 AA.

ABB78158;

DT	05-NOV-2002	(first entry)
XX		
DE	Amino acid sequence of a YggX homologue	

KM Superoxide damage; cell; YggX; *Salmonella enterica* serovar typhimurium;
KM hydroxyl radical; DNA damage; YggX homologue.

OS Unidentified.

PN US2002072118-A1.

PD 13-JUN-2002.

PF 18-SEP-2001; 2001US-00955502.

PR 22-SEP-2000; 2000US-0234588P.

PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.

PI Downs D, Gralnick JA;

DR WPI; 2002-589476/63.

PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from *Salmonella enterica* Serovar Typhimurium.

PS Example; Fig 1A; 16pp; English.

The specification describes a method for reducing superoxide damage to a CC cell. The method comprises engineering the cell to produce more than the native amount of YggX protein (a protein identified from *Salmonella enterica* serovar typhimurium) or its homolog, where the cells are rendered more resistant to superoxide damage. YggX reduces the oxidation of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from CC clusters. The resulting decrease in free-iron levels generates fewer

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.8933 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-10

Perfect score: 485
Sequence: 1 MARTVFCRLQKADGLDFQ.....VNFLFEKGVHIEGYTPPAK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pirl:*
2: pirl2:*
3: pirl3:*
4: pirl4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	485	100.0	90	2	C82320	conserved hypothet
2	402	82.9	91	2	A85954	hypothetical prote
3	402	82.9	91	2	A65082	hypothetical prote
4	402	82.9	91	2	F91108	hypothetical prote
5	394	81.2	90	2	C64013	hypothetical prote
6	389	80.2	91	2	AH0879	conserved hypothet
7	366	75.5	90	2	A10116	conserved hypothet
8	240	49.5	88	2	H81014	conserved hypothet
9	231	47.6	90	2	H83003	conserved hypothet
10	231	47.6	93	2	E84994	hypothetical prote
11	228	47.0	105	2	C82624	conserved hypothet
12	87	17.9	507	2	C81063	fumarate hydratase
13	87	17.9	546	2	A81807	fumarate hydratase
14	76	15.7	604	2	S66993	hypothetical prote
15	75	15.5	507	2	A83105	probable fumarase
16	73.5	15.2	91	2	H90521	hypothetical prote
17	71.5	14.7	3390	1	GNWVYD3	genome polypeptid
18	71	14.6	518	1	B46619	Ca2+/calmodulin-de
19	71	14.6	527	1	A31908	Ca2+/calmodulin-de
20	71	14.6	556	1	JC5636	Ca2+/calmodulin-de
21	70	14.4	542	1	A45025	Ca2+/calmodulin-de
22	69.5	14.3	204	1	MNN239	nonstructural prot
23	69.5	14.3	996	2	A71080	hypothetical prote
24	69.5	14.3	1008	2	H72310	conserved hypothet
25	68.5	14.1	166	2	F70562	hypothetical prote
26	68	14.0	379	2	T24654	hypothetical prote
27	68	14.0	478	1	A30355	Ca2+/calmodulin-de
28	68	14.0	478	1	S04365	Ca2+/calmodulin-de
29	68	14.0	543	2	T16015	hypothetical prote

30	68	14.0	549	2	T16016	hypothetical prote
31	68	14.0	4116	2	T13719	calo protein - fru
32	67	13.8	533	1	A34366	Ca2+/calmodulin-de
33	67	13.8	542	1	A26464	Ca2+/calmodulin-de
34	67	13.8	589	2	S68470	Ca2+/calmodulin-de
35	67	13.8	743	2	S19437	hypothetical prote
36	67	13.8	768	2	S43567	R01H10.7 protein (
37	67	13.8	996	2	JE0237	apolipoprotein E r
38	66.5	13.7	472	2	S74886	phytoene dehydroge
39	66.5	13.7	3391	1	GNWV26	genome polypeptid
40	66.5	13.7	3391	1	GNWVJA	genome polypeptid
41	66.5	13.7	3391	2	JS0219	polypeptid - deng
42	66	13.6	306	2	A97249	Zn-binding lipopro
43	66	13.6	518	1	S43845	Ca2+/calmodulin-de
44	66	13.6	583	2	T48365	hypothetical prote
45	65.5	13.5	635	2	S75668	DNA primase (EC 2.
46	65.5	13.5	1418	2	T37264	phospholipase C (E
47	65	13.4	389	2	S73910	probable serine/th
48	65	13.4	1931	2	A59234	slow myosin heavy
49	65	13.4	3396	1	A42551	genome polypeptid
50	64.5	13.3	401	2	C70159	translation elonga
51	64.5	13.3	683	2	AC2256	hypothetical prote
52	64.5	13.3	1206	2	E96507	hypothetical prote
53	64.5	13.3	3391	1	GNWV16	genome polypeptid
54	64	13.2	304	2	H96496	TNP2-like transpos
55	64	13.2	387	2	JC2484	xylian endo-1,3-bet
56	64	13.2	492	2	B72389	shikimate kinase/3
57	64	13.2	505	2	C82216	probable fumarate
58	63.5	13.1	347	2	S71436	farnesyl-pyrophosp
59	63.5	13.1	577	1	A41289	moesin - human
60	63.5	13.1	1010	2	F75134	hypothetical prote
61	63	13.0	253	2	F85060	hypothetical prote
62	63	13.0	265	2	C86516	hypothetical prote
63	63	13.0	265	2	D72105	KDO-transferase 2,
64	63	13.0	336	2	T04196	RNA-binding protei
65	63	13.0	399	2	T23470	hypothetical prote
66	63	13.0	504	2	F64143	probable GTPase/GT
67	63	13.0	593	2	C64097	probable soluble 1
68	63	13.0	629	2	T28217	hypothetical prote
69	63	13.0	909	1	QRXL1	LDL receptor 1 pre
70	63	13.0	909	1	QRXL12	LDL receptor 2 pre
71	63	13.0	1148	2	T13347	Cnn protein - frui
72	62.5	12.9	305	2	A75211	asparaginase (EC 3
73	62.5	12.9	577	1	S39804	moesin - pig
74	62.5	12.9	1119	2	T18491	hypothetical prote
75	62	12.8	330	2	S74456	regulatory protein

ALIGNMENTS

RESULT 1
C82320
conserved hypothetical protein VC0451 [imported] - Vibrio cholerae (strain N16961 serogrc
C/Species: Vibrio cholerae
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 05-Oct-2004
C/Accession: C82320
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: C82320
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <HEI>
A/Cross-references: UNIPARC:UPI00000C2CCF; GB:AE004132; GB:AE003852; NID:99654871; PIDN:1
A/Experimental source: BeroGroup O1; Strain N16961; biotype El Tor
C/Genetics:
A/Gene: VC0451
A/Map position: 1
C/Superfamily: fe(II) trafficking protein yggX

Query Match	100.0%;	Score 485;	DB 2;	length 90;
Best Local Similarity	100.0%;	Pred. No. 7.6e-43;		
Matches	90;	Conservative	0;	Mismatches 0;
			Indels	0;
			Gaps	0;

Qy 1 MARTVFCTRLQKADGDLDFQLYPGEGLKRIIPDNICKEAWAQWTKQMTLINEKLNMDP 600
|||
Db 1 MARTVFCTRLQKADGDLDFQLYPGEGLKRIIPDNICKEAWAQWTKQMTLINEKLNMDP 600

QY 61 EHRKLLSEQEMVNFLEFGKEVHI EGYTPPAK 90
|||
Db 61 EHRKLLSEQEMVNFLEFGKEVHI EGYTPPAK 90

RESULT 2
A85954

hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL93
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousts, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551

A;Gene: **yggX**
C;Superfamily: **fe(II) trafficking protein YggX**

Query Match	82.9%;	Score 402;	DB 2;	Length 91;
Best Local Similarity	83.3%;	Pred. No. 2.5e-34;		
Matches 75; Conservative		7; Mismatches 8;	Indels 0;	Gaps 0;

[illegible]

Qy	61	EHRKLLBQEMVNFLEFGKEVHIETGTPPAK	90
Db	61	EHRKLLBQEMVNFLEFGKEVHIETGTPEDK	90

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)

C/Species: *Escherichia coli*
C/Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C/Accession: A65082
R/Blatner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.U.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997
 A;Title: The complete genome sequence of *Escherichia coli* K-12.
 A;Reference number: A64720; MUID:97426617; PMID:9278503
 A;Accession: A65082
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-91 <BLAT>
 A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:9
 A;Experimental source: strain K-12, substrain MG1655
 C;Superfamily: fe(II) trafficking protein YggX

Query Match	82.9%;	Score 402;	DB 2;	Length 91;
Best Local Similarity	83.3%;	Pred. No. 2.5e-34;		
Matches 75; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0;

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0Y      1 MARTVFCTRLQKADGLDPOLYPGELGKRIFDNICKEAMAOQTOMTLINKEKLNTMP 600
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Db      1 MSRTIFCTFLQREAEQGFQLYPGEIGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 600
QY      61 EHRKLLQEQMVNPLFEGKEVHIEGYTPPAK 90
        |||||
Db      61 EHRKLLQEQMVNPLFEGKEVHIEGYTPPEK 90

```

RESULT 4
F91108

hypothetical protein EC63838 [imported] - Escherichia coli (strain O157:H7, substrain R)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C/Accession: F91108
R/Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A/Reference number: A99629; MUID:21156231; PMID:11258796

A;Gene: ECs3838
C;Superfamily: fe(II) trafficking protein ygxx

Query Match	82.9%	Score 402;	DB 2;	Length 91;
Best Local Similarity	83.3%	Pred. No. 2.5e-34;		
Matches 75; Conservative	7;	Mismatches 8;	Indels 0;	Gaps 0

```
Oy      1 MARTVFCTRLQKEADGIDFQLYPGELKRIFDNICBEAWAQWQTQMTMLINEKKLNMDP   60  
       :|||:|||::|||||::::|:|||||:|||||:  
Db      1 MSRTIFCTFLQREAGODFQLYPGELKRITYNELSKCAWAQWHQTMMLINEKKLNMNNA   60
```

Oy 61 EHRKLLBQEMVNFLEFGKEVHIIGTTPPAK 90
| | | | | | | | | | | | | | |
Db 61 EHRKLLBQEMVNFLEFGKEVHIIGTTPEDK 90

RESULT 5
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)

C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C/Accession: C64013
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, C.
, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995

A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;Title: Whole-genome random sequencing and assembly of *Haemophilus influenzae* Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <TIGR>
A;Cross-references: UNIPROT:P44048; UNIPARC:UPI000001.3B0A4; GB:U32760; GB:L42023; NID:315
C;Superfamily: Fe(II) trafficking protein Y9x

Query Match	81.2%;	Score 394;	DB 2;	Length 90;
Best Local Similarity	79.8%;	Pred. No. 1.6e-33;		
Matches	71;	Conservative	10;	Mismatches 8;
			Indels	0;
			Gaps	0;

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Oy      1 MARTVFCTRLÖKEADGDLDFÖLYPGEKGRIIPDNICEKANAQÖTKÖTMLINEKKNMMDP 6
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      1 MARTVFCEYLKKEAEGDLDFÖLYPGEKGRIIFDSVSKQWGEIICKÖTMLVNEKKNMNA 6

```

QY 61 EHRKLTGEQVNFLEFGKEVHIIEGYTPRA 89
|||
Db 61 EHRKLTGEQVNFLEFGKDVHIIEGYTPRS 89

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 82.7469 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-10
Perfect score: 485
Sequence: 1 MARTVFCTRLQKADGLDFQ.....VNFLPEGKEVHIEGYTPPAK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues
Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	485	100.0	90	1	FETP_VIBCH	Q9kur4 vibrio chol
2	442	91.1	90	1	FETP_VIBVU	Q8dcs5 vibrio vuln
3	442	91.1	90	1	FETP_VIBVY	Q7mhi4 vibrio vuln
4	432	89.1	90	1	FETP_VIBPA	Q87li5 vibrio para
5	407	83.9	90	1	FETP_PHOPR	Q6lwk7 photobacter
6	406	83.7	90	1	FETP_VIBF1	Q5e7t0 vibrio fisc
7	397	81.9	90	1	FETP_RCO57	POa8p4 escherichia
8	397	81.9	90	1	FETP_ECOLI	POa8p3 escherichia
9	397	81.9	90	1	FETP_SHIFL	POa8p5 shigella fl
10	394	81.2	90	1	FETP_HABIN	P44048 haemophilus
11	394	81.2	90	2	Q4QMD9_HAEI8	Q4qmd9 haemophilus
12	393	81.0	90	1	FETP_ECOL6	Q8fel9 escherichia
13	385	79.4	91	1	FETP_MANSM	Q65vt7 manheimia
14	384	79.2	90	1	FETP_SALCH	Q57k04 salmonella
15	384	79.2	90	1	FETP_SALPA	Q5pmu1 salmonella
16	384	79.2	90	1	FETP_SALTI	P67618 salmonella
17	384	79.2	90	1	FETP_SALTY	P67617 salmonella
18	383	79.0	90	1	FETP_PASMU	Q9cib9 pasteurella
19	381	78.6	90	1	FETP_ERWCT	Q6d8j9 erwina car
20	375	77.3	94	1	FETP_HAEDU	Q7vkb6 haemophilus
21	374	77.1	90	1	FETP_YERPS	Q66m3 yersinia ps
22	368	75.9	90	1	FETP_PHOL1	Q7n711 photorhabdu
23	366	75.5	90	1	FETP_YERPS	Q8zhe7 yersinia pe
24	353	72.8	90	1	FETP_IDILO	Q5gy58 idiomarina
25	347	71.5	92	1	FETP_SHEON	Q8ebx6 shewanella
26	257	53.0	90	1	FETP_BORBR	Q7wh06 bordetella
27	257	53.0	90	1	FETP_BORPA	Q7w9q2 bordetella
28	257	53.0	90	1	FETP_BORPE	Q7wvc4 bordetella
29	247	50.9	91	1	FETP_XANAC	Q8pjh7 xanthomonas
30	246	50.7	90	1	FETP_NITEU	Q82xf2 nitrosomona
31	244	50.3	92	1	FETP_XANOR	Q5gy22 xanthomonas

32	241	49.7	90	1	FETP_COXBU	Q83d06 coxiella bu
33	240	49.5	88	1	FETP_NEIG1	Q5f553 neisseria g
34	240	49.5	88	1	FETP_NEIMA	P67615 neisseria m
35	240	49.5	88	1	FETP_NEIMB	P67616 neisseria m
36	240	49.5	90	1	FETP_PSEPK	Q88r49 pseudomonas
37	238	49.1	91	1	FETP_BURMA	Q62iu9 burkholderi
38	238	49.1	91	1	FETP_BURPS	Q638j4 burkholderi
39	237	48.9	92	1	FETP_XANCP	Q8p829 xanthomonas
40	237	48.9	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
41	235	48.5	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
42	231	47.6	77	1	FETP_BUCAI	P57618 buchnera ap
43	231	47.6	90	1	FETP_PSEAE	Q9hu36 pseudomonas
44	230	47.4	90	2	Q4KJT2_PSEF5	Q4kt2 pseudomonas
45	228	47.0	90	1	FETP_PSESM	Q87uf5 pseudomonas
46	228	47.0	90	1	FETP_XYLFA	Q9pc73 xyliella fas
47	228	47.0	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
48	227	46.8	91	1	FETP_RALSO	Q8y010 ralsconia s
49	224.5	46.3	89	1	FETP_LEGPA	Q5x3x9 legionella
50	224.5	46.3	89	1	FETP_LEGPH	Q5zu80 legionella
51	223	46.0	90	1	FETP_XYLPFT	Q87d06 xyliella fas
52	223	46.0	90	2	Q4J228_AZOVI	Q4j228 azotobacter
53	222	45.8	90	1	FETP_METCA	Q60aj7 methylococc
54	221.5	45.7	89	1	FETP_LEGPL	Q5wvc4 legionella
55	218.5	45.1	90	1	FETP_AC1AD	Q6ffb3 acinetobact
56	218	44.9	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
57	217	44.7	78	1	FETP_WIGBR	Q8d3cs wigleswort
58	214	44.1	90	1	FETP_CHRVO	Q7nsr4 chromobacte
59	208	42.9	78	1	FETP_BUCAP	Q8k925 buchnera ap
60	208	42.9	87	1	FETP_FRATT	Q5nhj8 francisella
61	201	41.4	79	1	FETP_CANBF	Q7vr99 candidatus
62	186	38.4	87	1	FETP_BUCBP	Q89a44 buchnera ap
63	168.5	34.7	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
64	158	32.6	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
65	90.5	18.7	514	2	Q6A1Z9_DESPS	Q6alz9 desulfotale
66	87	17.9	507	2	Q9JYE9_NEIMB	Q9jye9 neisseria m
67	87	17.9	546	2	Q9JTE3_NEIMA	Q9jte3 neisseria m
68	85	17.5	508	2	Q7NSF0_CHRVO	Q7nsf0 chromobacte
69	84	17.3	507	2	Q88PF3_PSEPK	Q88pf3 pseudomonas
70	84	17.3	855	2	Q416W2_GIBZE	Q416w2 gibdarella
71	82	16.9	526	2	Q4PC52_USTMA	Q4pc52 ustilago ma
72	78.5	16.2	345	2	Q55821_9FLAV	Q55821 rocio virus
73	77	15.9	482	2	Q5NUY1_9BURK	Q5nuyl ralsconia m
74	76.5	15.8	996	2	Q9C925_ARATH	Q9c925 arabidopsis
75	76	15.7	604	2	Q12166_YEAST	Q12166 saccharomyc

ALIGNMENTS

RESULT 1
FETP_VIBCH
ID FETP_VIBCH STANDARD; PRT; 90 AA.
AC Q9KUR4;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedlocusNames=VC0451;
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301; DOI=10.1038/35020000;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.L.,
RA Ermolaeva M.D., Vamathevan J.J., Bass S., Qin H., Dragoi I.,
RA Sellers P., McDonald L.A., Utterback T.R., Fleischmann R.D.,
RA Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R.,
RA Mekalanos J.J., Venter J.C., Fraser C.M.;

RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
RL *cholerae*.";
CC Nature 406:477-483 (2000).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AE004132; AAF93624.1; -; Genomic_DNA.
DR TIGR; VC0451; -.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10647 MW; 972331B2600B3184 CRC64;

Query Match 100.0%; Score 485; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.5e-43;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWOTKQTMLINEKKLNWMDP 60
Db 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWOTKQTMLINEKKLNWMDP 60

QY 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPAK 90
Db 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPAK 90

RESULT 2
FETP_VIBVU
ID_FETP_VIBVU STANDARD; PRT; 90 AA.
AC Q8DCC5;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV11514;
OS *Vibrio vulnificus*.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OK NCBI_TaxID=672;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CMCP6;
RA Rhee J.H., Kim S.Y., Chung S.S., Kim J.J., Moon Y.H., Jeong H.,
RA Choy H.B.;
RT "Complete genome sequence of *Vibrio vulnificus* CMCP6.";
RL Submitted (DEC-2002) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; AE016801; AA009940.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR ProDom; PD029191; DUF495; 1.

KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 91.1%; Score 442; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 5.6e-39;
Matches 82; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 MARTVFCTRLQKEADGLDFQLYPGELGKRIFDNICKEAWAQWOTKQTMLINEKKLNWMDP 60
Db 1 MSRTVFCARLNKEADGLDFQLYPGELGKRIFDNISKEAWGQWQHQTMLINEKKLNWMDP 60

QY 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPAK 90
Db 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPSK 90

RESULT 3
FETP_VIBVY
ID_FETP_VIBVY STANDARD; PRT; 90 AA.
AC Q7MH14;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=VV2885;
OS *Vibrio vulnificus* (strain Y016).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; *Vibrio*.
OK NCBI_TaxID=196600;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RX PubMed=14656965; DOI=10.1101/gr.1295503;
RA Chen C.-Y., Wu K.-M., Chang Y.-C., Chang C.-H., Tsai H.-C.,
RA Liao T.-L., Liu Y.-M., Chen H.-J., Shen A.B.-T., Li J.-C., Su T.-L.,
RA Shao C.-P., Lee C.-T., Hor L.-I., Tsai S.-F.;
RT "Comparative genome analysis of *Vibrio vulnificus*, a marine
RT pathogen.";
RL Genome Res. 13:2577-2587 (2003).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR EMBL; BA000037; BAC95649.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Yg9X.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10614 MW; 7EA0CB75840A255C CRC64;

Query Match 91.1%; Score 442; DB 1; Length 90;
Best Local Similarity 91.1%; Pred. No. 5.6e-39;
Matches 82; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

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QY 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPAK 90
Db 61 EHRKLLLEQEMVNFLEFGKEVHIIEGYTPPSK 90

RESULT 4
FETP_VIBPA

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 21.0443 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502a-10
Perfect score: 485
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 segs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	231	47.6	122	2	US-09-252-991A-23355 Sequence 23355, A
4	218.5	45.1	92	2	US-09-328-352-5456 Sequence 5456, Ap
5	154	31.8	110	2	US-09-540-236-2859 Sequence 2859, Ap
6	76.5	15.8	525	2	US-09-540-236-2250 Sequence 2250, Ap
7	75	15.5	474	2	US-09-252-991A-24473 Sequence 24473, A
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9	71	14.6	556	2	US-10-096-960-4 Sequence 2, Appli
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11	71	14.6	565	2	US-10-096-960-2 Sequence 2, Appli
12	69	14.2	57	2	US-09-562-737-124 Sequence 124, App
13	68	14.0	73	2	US-09-513-999C-5376 Sequence 5376, Ap
14	68	14.0	217	2	US-09-543-681A-7862 Sequence 7862, Ap
15	68	14.0	292	2	US-09-328-352-5836 Sequence 5836, Ap
16	67	13.8	116	2	US-09-562-737-125 Sequence 125, App
17	67	13.8	516	2	US-09-820-790B-2 Sequence 2, Appli
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21	64.5	13.3	311	2	US-09-248-796A-26397 Sequence 26397, A
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24	64	13.2	737	2	US-09-949-016-7675 Sequence 7675, Ap
25	64	13.2	1676	2	US-09-949-016-7610 Sequence 7610, Ap
26	63	13.0	279	2	US-09-198-452A-221 Sequence 221, App
27	63	13.0	279	2	US-09-438-185A-205 Sequence 205, App

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71	59	12.2	817	1	US-08-381-931B-2	Sequence 2, Appli
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75	58.5	12.1	455	2	US-09-270-767-45790	Sequence 45790, A

ALIGNMENTS

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Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
PRIOR FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117, 747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 68.4449 Seconds
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Title: US-09-955-502A-10

Perfect score: 485
Sequence: 1 MARTVFCTRLQKADGLDFQ.....VNFLFEKGKVIHGYTPPAK 90

Scoring table: BLOSUM62
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Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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6	389	80.2	91	3	US-09-955-502-14
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8	387	79.8	91	3	US-09-955-502-17
9	387	79.6	87	3	US-09-955-502-7
10	386	79.6	87	3	US-09-955-502-6
11	375	77.3	87	3	US-09-955-502-8
12	375	77.3	87	3	US-09-955-502-18
13	375	77.3	91	3	US-09-955-502-20
14	366	75.5	90	3	US-09-955-502-19
15	350	72.2	78	3	US-09-955-502-9
16	347	71.5	88	3	US-09-955-502-2
17	249	51.3	87	3	US-09-955-502-3
18	249	51.3	87	3	US-09-955-502-3
19	241	49.7	88	3	US-09-955-502-33
20	240	49.5	88	3	US-09-955-502-26
21	240	49.5	88	3	US-09-955-502-27
22	240	49.5	88	3	US-09-955-502-28
23	235	48.5	86	3	US-09-955-502-4
24	231	47.6	76	3	US-09-955-502-21
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27	228	47.0	90	3	US-09-955-502-23

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29	226	46.6	87	3	US-09-955-502-30	Sequence 30, Appl
30	223	46.0	87	3	US-09-955-502-25	Sequence 25, Appl
31	215	44.3	87	3	US-09-955-502-32	Sequence 32, Appl
32	204	42.1	87	3	US-09-955-502-31	Sequence 31, Appl
33	87	17.9	546	4	US-10-282-122A-66021	Sequence 66021, A
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66	68	14.0	699	5	US-10-482-029-295	Sequence 35058, A
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74	67	13.8	503	5	US-10-635-398-16	
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; Sequence 10, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 90
; TYPE: PRT
; ORGANISM: Vibrio cholerae

US-09-955-502-10

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RESULT 2
US-09-95

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; Sequence 11, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIORITY FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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; LENGTH: 91

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; Sequence 12, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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; SEQ ID NO 12
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; LENGTH: 91

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US-09-95

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 33
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US-09-955-502-13

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RESULT 5
US-09-95

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; Sequence 5, Application US/09955502
; Patent No. US20020072118A1
: GENERAL INFORMATION:

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; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
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; TYPE: PRF
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US-09-955-502-5

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				Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 6.1294 Seconds
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Title: US-09-955-502A-10
Perfect score: 485
Sequence: 1 MARTVFCRLQKADGUDFQ.....VNFLFEKGVHIEGYTPPAK 90

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 segs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/PCR_NEW_PUB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	240	49.5	88	US-10-467-657-968	Sequence 968, App
2	68.5	14.1	179	US-10-467-657-6542	Sequence 6542, App
3	68	14.0	695	US-10-453-372-648	Sequence 648, App
4	68	14.0	775	US-10-453-372-656	Sequence 656, App
5	68	14.0	834	US-10-453-372-658	Sequence 658, App
6	67	13.8	700	US-10-995-561-922	Sequence 922, App
7	67	13.8	700	US-10-995-561-924	Sequence 924, App
8	66	13.6	336	US-10-453-372-640	Sequence 640, App
9	66	13.6	793	US-10-995-561-925	Sequence 925, App
10	66	13.6	804	US-10-453-372-650	Sequence 650, App
11	66	13.6	847	US-10-453-372-654	Sequence 654, App
12	66	13.6	857	US-10-453-372-652	Sequence 652, App
13	66	13.6	905	US-10-453-372-638	Sequence 638, App
14	66	13.6	905	US-10-453-372-662	Sequence 662, App
15	66	13.6	905	US-10-453-372-664	Sequence 664, App
16	66	13.6	963	US-10-995-561-923	Sequence 923, App
17	66	13.6	963	US-10-453-372-660	Sequence 660, App
18	66	13.6	1012	US-10-453-372-646	Sequence 646, App
19	63.5	13.1	577	US-11-072-175-187	Sequence 187, App
20	63	13.0	266	US-09-995-493-6	Sequence 6, Appli
21	63	13.0	593	US-11-194-246-317	Sequence 317, Appl
22	61	12.6	1871	US-10-877-346-42	Sequence 42, Appl
23	61	12.6	3433	US-10-714-781A-67	Sequence 67, Appl
24	57.5	11.9	242	US-11-022-562-220	Sequence 220, App
25	57.5	11.9	278	US-11-098-686-10664	Sequence 10664, A

26	57	11.8	667	6	US-10-793-626-198	Sequence 198, App
27	56	11.5	177	6	US-10-467-657-1658	Sequence 1658, Ap
28	56	11.5	359	7	US-11-087-227-8	Sequence 8, Appli
29	56	11.5	359	7	US-11-192-450-6	Sequence 6, Appli
30	56	11.5	404	7	US-11-087-227-6	Sequence 6, Appli
31	56	11.5	404	7	US-11-192-450-3	Sequence 3, Appli
32	56	11.5	1122	6	US-10-995-561-705	Sequence 705, App
33	56	11.5	1129	6	US-10-995-561-706	Sequence 706, App
34	55.5	11.4	397	7	US-11-098-686-10901	Sequence 10901, A
35	55	11.3	198	7	US-11-182-016-43	Sequence 43, Appl
36	55	11.3	235	7	US-11-098-686-11270	Sequence 11270, A
37	55	11.3	1813	6	US-10-495-083-10	Sequence 10, Appl
38	54.5	11.2	349	6	US-10-821-234-1387	Sequence 1387, Ap
39	54.5	11.2	752	7	US-11-072-512-3003	Sequence 3003, Ap
40	54.5	11.2	765	7	US-11-120-308-84	Sequence 84, Appl
41	54.5	11.2	818	7	US-11-120-308-94	Sequence 94, Appl
42	54	11.1	305	7	US-11-156-084-178	Sequence 178, App
43	54	11.1	319	6	US-10-793-626-2760	Sequence 2760, Ap
44	54	11.1	1194	7	US-11-098-686-10270	Sequence 10270, A
45	54	11.1	1678	7	US-11-124-367A-340	Sequence 340, App
46	54	11.1	1678	7	US-11-124-367A-341	Sequence 341, App
47	53.5	11.0	58	6	US-10-957-887B-82	Sequence 82, Appl
48	53.5	11.0	243	7	US-11-214-796-2	Sequence 2, Appli
49	53.5	11.0	286	7	US-11-082-389-88	Sequence 88, Appl
50	53.5	11.0	455	6	US-10-714-887-212	Sequence 212, App
51	53.5	11.0	508	6	US-10-934-944-174	Sequence 174, App
52	53.5	11.0	516	7	US-11-135-604-2	Sequence 2, Appli
53	53.5	11.0	532	7	US-11-135-604-4	Sequence 4, Appli
54	53.5	11.0	537	7	US-11-135-604-6	Sequence 6, Appli
55	53.5	11.0	657	7	US-11-072-512-2529	Sequence 2529, Ap
56	53.5	11.0	731	6	US-10-613-744-10	Sequence 10, Appl
57	53.5	11.0	767	7	US-11-055-557-14	Sequence 14, Appl
58	53.5	11.0	767	7	US-11-055-557-14	Sequence 14, Appl
59	53.5	11.0	1613	7	US-11-108-528-84	Sequence 84, Appl
60	53.5	11.0	283	7	US-11-165-067A-21	Sequence 21, Appl
61	53	10.9	478	6	US-10-821-234-915	Sequence 915, App
62	53	10.9	521	6	US-10-934-944-216	Sequence 216, App
63	53	10.9	521	6	US-10-934-944-216	Sequence 216, App
64	53	10.9	600	7	US-11-072-512-3845	Sequence 3845, Ap
65	53	10.9	2665	7	US-11-124-368A-214	Sequence 214, App
66	53	10.9	2668	7	US-11-124-368A-215	Sequence 215, App
67	53	10.9	508	7	US-11-072-512-2186	Sequence 2186, Ap
68	52.5	10.8	723	5	US-09-934-948-2	Sequence 2, Appli
69	52.5	10.8	723	5	US-09-934-948-6	Sequence 6, Appli
70	52.5	10.8	723	5	US-09-934-948-6	Sequence 6, Appli
71	52.5	10.8	1432	6	US-10-510-386-218	Sequence 218, App
72	52.5	10.8	708	7	US-11-196-475-76	Sequence 76, Appl
73	52	10.7	783	7	US-11-192-219-7	Sequence 7, Appli
74	52	10.7	894	7	US-11-202-330-2	Sequence 2, Appli
75	52	10.7				

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; PRIOR FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin9, version 1.04

```

; SEQ ID NO 968
;
; LENGTH: 88
;
; TYPE: PRT
;
; ORGANISM: Neisseria gonorrhoeae
;
US-10-467-657-968

```

Query Match	49.5%	Score 240;	DB 6;	Length 88;
Best Local Similarity	50.6%	Pred. No. 6.9e-22;		
Matches 44;	Conservative 14;	Mismatches 29;	Indels 0;	Gaps 0;

```
Oy      1 MARTVFCTRLQKADGIDFQLYPGELGRIFDNI CKEAWAQOTKTQMTLINEKKLNMPD    60  
        ||| :|||:|||||:::||| ||||| ::||  
Db      1 MARMVPCVKLNEAEGMKPPPLPNELGRIRIFENYSQEAWAAWTRHQMTLINENRSLADP   60
```

Qy	61	EHRKLL	QEMVNF	LFECKE	VHIEGY	TP	87
		: :	:		:		
Db	61	RAREYLA	QMEQYF	FGDGAD	AVQGY	TP	87

RESULT 2
US-10-46

```

; Sequence 6542, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:

```

; APPLICANT: CHIRON SPA
 ; APPLICANT: FONTANA Maria Rita
 ; APPLICANT: PIZZA Mariagrazia
 ; APPLICANT: MASIGNANI Vega
 ; APPLICANT: MONACI Elisabetta
 ; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 ; FILE REFERENCE:

; CURRENT APPLICATION NUMBER: US/10/467,
 ; CURRENT FILING DATE: 2003-08-11
 ; PRIOR APPLICATION NUMBER: GB-0103424.8

```

; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwinn9, version 1.04
; SEQ ID NO 6542

```

```

; ORGANISM: Neisseria gonorrhoeae
; TYPE: PRT
US-10-467-657-6542

```

Query Match	14.1%;	Score 68.5;	DB 6;	Length 179;
Best Local Similarity	34.1%;	Pred. No. 0.46;		
Matches 15;	Conservative 10;	Mismatches 14;	Indels 5;	Gaps 1;

```
QY      40 AQWQTQMILINEKKLNMDPEHRKLLQEEMVNPFLFEGKEVHIE    83  
        |::|::|||::|::|::|::|:  
Db     2 ASWTGDEVLLNGKILTRDPAHKRL-----VNMLDKGEELPVD   40
```

RESULT 3
US-10-45

US-10-453-372-648
; Sequence 648, Application US/10453372
; Publication No. US20060003323A1

GENERAL INFORMATION:
APPLICANT: Alsobrook, et al.
TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD

```

; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
;

```

; CURRENT FILING DATE: 2003-06-03
 ; PRIOR APPLICATION NUMBER: 09/789390
 ; PRIORITY FILING DATE: 2001-03-23

; PRIOR FILING DATE: 2001-02-23
 ; PRIOR APPLICATION NUMBER: 60/185967
 ; PRIOR FILING DATE: 2000-03-01

/ ENION FILING DATE: 2000-03-01
 / PRIOR APPLICATION NUMBER: 09/823187
 / PRIOR FILING DATE: 2001-03-29

PRIOR APPLICATION NUMBER: 60/195792
PRIOR FILING DATE: 2000-03-10

PRIOR APPLICATION NUMBER: 09/839446
PRIOR FILING DATE: 2001-03-19

PRIOR APPLICATION NUMBER: 60/199476

;
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
;

;
 ; PRIOR FILING DATE: 2001-08-24
 ;
 ; PRIOR APPLICATION NUMBER: 60/227800
 ;
 ; PRIOR FILING DATE: 2000-08-25
 ;

```

; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 648

```

TYPE: PRT
ORGANISM: Homo sapiens
US-10-453-372-648

Query Match	14.0%;	Score 68;	DB 6;	Length 695;
Best Local Similarity	32.7%;	Pred. No. 2.8;		
Matches 17;	Conservative	9;	Mismatches	20;
			Indels	

```
QY      39 WAQWQTKTMLINEKKNMMDPEHRKLLLEQEMVNFLEGEKVHIEGYTPPAK 90
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      639 WRNWKRK-----NTKSMNFDNVPYRKTEEEDEDEDLHGRTAQI-GHVPYPAR 684
```

RESULT 4
US-10-453-372-656

US-10-453-372-656
; Sequence 656, Application US/10453372
; Publication No. US20060003323A1

```

; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHODS
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
;

```

PRIOR FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 60/185967
PRIOR FILING DATE: 2000-03-01

;
 ;
 ; PRIOR FILING DATE: 2001-03-29
 ;
 ; PRIOR APPLICATION NUMBER: 60/195792
 ;
 ; PRIOR FILING DATE: 2000-03-10
 ;

PRIOR FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 60/199476
PRIOR FILING DATE: 2000-03-25

;
 ; PRIOR APPLICATION NUMBER: 03/883118
 ;
 ; PRIOR FILING DATE: 2001-05-23
 ;
 ; PRIOR APPLICATION NUMBER: 60/208263
 ;
 ; PRIOR FILING DATE: 2000-05-31
 ;

? PRIOR APPLICATION NUMBER: 03/959396
 ? PRIOR FILING DATE: 2001-08-24
 ? PRIOR APPLICATION NUMBER: 60/227800
 ? PRIOR FILING DATE: 2000-08-25

```

; Remaining prior application data removed - see file wdgprer of FAULT
;
; NUMBER OF SEQ ID NOS: 1609
;
; SOFTWARE: Curaseq1ist version 0.1
;
; SEQ ID NO 656

```

```

; LENGTH: 775
; TYPE: PRT
; ORGANISM: Homo sapiens
ITS-10-453-372-656

```

Query Match	14.0%;	Score 68;	DB 6;	Length 775;
Best Local Similarity	32.7%;	Pred. No. 3.2;		
Matches 17: Conservative	9;	Mismatches 20;	Indels 6;	Gaps 2

```

QY      39 WAQMOTKQTMLENEKLNMMDEPHRKLLEQEMVNFLEEGKEVHIIEGYTPPAK  90
      | | : | | : | : | : | : | : | : | : | : | : | : | : | : | :
Db      719 WRNWKRR-----NTKSMNFNDNPYRKTEEEDEDEDLHGRTAQI-GHYVPPAR  764

```

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 86.765 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486

Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NFLFEGRVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*

1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match length	ID	Description
1	486	100.0	91 5 ABB78158	Abb78158 Amino aci
2	486	100.0	91 5 ABB78157	Abb78157 Amino aci
3	486	100.0	91 5 ABB78156	Abb78156 Amino aci
4	469	96.5	91 5 ABB78161	Abb78161 Amino aci
5	469	96.5	91 5 ABB78159	Abb78159 Amino aci
6	469	96.5	91 5 ABB78162	Abb78162 Amino aci
7	455	93.6	91 5 ABB78163	Abb78163 Amino aci
8	453	93.2	88 5 ABB78160	Abb78160 Amino aci
9	450	92.6	107 7 ABO65445	Abbo65445 Klebsiell
10	402	82.7	90 5 ABB78155	Abb78155 Amino aci
11	396	81.5	90 5 ABB78165	Abb78165 Amino aci
12	395	81.3	78 5 ABB78164	Abb78164 Amino aci
13	389	80.0	93 7 ADF05158	Adf05158 Bacterial
14	388	79.8	91 5 ABB78150	Abb78150 Amino aci
15	387	79.6	87 5 ABB78152	Abb78152 Amino aci
16	379	78.0	87 5 ABB78151	Abb78151 Amino aci
17	373	76.7	87 5 ABB78153	Abb78153 Amino aci
18	332	68.3	88 5 ABB78154	Abb78154 Amino aci
19	265	54.5	76 5 ABB78166	Abb78166 Amino aci
20	255	52.5	87 5 ABB78148	Abb78148 Amino aci
21	255	52.5	87 5 ABB78147	Abb78147 Amino aci
22	241	49.6	86 5 ABB78149	Abb78149 Amino aci
23	231.5	47.6	89 9 AEB841576	Aeb841576 L. pneumo
24	231.5	47.6	95 9 AEB38294	Aeb38294 L. pneumo

25	231	47.5	87 5	ABB78170	Abb78170 Amino aci
26	231	47.5	122 7	ABO74609	Abbo74609 Pseudomon
27	227	46.7	88 5	ABB78178	Abb78178 Amino aci
28	227	46.7	90 5	ABB78168	Abb78168 Amino aci
29	225	46.3	87 5	ABB78169	Abb78169 Amino aci
30	216.5	44.5	90 5	ABB78167	Abb78167 Amino aci
31	213	43.8	88 5	ABB78171	Abb78171 Amino aci
32	213	43.8	88 5	ABB78172	Abb78172 Amino aci
33	213	43.8	88 5	ABB78173	Abb78173 Amino aci
34	213	43.8	88 6	ABP77219	Abp77219 N. gonorr
35	206	42.4	87 5	ABB78175	Abb78175 Amino aci
36	200	41.2	87 5	ABB78177	Abb78177 Amino aci
37	200	41.2	87 5	ABB78174	Abb78174 Amino aci
38	200	41.2	87 5	ABB78176	Abb78176 Amino aci
39	199.5	41.0	92 6	ADA34169	Ada34169 Acinetoba
40	131	27.0	110 8	ADL05173	Adl05173 M. catarr
41	83	17.1	506 3	AAV74371	Aay74371 Neisseria
42	83	17.1	1647 4	ABG10750	Abg10750 Novel hum
43	81	16.7	507 6	ABU40210	Abu40210 Protein e
44	78	16.0	507 3	AAV74372	Aay74372 Neisseria
45	78	16.0	507 3	AAV74373	Aay74373 Neisseria
46	78	16.0	546 6	ABU38097	Abu38097 Protein e
47	76	15.6	548 4	AAE04737	Aae04737 Brugia ma
48	75	15.4	309 8	ADN46828	Adn46828 Thermococ
49	74.5	15.3	632 8	ADS29711	Ads29711 Bacterial
50	72	14.8	474 7	ABO75727	Abso75727 Pseudomon
51	71.5	14.7	679 9	ADZ85056	Adz85056 Partial F
52	71	14.6	311 7	ADM26256	Adm26256 Hyperther
53	70.5	14.5	285 4	AAE92683	Aae92683 Human pro
54	70.5	14.5	614 6	ABU11747	Abu11747 Human MDD
55	70.5	14.5	614 9	ADX06837	Adx06837 Cyclin-de
56	70.5	14.5	614 9	ADY16108	Ady16108 PRO polyp
57	70.5	14.5	764 5	ABB77432	Abb77432 Human tum
58	70.5	14.5	764 7	ADC99062	Adc99062 Human KKP
59	70.5	14.5	817 4	AAE38657	Aae38657 Human pol
60	70.5	14.5	863 4	AAE38656	Aae38656 Human pol
61	70.5	14.5	1135 8	ADS10706	Ads10706 Human the
62	70.5	14.5	1181 8	ADS10708	Ads10708 Human the
63	70.5	14.5	1186 8	ADS10709	Ads10709 Human the
64	70.5	14.5	1188 8	ADH45460	Adh45460 Human mol
65	70.5	14.5	1206 5	ADH48860	Adh48860 NOV61 pro
66	70.5	14.5	1214 7	ADK65785	Adk65785 Angiogene
67	69.5	14.3	374 4	AAE39682	Aae39682 Human pol
68	69.5	14.3	389 4	AAE41468	Aae41468 Human pol
69	69.5	14.3	481 5	AAU93169	Aau93169 Arabidops
70	69.5	14.3	481 7	ADD30148	Add30148 Plant yie
71	69.5	14.3	481 7	ADE31497	Ade31497 Plant yie
72	69.5	14.3	481 8	ADI41933	Adi41933 Plant tra
73	69.5	14.3	485 5	AAE08447	Aeb08447 Human lat
74	69.5	14.3	488 4	AAE94458	Aab94458 Human pro
75	69.5	14.3	488 4	AAE67252	Aag67252 Amino aci

ALIGNMENTS

RESULT 1
ABB78158
ID ABB78158 standard; protein; 91 AA.
XX ABB78158;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
XX hydroxyl radical; DNA damage; YggX homologue.
OS Unidentified.
XX
XX US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 60

QY 61 EHRKLLQEQEMVNFLEEGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEQEMVNFLEEGKEVHIIEGYTPEDKK 91

RESULT 2
ABB78157
ID ABB78157 standard; protein; 91 AA.
XX
AC ABB78157;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Unidentified.

XX US2002072118-A1.
XX
PD 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.
XX
PF 22-SEP-2000; 2000US-0234588P.

XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 91 AA;

Query Match 100.0%; Score 486; DB 5; Length 91;
Best Local Similarity 100.0%; Pred. No. 3.1e-48;
Matches 91; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 60
Db 1 MSRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNA 60

QY 61 EHRKLLQEQEMVNFLEEGKEVHIIEGYTPEDKK 91
Db 61 EHRKLLQEQEMVNFLEEGKEVHIIEGYTPEDKK 91

RESULT 3
ABB78156
ID ABB78156 standard; protein; 91 AA.
XX
AC ABB78156;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Escherichia coli.

XX US2002072118-A1.
XX
PD 13-JUN-2002.

XX 18-SEP-2001; 2001US-00955502.
XX
PF 22-SEP-2000; 2000US-0234588P.

XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.

XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.

XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 14.0477 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAEAGQDFQ.....NFLPEGKEVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR 80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	486	100.0	91	2	A85954	hypothetical prote
2	486	100.0	91	2	A65082	hypothetical prote
3	486	100.0	91	2	F91108	hypothetical prote
4	469	96.5	91	2	AH0879	conserved hypothet
5	402	82.7	90	2	C82320	conserved hypothet
6	396	81.5	90	2	AI0116	conserved hypothet
7	387	79.6	90	2	C64013	hypothetical prote
8	265	54.5	93	2	E84994	hypothetical prote
9	231	47.5	90	2	H83003	conserved hypothet
10	226	46.5	105	2	C82624	conserved hypothet
11	213	43.8	88	2	H81014	conserved hypothet
12	78	16.0	507	2	C81063	fumarate hydratase
13	78	16.0	546	2	A81807	fumarate hydratase
14	76	15.6	548	2	A54510	protein unc-73b [1
15	75.5	15.5	1638	2	D87749	guanine nucleotide
16	75.5	15.5	2488	2	T42739	hypothetical prote
17	74.5	15.3	683	2	AC2256	hypothetical prote
18	72	14.8	265	2	T46013	hypothetical prote
19	72	14.8	447	2	T16527	hypothetical prote
20	72	14.8	507	2	A83105	probable fumarase
21	72	14.8	511	2	A99574	ABC transporter at
22	69	14.2	258	2	A97991	hypothetical prote
23	69	14.2	258	2	E95121	phosphoesterase, p
24	69	14.2	548	2	A28209	60K filarial antig
25	69	14.2	1119	2	T15842	hypothetical prote
26	68	14.0	2672	2	A48126	translation activa
27	67.5	13.9	209	2	I64172	hypothetical prote
28	67	13.8	235	2	G65212	hypothetical prote
29	67	13.8	324	2	T05429	hypothetical prote

30	67	13.8	433	2	A70465	probable GTP bindi
31	67	13.8	447	2	JC2076	alpha-1,3-mannosyl
32	66.5	13.7	544	2	T40058	probable chromatin
33	66.5	13.7	1260	2	T04440	hypothetical prote
34	66	13.6	593	2	C64097	probable soluble 1
35	66	13.6	689	2	F83902	beta-galactosidase
36	65.5	13.5	173	2	H86869	hypothetical prote
37	65.5	13.5	305	2	A75211	asparaginase (EC 3
38	65.5	13.5	323	2	A90536	lipoprotein (impor
39	65.5	13.5	365	2	B54128	hypothetical prote
40	65.5	13.5	821	2	AI2417	hypothetical prote
41	65	13.4	251	2	E90428	hypothetical prote
42	65	13.4	330	2	S74456	regulatory protein
43	65	13.4	445	1	XUHUW8	alpha-1,3-mannosyl
44	65	13.4	456	2	G71152	hypothetical prote
45	65	13.4	1008	2	H85055	probable transposo
46	65	13.4	1141	2	T29185	hypothetical prote
47	65	13.4	1230	2	S56850	SMC1 protein homol
48	64.5	13.3	245	2	AG2300	hypothetical prote
49	64.5	13.3	305	2	A71247	probable L-asparag
50	64.5	13.3	495	2	AH0985	probable zinc-prot
51	64.5	13.3	859	2	T29630	hypothetical prote
52	64	13.2	220	2	S62410	hypothetical prote
53	64	13.2	438	2	T37786	probable RNA-bindi
54	64	13.2	447	1	A38561	alpha-1,3-mannosyl
55	64	13.2	583	2	T48365	hypothetical prote
56	64	13.2	604	2	S66993	hypothetical prote
57	64	13.2	990	2	T43445	hypothetical prote
58	64	13.2	1051	2	S27002	phospholipase C (E
59	64	13.2	1234	2	S52099	phospholipase C be
60	64	13.2	1234	2	I38994	phospholipase C-be
61	63.5	13.1	91	2	H90521	hypothetical prote
62	63.5	13.1	243	2	T29635	hypothetical prote
63	63.5	13.1	460	2	T00639	hypothetical prote
64	63.5	13.1	591	1	FOVWVM	98g polypeptide -
65	63	13.0	880	2	AE0179	probable ATPase ch
66	63	13.0	1251	2	A56677	neuronal cell cycl
67	63	13.0	1327	2	T14594	guanidine nucleoti
68	63	13.0	1611	1	WMTMPV	183K protein - pep
69	62.5	12.9	483	1	SVSEST	glutamate-tRNA lig
70	62.5	12.9	551	2	B84106	hypothetical prote
71	62.5	12.9	555	2	C96667	unknown protein, 7
72	62.5	12.9	617	2	B71071	probable prolly en
73	62.5	12.9	964	1	T04325	probable ATP-depen
74	62.5	12.9	1417	2	T00661	hypothetical prote
75	62	12.8	169	2	PN0560	phytochrome - long

ALIGNMENTS

RESULT 1
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL9:
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C:Accession: A85954
R:Perma, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhe
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, B.; Potamousis, K.; Apodaca
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85954
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-91 <STO>
A:Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AB005174; NID:G12517511; 1
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: yggX
C:Superfamily: fe(II) trafficking protein YggX
Query Match 100.0%; Score 486; DB 2; Length 91;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 83.6663 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-11
Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAEQDFQ.....NFLFEKGVHIEGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : UniProt_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	481	99.0	90	1	FETP_ECO57
2	481	99.0	90	1	FETP_ECOLI
3	481	99.0	90	1	FETP_SHIFL
4	477	98.1	90	1	FETP_ECOL6
5	464	95.5	90	1	FETP_SALCH
6	464	95.5	90	1	FETP_SALPA
7	464	95.5	90	1	FETP_SALTI
8	464	95.5	90	1	FETP_SALTY
9	411	84.6	90	1	FETP_ERWCT
10	404	83.1	90	1	FETP_YERPS
11	402	82.7	90	1	FETP_VIBCH
12	402	82.7	90	1	FETP_VIBVU
13	402	82.7	90	1	FETP_VIBBY
14	399	82.1	90	1	FETP_VIBPA
15	396	81.5	90	1	FETP_YERPE
16	389	80.0	90	1	FETP_MANSN
17	387	79.6	90	1	FETP_HAENI
18	387	79.6	90	2	Q4QMD9_HAB18
19	382	78.6	90	1	FETP_PHOPR
20	381	78.4	90	1	FETP_PHOHL
21	379	78.0	90	1	FETP_PASMU
22	373	76.7	94	1	FETP_HABDU
23	366	75.3	90	1	FETP_VIBF1
24	335	68.9	90	1	FETP_IDILO
25	332	68.3	92	1	FETP_SHEON
26	265	54.5	77	1	FETP_BUCAL
27	255	52.5	90	1	FETP_BORBR
28	255	52.5	90	1	FETP_BORPA
29	255	52.5	90	1	FETP_BORPE
30	247	50.8	78	1	FETP_BUCAP
31	235	48.4	78	1	FETP_WIGBR

32	231.5	47.6	89	1	FETP_LEGPA	Q5x3x9 legionella
33	231.5	47.6	89	1	FETP_LEGPH	Q5zu80 legionella
34	231	47.5	90	1	FETP_PSEAE	Q9hu36 pseudomonas
35	231	47.5	91	1	FETP_XANAC	Q8pjh7 xanthomonas
36	228.5	47.0	89	1	FETP_LEGPL	Q5wvc4 legionella
37	227	46.7	90	1	FETP_COXBU	Q83d06 coxiella bu
38	227	46.7	90	1	FETP_PSESM	Q87uf5 pseudomonas
39	227	46.7	90	2	Q4ZLP3_PSESY	Q4zlp3 pseudomonas
40	226	46.5	90	1	FETP_XYLFY	Q9pc73 xylella fas
41	225	46.3	90	1	FETP_PSEPK	Q88r49 pseudomonas
42	225	46.3	92	1	FETP_XANOR	Q5gy22 xanthomonas
43	223	45.9	90	2	Q4J228_AZOVI	Q4j228 azotobacter
44	222	45.7	90	1	FETP_XYLFY	Q87d06 xylella fas
45	222	45.7	92	1	FETP_XANCP	Q8p829 xanthomonas
46	222	45.7	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
47	220	45.3	90	1	FETP_NITEU	Q82xf2 nitrosomona
48	215	44.2	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
49	214	44.0	87	1	FETP_BUCBP	Q89a44 buchnera ap
50	213	43.8	88	1	FETP_NEIG1	Q5f553 neisseria g
51	213	43.8	88	1	FETP_NEIMA	P67615 neisseria m
52	213	43.8	88	1	FETP_NEIMB	P67616 neisseria m
53	212	43.6	79	1	FETP_CANBF	Q7vrg9 candidatus
54	212	43.6	90	2	Q4KJT2_PSEF5	Q4kjt2 pseudomonas
55	211	43.4	90	1	FETP_CHRVO	Q7nsr4 chromobacte
56	207	42.6	91	2	Q4LS19_9BURK	Q4ls19 burkholderi
57	206	42.4	91	1	FETP_BURMA	Q621s9 burkholderi
58	206	42.4	91	1	FETP_BURPS	Q63s14 burkholderi
59	206	42.4	91	1	FETP_RALSO	Q8y010 ralstonia s
60	200	41.2	90	1	FETP_METCA	Q60aj7 methylococc
61	199	40.9	87	1	FETP_FRATT	Q5nhj8 francisella
62	194.5	40.0	90	1	FETP_ACTIAD	Q6ffb3 acinetobact
63	144	29.6	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	142	29.2	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
65	90.5	18.6	482	2	Q5NUY1_9BURK	Q5nuyl ralstonia m
66	85.5	17.6	514	2	Q6A1Z9_DESPS	Q6a1z9 desulfotale
67	81	16.7	507	2	Q88PF3_PSEPK	Q88pf3 pseudomonas
68	81	16.7	508	2	Q7NSFO_CHRVO	Q7nsfo chromobacte
69	80	16.5	486	2	Q7WX51_ALCEU	Q7wx51 alcaligenes
70	78.5	16.2	760	2	Q4YVR2_PLABE	Q4yvr2 plasmodium
71	78	16.0	507	2	Q9JYE3_NEIMB	Q9jye3 neisseria m
72	78	16.0	546	2	Q9JTE3_NEIMA	Q9jte3 neisseria m
73	78	16.0	2248	2	Q4UB40_THEAN	Q4ub40 theileria a
74	77.5	15.9	337	2	Q81AR8_BACCR	Q81ar8 bacillus ce
75	77.5	15.9	1123	2	Q7RJL0_PLAYO	Q7rjl0 plasmodium

ALIGNMENTS

RESULT 1
FETP_ECO57
ID FETP_ECO57 STANDARD; PRT; 90 AA.
AC P0A8P4; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yggX; OrderedLocustNames=z4307, Ecs3838;
OS Escherichia coli O157:H7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=83334;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=O157:H7 / EDL933 / ATCC 700927 / EHEC;
RX MEDLINE=21074935; PubMed=11206551; DOI=10.1038/35054089;
RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamoudis K.,
RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA Welch R.A., Blattner F.R.;
RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";


```
RL Nature 409:529-533(2001).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=0157:H7 / Sakai / RIMD 0509952 / EHEC;
RX MEDLINE=21156231; PubMed=11258796;
RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA Tida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT "Complete genome sequence of enterohemorrhagic Escherichia coli
RT O157:H7 and genomic comparison with a laboratory strain K-12.";
RL DNA Res. 8:11-22(2001).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -!- SUBUNIT: Monomer (By similarity).
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC
CC EMBL; AB005174; AAG58093.1; -; Genomic DNA.
CC EMBL; BA000007; BAB37261.1; -; Genomic DNA.
CC PIR; A85954; A85954.
CC PIR; F91108; F91108.
CC HAMAP; MF_00686; -, 1.
CC InterPro; IPR007457; Yg9X.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.
CC ProDom; PD029191; DUF495; 1.
CC Complete proteome; Iron.
CC INIT_MET 0 By similarity.
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNAE 61
Db 1 SRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNAE 60
Qy 62 HRKLEQEMVNFLEGKEVHIEGYTPEDKK 91
Db 61 HRKLEQEMVNFLEGKEVHIEGYTPEDKK 90

RESULT 2
FETP_ECOLI STANDARD; PRT; 90 AA.
AC POA8P3; P52065;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Name=yg9X; Ordered locus Names=b2962;
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Colado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
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RN [2]
RP PARTIAL PROTEIN SEQUENCE OF 1-12.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
RT in the genome of Escherichia coli K-12.";
RL Electrophoresis 18:1259-1313(1997).
RN [3]
RP PROTEIN SEQUENCE OF 1-10.
RC STRAIN=K12;
RX MEDLINE=99085675; PubMed=9868784;
RA Wasinger V.C., Humphrey-Smith I.;
RT "Small genes/gene-products in Escherichia coli K-12.";
RL FEMS Microbiol. Lett. 169:375-382(1998).
RN [4]
RP IDENTIFICATION BY MASS SPECTROMETRY.
RX MEDLINE=99420866; PubMed=10493123;
RX DOI=10.1002/(SICI)1522-2683(19990801)20:11<2181::AID-ELPS2181>3.CO;2-H;
RA Fountoulakis M., Takacs M.-F., Berndt P., Langen H., Takacs B.;
RT "Enrichment of low abundance proteins of Escherichia coli by
RT hydroxyapatite chromatography.";
RL Electrophoresis 20:2181-2195(1999).
RN [5]
RP INDUCTION, AND FUNCTION.
RC STRAIN=K12 / GC4468;
RX PubMed=14594836; DOI=10.1128/JB.185.22.6624-6632.2003;
RA Pomposiello P.J., Koutsolioutsou A., Carrasco D., Demple B.;
RT "SoxRS-regulated expression and genetic analysis of the yg9X gene of
RT Escherichia coli.";
RL J. Bacteriol. 185:6624-6632(2003).
RN [6]
RP STRUCTURE BY NMR, AND FUNCTION.
RX PubMed=15883188; DOI=10.1110/PS.051358105;
RA Osborne M.J., Siddiqui N., Landgraf D., Pomposiello P.J., Gehring K.;
RT "The solution structure of the oxidative stress-related protein Yg9X
RT from Escherichia coli.";
RL Protein Sci. 14:1673-1678(2005).
CC -!- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes. Necessary to
CC maintain high levels of aconitase under oxidative stress.
CC -!- SUBUNIT: Monomer (Probable).
CC -!- INDUCTION: By oxidative stress and SoxS.
CC -!- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC
CC EMBL; U28377; AAA69129.1; -; Genomic DNA.
CC EMBL; U00096; AAC75999.1; -; Genomic DNA.
CC PIR; A65082; A65082.
CC PDB; 1YHD; NMR; A=1-90.
CC SWISS-2DPAGE; POA8P3; COLI.
CC Echobase; EB2809; -.
CC Ecogene; EG12984; Yg9X.
CC HAMAP; MF_00686; -, 1.
CC InterPro; IPR007457; Yg9X.
CC Pfam; PF04362; DUF495; 1.
CC PIRSF; PIRSF029827; Fe traffic_Yg9X; 1.
CC ProDom; PD029191; DUF495; 1.
CC 3D-structure; Complete proteome; Direct protein sequencing; Iron.
CC INIT_MET 0
CC SEQUENCE 90 AA; 10821 MW; D7C66C2A35B62402 CRC64;

Query Match 99.0%; Score 481; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 4.5e-41;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 SRTIFCTFLQREAGQDFQLYPGELGKRIYNEISKEAWAQWQHQTMLINEKLNMMNAE 61
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 21.2781 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-11

Perfect score: 486
Sequence: 1 MSRTIFCTFLQREAGQDFQ.....NPLFEKGKWHIGYTPEDKK 91

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Issued Patents AA:*
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4: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	450	92.6	107	2	US-09-489-039A-11962
2	389	80.0	93	2	US-09-543-681A-5443
3	231	47.5	122	2	US-09-252-991A-23355
4	199.5	41.0	92	2	US-09-328-352-5456
5	131	27.0	110	2	US-09-540-236-2859
6	76	15.6	548	2	US-09-167-299-3
7	72	14.8	474	2	US-09-252-991A-24473
8	70.5	14.5	1214	2	US-10-164-595-24
9	67.5	13.9	184	2	US-09-325-932A-66
10	67.5	13.9	546	1	US-08-533-669A-2
11	67.5	13.9	546	2	US-09-183-861-2
12	67.5	13.9	546	2	US-09-022-765-2
13	67.5	13.9	546	2	US-09-551-974A-2
14	67.5	13.9	546	2	US-09-565-501A-2
15	67.5	13.9	546	2	US-09-639-206A-2
16	67.5	13.9	546	2	US-09-874-923-2
17	67.5	13.9	546	2	US-08-798-841-2
18	67.5	13.9	982	2	US-09-551-974A-95
19	67.5	13.9	982	2	US-09-565-501A-95
20	67.5	13.9	982	2	US-09-639-206A-95
21	67.5	13.9	982	2	US-09-874-923-95
22	67.5	13.9	1427	2	US-09-551-974A-97
23	67.5	13.9	1427	2	US-09-565-501A-97
24	67.5	13.9	1427	2	US-09-639-206A-97
25	67.5	13.9	1427	2	US-09-874-923-97
26	67.5	13.9	1641	2	US-09-551-974A-96
27	67.5	13.9	1641	2	US-09-565-501A-96

28	67.5	13.9	1641	2	US-09-639-206A-96	Sequence 96, Appl
29	67.5	13.9	1641	2	US-09-874-923-96	Sequence 96, Appl
30	65.5	13.5	395	2	US-09-914-098-46	Sequence 46, Appl
31	65	13.4	292	2	US-09-328-352-5836	Sequence 5836, Ap
32	64.5	13.3	209	2	US-09-252-991A-20905	Sequence 20905, A
33	64	13.2	227	2	US-09-270-767-58283	Sequence 58283, A
34	64	13.2	280	2	US-09-323-998E-37	Sequence 37, Appl
35	64	13.2	448	2	US-09-270-767-42959	Sequence 42959, A
36	64	13.2	534	2	US-09-312-762A-5	Sequence 5, Appli
37	63.5	13.1	591	2	US-09-370-368-8	Sequence 8, Appli
38	63	13.0	525	2	US-09-540-236-2250	Sequence 2250, Ap
39	63	13.0	569	2	US-09-107-532A-6689	Sequence 6689, Ap
40	62.5	12.9	325	2	US-09-134-000C-4346	Sequence 4346, Ap
41	62.5	12.9	544	2	US-09-248-796A-18911	Sequence 18911, A
42	62.5	12.9	798	2	US-09-861-451A-12	Sequence 12, Appl
43	62	12.8	959	2	US-09-543-681A-6879	Sequence 6879, Ap
44	62	12.8	1394	2	US-09-248-796A-19555	Sequence 19555, A
45	62	12.8	1501	2	US-09-710-279-2850	Sequence 2850, Ap
46	62	12.8	1529	2	US-09-134-001C-3945	Sequence 3945, Ap
47	61.5	12.7	57	2	US-09-562-737-124	Sequence 124, App
48	61.5	12.7	116	2	US-09-562-737-125	Sequence 125, App
49	61.5	12.7	311	2	US-09-248-796A-26397	Sequence 26397, A
50	61.5	12.7	419	2	US-09-543-681A-7295	Sequence 7295, Ap
51	61.5	12.7	680	2	US-09-298-924-4	Sequence 4, Appli
52	61.5	12.7	720	1	US-08-840-236-1	Sequence 1, Appli
53	61.5	12.7	720	1	US-08-505-448A-1	Sequence 1004, Ap
54	61	12.6	308	2	US-09-198-452A-1004	Sequence 16, Appl
55	61	12.6	444	2	US-09-861-451A-16	Sequence 934, App
56	61	12.6	480	2	US-09-438-185A-934	Sequence 4802, Ap
57	60.5	12.4	139	2	US-09-513-999C-4802	Sequence 4800, Ap
58	60.5	12.4	258	2	US-09-513-999C-4800	Sequence 6012, Ap
59	60.5	12.4	264	2	US-09-949-016-6012	Sequence 11703, A
60	60.5	12.4	276	2	US-09-949-016-11703	Sequence 48, Appl
61	60.5	12.4	404	2	US-09-873-404-2	Sequence 2, Appli
62	60.5	12.4	640	2	US-09-270-767-41085	Sequence 2, Appli
63	60.5	12.4	640	2	US-09-270-767-56301	Sequence 56301, A
64	60.5	12.4	640	2	US-09-270-767-46116	Sequence 8705, Ap
65	60	12.3	98	2	US-09-270-767-41085	Sequence 32, Appl
66	60	12.3	98	2	US-09-270-767-56301	
67	60	12.3	184	2	US-09-270-767-61671	
68	60	12.3	271	2	US-09-248-796A-19265	
69	60	12.3	279	2	US-09-198-452A-221	
70	60	12.3	279	2	US-09-438-185A-205	
71	60	12.3	331	2	US-09-328-352-6400	
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73	60	12.3	389	2	US-09-270-767-46116	
74	60	12.3	410	2	US-09-949-016-8705	
75	60	12.3	411	2	US-09-886-319A-32	

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-2

Perfect score: 461
Sequence: 1 MSRIVNCVKLKREAGIDFP.....QQMERFLPEDGTVEAQGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 75 summaries

Database :

1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	461	100.0	90	1	FETP_BORBR
2	461	100.0	90	1	FETP_BORPA
3	461	100.0	90	1	FETP_BORPB
4	313	67.9	91	1	FETP_RALSO
5	304	65.9	91	2	Q4LS19_9BURK
6	300	65.1	91	1	FETP_BURMA
7	300	65.1	91	1	FETP_BURPS
8	297	64.4	90	1	FETP_CHRVO
9	290	62.9	88	1	FETP_NEIGI
10	290	62.9	88	1	FETP_NEIMA
11	290	62.9	88	1	FETP_NEIMB
12	286	62.0	90	1	FETP_NITEU
13	260	56.4	90	1	FETP_METCA
14	256	55.5	90	1	FETP_HABIN
15	256	55.5	90	2	Q4QMD9_HABIS8
16	256	55.5	91	1	FETP_MANSN
17	256	55.5	92	1	FETP_SHEON
18	255	55.3	90	1	FETP_VIBPA
19	254	55.1	90	1	FETP_IDILO
20	252	54.7	90	1	FETP_VIBFI
21	251	54.4	90	1	FETP_PASMU
22	250	54.2	90	1	FETP_ECO57
23	250	54.2	90	1	FETP_ECOLI
24	250	54.2	90	1	FETP_SHIFL
25	250	54.2	90	1	FETP_VIBVU
26	250	54.2	90	1	FETP_VIBVY
27	249	54.0	89	1	FETP_LEGPA
28	249	54.0	89	1	FETP_LEGPH
29	249	54.0	89	1	FETP_VIBCH
30	248	53.8	89	1	FETP_LEGPL
31	247	53.6	90	1	FETP_PHOPR

32	246	53.4	90	1	FETP_ECOL6	Q8fe19 escherichia
33	246	53.4	90	1	FETP_PHOLL	Q7n711 photorhabdu
34	244	52.9	90	1	FETP_SALCH	Q57k04 salmoneilla
35	244	52.9	90	1	FETP_SALPA	Q5pmn1 salmoneilla
36	244	52.9	90	1	FETP_SALTI	Q67618 salmoneilla
37	244	52.9	90	1	FETP_SALTY	P67617 salmoneilla
38	243	52.7	94	1	FETP_HAEDU	Q7vkb6 haemophilus
39	240	52.1	90	1	FETP_PSEAE	Q9hu36 pseudomonas
40	239	51.8	90	1	FETP_ERWCT	Q6d8j9 erwina car
41	239	51.8	90	2	Q4J228_AZOV1	Q4j228 azotobacter
42	234	50.8	90	1	FETP_YERPS	Q666m3 yersinia ps
43	231.5	50.2	90	1	FETP_AC1AD	Q6f6b3 acinetobact
44	231	50.1	91	1	FETP_XANAC	Q8pjh7 xanthomonas
45	230	49.9	90	1	FETP_COXBU	Q83d06 coxiella bu
46	226	49.0	90	1	FETP_YERPE	Q8zhe7 yersinia pe
47	223	48.4	92	1	FETP_XANOR	Q5gy22 xanthomonas
48	222	48.2	90	1	FETP_PSEBP	Q88r49 pseudomonas
49	222	48.2	92	1	FETP_XANCP	Q8p829 pseudomonas
50	222	48.2	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
51	220	47.7	78	1	FETP_BUCAP	Q8k925 buchnera ap
52	218	47.3	90	1	FETP_PSESM	Q87uf5 pseudomonas
53	218	47.3	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
54	214	46.4	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
55	214	46.4	90	2	Q4KJT2_PSEF5	Q4kjt2 pseudomonas
56	213	46.2	79	1	FETP_CANBF	Q7vr99 candidatus
57	212	46.0	90	1	FETP_XYLFY	Q87d06 xylella fas
58	205	44.5	90	1	FETP_XYLFA	Q9pc73 xylella fas
59	200	43.4	77	1	FETP_BUCAI	P57618 buchnera ap
60	193	41.9	78	1	FETP_WIGBR	Q8d3c5 wigleswort
61	184	39.9	87	1	FETP_FRATY	Q5nhj8 francisella
62	178	38.6	92	2	Q4NWQ4_9DELT	Q4nwq4 anaeromyxob
63	175	38.0	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	157	34.1	87	1	FETP_BUCBP	Q89a44 buchnera ap
65	79.5	17.2	116	2	Q6UFK7_9HIV1	Q6ufk7 human immun
66	77	16.7	330	2	Q5DA35_SCHJA	Q5da35 schistosoma
67	77	16.7	2410	2	Q5AZ49_EMENT	Q5az49 aspergillus
68	76.5	16.6	207	1	COAE_STAAM	P63830 staphylococ
69	76.5	16.6	207	1	COAE_STAN	P63831 staphylococ
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71	76.5	16.6	207	1	COAE_STAAS	Q6g8n8 staphylococ
72	76.5	16.6	207	1	COAE_STAAS	P63832 staphylococ
73	76.5	16.6	207	2	Q5HF85_STAAC	Q5hf85 staphylococ
74	76.5	16.6	749	2	Q9CGA2_LACLA	Q9cgaz lactococcus
75	75.5	16.4	116	2	Q6WS71_9HIV1	Q6ws71 human immun

ALIGNMENTS

RESULT 1
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ID FETP_BORBR STANDARD; PRT; 90 AA.
AC Q7WH06;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN Ordered locus names=BB3405;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltham T., Goble A., Hamlin N., Hauser H., Holroyd S., Jags K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,


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RA Rabbिनowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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CC EMBL; BX640447; CAB33897.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNEENRLNLADA 60
Db 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNEENRLNLADA 60

QY 61 PAKRYLQQQOMERFLFEDGTVEAAGYVP 87
Db 61 PAKRYLQQQOMERFLFEDGTVEAAGYVP 87

RESULT 2
FETP_BORPA
ID FETP_BORPA STANDARD; PRT; 90 AA.
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP1703;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabbिनowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
```

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CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNEENRLNLADA 60
Db 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNEENRLNLADA 60

QY 61 PAKRYLQQQOMERFLFEDGTVEAAGYVP 87
Db 61 PAKRYLQQQOMERFLFEDGTVEAAGYVP 87

RESULT 3
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ID FETP_BORPE STANDARD; PRT; 90 AA.
AC Q7VWC4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BP2336;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tohama 1 / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtmann M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neil S., Ormond D., Price C.,
RA Rabbिनowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC EMBL; BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds

(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-2

Perfect score: 461

Sequence: 1 MSRIYVCVKIKRAEGLDFP.....QOMERFLFEDGTVEAGGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 75 summaries

Database :

Issued_Patents_AA:*
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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	52.7	107	2	US-09-489-039A-11962
2	242	52.5	93	2	US-09-543-681A-5443
3	240	52.1	122	2	US-09-252-991A-23355
4	230.5	50.0	92	2	US-09-328-352-5456
5	164	35.6	110	2	US-09-540-236-2859
6	72.5	15.7	303	2	US-09-902-540-13601
7	70.5	15.3	200	2	US-09-710-279-1186
8	70.5	15.3	200	2	US-09-710-279-2390
9	70.5	15.3	208	2	US-09-134-001C-3785
10	67.5	14.6	504	1	US-08-441-139-18
11	67.5	14.6	521	1	US-08-557-122A-32
12	67.5	14.6	521	2	US-09-262-666-32
13	67.5	14.6	522	2	US-09-368-588-2
14	67.5	14.6	530	1	US-08-557-122A-35
15	67.5	14.6	530	2	US-09-262-666-35
16	67	14.5	381	2	US-09-949-016-9788
17	67	14.5	381	2	US-09-964-899-13
18	66.5	14.4	591	2	US-09-370-368-8
19	66	14.3	503	2	US-09-058-260-26
20	65	14.1	366	2	US-08-928-213B-59
21	64.5	14.0	805	1	US-08-045-806-2
22	64.5	14.0	805	1	US-08-366-051B-2
23	64	13.9	856	2	US-09-252-991A-17850
24	64	13.9	1493	2	US-09-713-273A-20
25	63.5	13.8	219	2	US-08-928-213B-61
26	63.5	13.8	498	2	US-09-058-260-16
27	63.5	13.8	503	1	US-08-781-802-2

28	63.5	13.8	503	1	US-08-781-802-10	Sequence 10, Appl
29	63.5	13.8	503	1	US-08-781-802-12	Sequence 12, Appl
30	63.5	13.8	503	2	US-08-694-078-2	Sequence 2, Appli
31	63.5	13.8	503	2	US-09-058-260-2	Sequence 2, Appli
32	63.5	13.8	503	2	US-09-058-260-10	Sequence 10, Appl
33	63.5	13.8	503	2	US-09-058-260-12	Sequence 12, Appl
34	63.5	13.8	503	2	US-09-058-260-28	Sequence 28, Appl
35	63.5	13.8	503	2	US-09-058-260-30	Sequence 30, Appl
36	63.5	13.8	1242	2	US-09-107-532A-5241	Sequence 5241, Ap
37	63	13.7	581	2	US-09-713-273A-12	Sequence 12, Appl
38	63	13.7	2532	2	US-09-215-694-10	Sequence 10, Appl
39	63	13.7	2532	2	US-10-109-310-10	Sequence 10, Appl
40	62.5	13.6	666	2	US-09-270-767-62249	Sequence 62249, A
41	62.5	13.6	721	2	US-09-489-039A-7804	Sequence 46645, A
42	62.5	13.6	839	2	US-09-489-039A-13252	Sequence 13252, A
43	62	13.4	862	1	US-08-685-118-2	Sequence 2, Appli
44	62	13.4	862	1	US-08-915-495-2	Sequence 2, Appli
45	62	13.4	862	1	US-08-914-520-2	Sequence 2, Appli
46	62	13.4	862	2	US-09-853-180B-4	Sequence 4, Appli
47	62	13.4	864	2	US-09-949-016-7758	Sequence 7758, Ap
48	62	13.4	979	2	US-09-543-681A-5466	Sequence 5466, Ap
49	61.5	13.3	391	2	US-09-489-039A-7804	Sequence 7804, Ap
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51	61.5	13.3	518	2	US-09-746-390-4	Sequence 2, Appli
52	61.5	13.3	1464	2	US-09-045-360-2	Sequence 2, Appli
53	61.5	13.3	1464	2	US-09-713-273A-21	Sequence 21, Appl
54	61.5	13.3	1464	2	US-10-038-224-2	Sequence 2, Appli
55	61.5	13.3	1464	2	US-09-746-390-2	Sequence 2, Appli
56	61	13.2	185	2	US-09-107-532A-5608	Sequence 5608, Ap
57	61	13.2	312	2	US-09-605-703B-2656	Sequence 2656, Ap
58	61	13.2	1245	1	US-08-158-232-8	Sequence 8, Appli
59	61	13.2	1245	1	US-08-304-626-8	Sequence 8, Appli
60	61	13.2	1245	1	US-08-611-928-8	Sequence 8, Appli
61	61	13.2	1245	2	US-09-173-891-8	Sequence 8, Appli
62	61	13.2	1245	2	US-09-716-964B-87	Sequence 87, Appl
63	60.5	13.1	81	2	US-10-290-579A-138	Sequence 138, App
64	60.5	13.1	314	2	US-09-252-991A-18752	Sequence 18752, A
65	60	13.0	563	2	US-09-949-016-10801	Sequence 10801, A
66	60	13.0	713	2	US-09-540-236-3595	Sequence 3595, Ap
67	59.5	12.9	447	2	US-09-902-540-13195	Sequence 13195, A
68	59.5	12.9	623	2	US-10-104-047-3378	Sequence 3378, Ap
69	59.5	12.9	5037	2	US-09-424-783-4	Sequence 4, Appli
70	59	12.8	226	2	US-10-104-047-3820	Sequence 3820, Ap
71	59	12.8	265	2	US-09-710-279-174	Sequence 174, App
72	59	12.8	309	2	US-09-248-796A-14939	Sequence 14939, A
73	59	12.8	371	2	US-10-104-047-3421	Sequence 3421, Ap
74	59	12.8	437	2	US-09-134-001C-5342	Sequence 5342, Ap
75	59	12.8	520	2	US-09-328-352-7451	Sequence 7451, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-11962
Sequence 11962, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
CURRENT APPLICATION NUMBER: US/09/489, 039A
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US 60/117,747
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 11962
LENGTH: 107
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

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RESULT 2
US-09-543-681A-5443
: Sequence 5443, Application US/09543681A

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; APPLICANT: GARY BRETTON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 5443
; LENGTH: 93
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-5443

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4 MSRTIFCTFLNKEADGLDPQLYPGELGKRIPNEISKEAWGQMAKQTMLINEKCLNTMNP 63
Db

QY	61	RARKYLQOQMERFLFEDGTVEAQGYVP	87
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RESULT 3
US-09-252-991A-23355
: Sequence 23355, Application US/09252991A

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: GENERAL INFORMATION:
: APPLICANT: Marc J. Rubenfield et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
: TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: 107196.136
: CURRENT APPLICATION NUMBER: US/09/252,991A
: CURRENT FILING DATE: 1999-02-18
: PRIOR APPLICATION NUMBER: US 60/074,788
: PRIOR FILING DATE: 1998-02-18
: PRIOR APPLICATION NUMBER: US 60/094,190
: PRIOR FILING DATE: 1998-07-27
: NUMBER OF SEQ ID NOS: 33142
: SEQ ID NO 23355
: LENGTH: 122
: TYPE: PRT
: ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23355

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Query Match	52.1%	Score 240;	DB 2;	Length 122;
Best Local Similarity	50.6%	Pred. No. 2.4e-23;		
Matches 44;	Conservative 16;	Mismatches 27;	Indels 0;	Gaps 0;

1 MSRI VNCVKLKREAEGLDFPPYPGELGTRIWQI SKEAWEWKQIQTRLVNENRNLADA 60

Db 33 MSRTVMCRKYHEELPGIDRPPYPGAKAGEDITYNNVSRKAWDEMOIKQHTMLINERLNMNNA 922

Qy 61 RARKYLQOQOMERFLFEDGTVEAQGYVP 87

Db 93 EDRKFLQOEMDKFLSGEDYAKADGYVP 119

RESULT 4
US-09-328-352-5456

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: APPLICANT: Gary L. Breton et al.
: TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
: TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
: FILE REFERENCE: GTC99-03PA
: CURRENT APPLICATION NUMBER: US/09/328,352
: CURRENT FILING DATE: 1999-06-04
: NUMBER OF SEQ ID NOS: 8252
: SEQ ID NO 5456
: LENGTH: 92
: TYPE: PRT
: ORGANISM: Acinetobacter baumannii
US-09-328-352-5456

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RESULT 5
US-09-540-236-2859
Sequence 2859, Application US/09540236

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; GENBANK ENTRY INFORMATION
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; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CATAR
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2005-001
; CURRENT APPLICATION NUMBER: US/09/540,236
; CURRENT FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 3840
; SEQ ID NO 2859
; LENGTH: 110
; TYPE: PRT
; ORGANISM: M.catarrhalis
US-09-540-236-2859

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Best Local Similarity	38.1%	Pred. No. 1.6e-13;		
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DQ

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:
| : | : | : | : | : | : | : | :
DB

24 MVECRKYQONLPKLPNPFPFNAKGEIQTDTISAKANNAMLEQLTMLINEKHLSMIDPOAK 83

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RESULT 6
US-09-902-540-13601
; Sequence 13601, Application US/09902540

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-2
Perfect score: 461
Sequence: 1 MSRIVNCVKLRKRAEGIDFP.....QCMERFLFEDGTVEAQGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 segs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	461	100.0	87	3	US-09-955-502-3 Sequence 3, Appli
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4	300	65.1	87	3	US-09-955-502-29 Sequence 29, Appl
5	300	65.1	87	3	US-09-955-502-30 Sequence 30, Appl
6	290	62.9	88	3	US-09-955-502-26 Sequence 26, Appl
7	290	62.9	88	3	US-09-955-502-27 Sequence 27, Appl
8	290	62.9	88	3	US-09-955-502-28 Sequence 28, Appl
9	275	59.7	87	3	US-09-955-502-31 Sequence 31, Appl
10	260	56.4	87	3	US-09-955-502-32 Sequence 32, Appl
11	260	56.4	91	3	US-09-955-502-5 Sequence 5, Appli
12	256	55.5	87	3	US-09-955-502-7 Sequence 7, Appli
13	256	55.5	88	3	US-09-955-502-9 Sequence 9, Appli
14	255	55.3	91	3	US-09-955-502-11 Sequence 11, Appl
15	255	55.3	91	3	US-09-955-502-12 Sequence 12, Appl
16	255	55.3	91	3	US-09-955-502-13 Sequence 13, Appl
17	251	54.4	87	3	US-09-955-502-6 Sequence 6, Appl
18	249	54.0	88	3	US-09-955-502-15 Sequence 15, Appl
19	249	54.0	90	3	US-09-955-502-10 Sequence 10, Appl
20	249	54.0	91	3	US-09-955-502-14 Sequence 14, Appl
21	249	54.0	91	3	US-09-955-502-16 Sequence 16, Appl
22	249	54.0	91	3	US-09-955-502-17 Sequence 17, Appl
23	243	52.7	87	3	US-09-955-502-8 Sequence 8, Appli
24	242	52.5	91	3	US-09-955-502-18 Sequence 18, Appl
25	240	52.1	87	3	US-09-955-502-25 Sequence 25, Appl
26	230	49.9	88	3	US-09-955-502-33 Sequence 33, Appl
27	226	49.0	90	3	US-09-955-502-20 Sequence 20, Appl

28	222	48.2	78	3	US-09-955-502-19	Sequence 19, Appl
29	222	48.2	87	3	US-09-955-502-24	Sequence 24, Appl
30	218	47.3	90	3	US-09-955-502-23	Sequence 23, Appl
31	205	44.5	89	3	US-09-955-502-22	Sequence 22, Appl
32	200	43.4	76	3	US-09-955-502-21	Sequence 21, Appl
33	76.5	16.6	207	5	US-10-857-625-698	Sequence 698, App
34	70.5	15.3	208	4	US-10-724-972A-6021	Sequence 6021, Ap
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36	69	15.0	373	4	US-10-437-963-107538	Sequence 107538,
37	69	15.0	428	4	US-10-437-963-146305	Sequence 146305,
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45	67	14.5	381	3	US-09-964-899-13	Sequence 13, Appl
46	67	14.5	381	5	US-10-975-523-13	Sequence 13, Appl
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48	67	14.5	1602	4	US-10-437-963-114183	Sequence 114183,
49	66.5	14.4	591	3	US-09-827-822-8	Sequence 8, Appli
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52	66	14.3	997	5	US-10-485-710-117	Sequence 117, App
53	65.5	14.2	348	4	US-10-437-963-121938	Sequence 121938,
54	65.5	14.2	596	4	US-10-437-963-130475	Sequence 130475,
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57	65	14.1	323	5	US-10-732-923-10032	Sequence 10032, A
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63	65	14.1	2073	4	US-10-437-963-180266	Sequence 180266,
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69	64.5	14.0	513	6	US-11-097-143-9255	Sequence 9255, Ap
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72	64.5	14.0	805	4	US-10-744-544-14	Sequence 14, Appl
73	64.5	14.0	818	4	US-10-437-963-156121	Sequence 156121,
74	64.5	14.0	890	4	US-10-437-963-156221	Sequence 156221,
75	64.5	14.0	897	4	US-10-437-963-165505	Sequence 165505,

ALIGNMENTS

RESULT 1

US-09-955-502-2

; Sequence 2, Application US/09955502

; Patent No. US20020072118A1

; GENERAL INFORMATION:

; APPLICANT: Downs, Diana M.

; APPLICANT: Gralnicks, Jeff A.

; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and

; FILE REFERENCE: 960296.97559

; CURRENT APPLICATION NUMBER: US/09/955,502

; PRIOR FILING DATE: 2001-09-18

; PRIOR APPLICATION NUMBER: 60/234,588

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 2

; LENGTH: 87

; TYPE: PRT

; ORGANISM: Bordetella pertussis

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
(without alignments)
218.595 Million cell updates/sec

Title: US-09-955-502A-2
Perfect score: 461
Sequence: 1 MSRIVNCVKKREAEGLDFP.....QQMERFLPEDGTVEAQGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : Published Applications AA New:*
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2: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
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4: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	290	62.9	88	US-10-467-657-968	Sequence 968, Appl
2	70.5	15.3	200	US-10-793-626-1186	Sequence 1186, Ap
3	70.5	15.3	200	US-10-793-626-2390	Sequence 2390, Ap
4	67	14.5	1320	US-11-098-686-10831	Sequence 10831, A
5	64.5	14.0	567	US-11-033-039-1279	Sequence 1279, Ap
6	64.5	14.0	805	US-11-108-539-2	Sequence 2, Appli
7	62.5	13.6	483	US-11-137-465-40	Sequence 40, Appl
8	61.5	13.3	832	US-11-098-686-10182	Sequence 10182, A
9	60	13.0	240	US-11-044-111-10	Sequence 10, Appl
10	59.5	12.9	623	US-11-072-512-3378	Sequence 3378, Ap
11	59	12.8	226	US-11-072-512-3820	Sequence 3820, Ap
12	59	12.8	265	US-10-793-626-174	Sequence 174, App
13	59	12.8	371	US-11-072-512-3421	Sequence 3421, Ap
14	59	12.8	805	US-10-927-641-77	Sequence 77, Appl
15	58.5	12.7	662	US-11-072-175-184	Sequence 184, App
16	58	12.6	919	US-10-821-234-951	Sequence 951, App
17	57.5	12.5	104	US-11-120-308-74	Sequence 74, Appl
18	57.5	12.5	398	US-10-793-626-44	Sequence 44, Appl
19	57.5	12.5	398	US-10-793-626-1498	Sequence 1498, Ap
20	57.5	12.5	897	US-10-821-234-1523	Sequence 1523, Ap
21	57	12.4	212	US-11-044-111-6	Sequence 6, Appli
22	57	12.4	212	US-11-044-111-26	Sequence 26, Appl
23	57	12.4	239	US-11-044-111-5	Sequence 5, Appli
24	57	12.4	239	US-11-044-111-25	Sequence 25, Appl
25	57	12.4	240	US-11-044-111-9	Sequence 9, Appli

26	57	12.4	464	6	US-10-959-322-5	Sequence 5, Appli
27	57	12.4	809	7	US-11-072-512-3367	Sequence 3367, Ap
28	57	12.4	1056	7	US-11-044-111-22	Sequence 22, Appl
29	56	12.1	183	7	US-11-072-512-3180	Sequence 3180, Ap
30	56	12.1	702	7	US-11-072-512-2154	Sequence 2154, Ap
31	56	12.1	1076	6	US-10-467-657-7916	Sequence 7916, Ap
32	55.5	12.0	237	6	US-10-467-657-570	Sequence 570, App
33	55.5	12.0	497	7	US-11-010-239-85	Sequence 85, Appl
34	55.5	12.0	522	7	US-11-072-512-3665	Sequence 3665, Ap
35	55.5	12.0	563	7	US-11-040-218-23	Sequence 23, Appl
36	55.5	12.0	625	7	US-11-072-512-3210	Sequence 3210, Ap
37	55.5	12.0	3353	7	US-11-037-243-64	Sequence 64, Appl
38	55	11.9	519	7	US-11-099-691-10	Sequence 10, Appl
39	54.5	11.8	356	7	US-11-143-986-8	Sequence 8, Appli
40	54.5	11.8	356	7	US-11-143-986-9	Sequence 9, Appli
41	54.5	11.8	1275	6	US-10-724-598-49	Sequence 49, Appl
42	54.5	11.8	1340	7	US-11-070-575-6	Sequence 6, Appli
43	54.5	11.8	1344	7	US-11-091-643-20	Sequence 20, Appl
44	54.5	11.8	1659	7	US-11-072-175-205	Sequence 205, App
45	54.5	11.8	2080	7	US-11-124-367A-364	Sequence 364, App
46	54.5	11.8	2542	7	US-11-124-367A-363	Sequence 363, App
47	54	11.7	331	7	US-11-098-686-10431	Sequence 10431, A
48	53.5	11.6	372	6	US-10-467-657-2318	Sequence 2318, Ap
49	53.5	11.6	599	7	US-11-109-157A-3	Sequence 3, Appli
50	53.5	11.6	1373	7	US-11-098-686-11150	Sequence 11150, A
51	53.5	11.6	1686	7	US-11-109-157A-1	Sequence 1, Appli
52	53.5	11.6	1686	7	US-11-226-701-2	Sequence 2, Appli
53	53.5	11.6	2250	6	US-10-922-232B-57	Sequence 57, Appl
54	53.5	11.6	2630	7	US-11-186-731-2	Sequence 2, Appli
55	53.5	11.6	4060	6	US-10-922-232B-55	Sequence 55, Appl
56	53.5	11.6	6738	6	US-10-922-232B-56	Sequence 56, Appl
57	53.5	11.6	7968	7	US-11-186-731-5	Sequence 5, Appli
58	53	11.5	200	7	US-11-194-246-402	Sequence 402, App
59	53	11.5	240	7	US-11-007-282-8	Sequence 8, Appli
60	53	11.5	240	7	US-11-007-282-13	Sequence 13, Appl
61	53	11.5	240	7	US-11-007-282-14	Sequence 14, Appl
62	53	11.5	258	7	US-11-007-282-6	Sequence 6, Appli
63	53	11.5	342	7	US-11-156-084-25	Sequence 25, Appl
64	53	11.5	342	7	US-11-156-084-44	Sequence 44, Appl
65	53	11.5	369	7	US-11-156-084-45	Sequence 45, Appl
66	53	11.5	384	7	US-11-098-686-10752	Sequence 10752, A
67	53	11.5	453	7	US-11-072-512-3394	Sequence 3394, Ap
68	53	11.5	618	6	US-10-454-437-396	Sequence 396, App
69	53	11.5	619	7	US-11-156-084-24	Sequence 24, Appl
70	53	11.5	784	6	US-10-517-939-324	Sequence 324, App
71	52.5	11.4	143	6	US-10-793-626-1714	Sequence 1714, Ap
72	52.5	11.4	237	7	US-11-044-111-11	Sequence 11, Appl
73	52.5	11.4	362	6	US-10-517-939-88	Sequence 88, Appl
74	52.5	11.4	471	6	US-10-770-726-68	Sequence 68, Appl
75	52.5	11.4	471	7	US-11-152-366-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: Seqwin99, version 1.04

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; SEQ ID NO 968
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-657-968

Query Match      62.9%; Score 290; DB 6; Length 88;
Best Local Similarity 60.9%; Pred. No. 3.5e-27;
Matches 53; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

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Db 1 MARWVFCVCLKKEAEGMKFPPLPNELGKRIFENVSQEAWAATRRHQTMLINEIRLSLADP 60
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 61 RARKYLOQQOMERFLFEDGTVEAQGYVP 87
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 61 RAREYLAQQMEQYFFGADAVQGYVP 87
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```
RESULT 2
US-10-793-626-1186
; Sequence 1186, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1186
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-1186
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Query Match      15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDPP-PYPGELGTRIWQQISKEAWEW--KQIQ-TRLVNVNRLNLADARARKY----- 65
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Db 109 MDIPLLYENEL-----QDTVDEVVVVYTSIQIDRLMERNNLSLEDAKARVYSIQSIDK 163
   :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 66 -----LQQQMERFLFEDGTVEAQ 83
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 164 KSRMADHVIDNLGDKLELKQNLQKLLEEGYIQSE 198
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```
RESULT 3
US-10-793-626-2390
; Sequence 2390, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2390
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2390

Query Match      15.3%; Score 70.5; DB 6; Length 200;
Best Local Similarity 26.3%; Pred. No. 0.38;
Matches 25; Conservative 15; Mismatches 22; Indels 33; Gaps 5;

QY 17 LDPP-PYPGELGTRIWQQISKEAWEW--KQIQ-TRLVNVNRLNLADARARKY----- 65
   :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 109 MDIPLLYENEL-----QDTVDEVVVVYTSIQIDRLMERNNLSLEDAKARVYSIQSIDK 163
   :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 66 -----LQQQMERFLFEDGTVEAQ 83
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 164 KSRMADHVIDNLGDKLELKQNLQKLLEEGYIQSE 198
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RESULT 4
US-11-098-686-10831
; Sequence 10831, Application US/11098686
; Publication No. US20060024696A1
; GENERAL INFORMATION:
; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10831
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10831
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Query Match      14.5%; Score 67; DB 7; Length 1320;
Best Local Similarity 31.5%; Pred. No. 9.4;
Matches 23; Conservative 11; Mismatches 25; Indels 14; Gaps 3;

QY 5 VNCVKLKREAEGLDFFPYPGELGTRIWQQISKEAWEWKQIQTRLVNVNRLNLA---DAR 61
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Db 217 LNLESLHKSKELEQQQYHLKRLDIWHQ-----WEWRLLIQTRLEHLPPISAFPDGA 271
   :|||:|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

QY 62 ARKYLQQQMERFL 74
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 272 AR-----MERAL 278
   |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
```

```
RESULT 5
US-11-033-039-1279
; Sequence 1279, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model
Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461
Sequence: 1 MSRVNCVKLKREAEGLDFP.....QQMERFLFEDGTVEAQGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980a.*
- 2: Geneseqp1990a.*
- 3: Geneseqp2000a.*
- 4: Geneseqp2001a.*
- 5: Geneseqp2002a.*
- 6: Geneseqp2003a.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004a.*
- 9: Geneseqp2005a.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	5	ABB78148 Amino aci
2	461	100.0	87	5	ABB78147 Amino aci
3	443.5	96.2	86	5	ABB78149 Amino aci
4	300	65.1	87	5	ABB78175 Amino aci
5	294	63.8	87	5	ABB78174 Amino aci
6	290	62.9	88	5	ABB78171 Amino aci
7	290	62.9	88	5	ABB78172 Amino aci
8	290	62.9	88	5	ABB78173 Amino aci
9	290	62.9	88	6	ABP77219 N. gonorr
10	275	59.7	87	5	ABB78176 Amino aci
11	260	56.4	87	5	ABB78177 Amino aci
12	260	56.4	91	5	ABB78150 Amino aci
13	256	55.5	87	5	ABB78152 Amino aci
14	256	55.5	88	5	ABB78154 Amino aci
15	255	55.3	91	5	ABB78158 Amino aci
16	255	55.3	91	5	ABB78157 Amino aci
17	255	55.3	91	5	ABB78156 Amino aci
18	251	54.4	87	5	ABB78151 Amino aci
19	249	54.0	88	5	ABB78160 Amino aci
20	249	54.0	89	9	ABB41576 L. pneumo
21	249	54.0	90	5	ABB78155 Amino aci
22	249	54.0	91	5	ABB78161 Amino aci
23	249	54.0	91	5	ABB78159 Amino aci
24	249	54.0	91	5	ABB78162 Amino aci

25	249	54.0	95	9	AEB38294	L. pneumo
26	243	52.7	87	5	ABB78153	Amino aci
27	243	52.7	107	7	ABO65445	Klebsiell
28	242	52.5	91	5	ABB78163	Amino aci
29	242	52.5	93	7	ADF05158	Bacterial
30	240	52.1	87	5	ABB78170	Amino aci
31	240	52.1	122	7	ABO74609	Pseudomon
32	230.5	50.0	92	6	ADA34169	Acinetoba
33	230	49.9	88	5	ABB78178	Amino aci
34	226	49.0	90	5	ABB78165	Amino aci
35	222	48.2	78	5	ABB78164	Amino aci
36	222	48.2	87	5	ABB78169	Amino aci
37	218	47.3	90	5	ABB78168	Amino aci
38	200	43.4	76	5	ABB78166	Amino aci
39	197.5	42.8	90	5	ABB78167	Amino aci
40	164	35.6	110	8	ADL05173	M. catarr
41	76.5	16.6	207	6	ABM73508	Staphyloc
42	76.5	16.6	207	9	ADV16859	Staphyloc
43	76.5	16.6	207	9	ADW94758	Prolifera
44	76.5	16.6	749	5	ABB54524	Lactococc
45	72.5	15.7	303	9	ABM94402	M. xanthu
46	70.5	15.3	200	4	AAG82648	S. epider
47	70.5	15.3	200	4	AAG82046	S. epider
48	70.5	15.3	208	5	ABP38940	Staphyloc
49	70.5	15.3	208	8	ADS06726	Staphyloc
50	70.5	15.3	308	6	ABM70179	Photorhab
51	69.5	15.1	1233	8	ADQ66727	Novel hum
52	69	15.0	124	9	ADX40209	HIV Rev p
53	69	15.0	527	6	ADB06106	Alloiococ
54	69	15.0	528	6	ADB06108	Alloiococ
55	68.5	14.9	529	5	AAE26857	Anabaena
56	68.5	14.9	720	7	ADF29270	Bacterial
57	68.5	14.9	720	7	ADG32479	Pasteurel
58	67.5	14.6	522	2	AAW69726	Saccharom
59	67.5	14.6	522	9	ABB13006	Yeast pro
60	67.5	14.6	522	9	ABB50108	Yeast dis
61	67.5	14.6	526	2	AAR26174	Protein d
62	67.5	14.6	530	9	ABB13007	Yeast alt
63	67.5	14.6	530	9	ABB50109	Yeast dis
64	67.5	14.6	714	8	ADN20031	Bacterial
65	67	14.5	381	5	AAO20498	Human amy
66	67	14.5	389	4	AAH80170	Human pro
67	67	14.5	593	6	ABR39276	Protein s
68	67	14.5	678	5	ABB47819	Listeria
69	66.5	14.4	591	2	AAAY41141	Mouse mam
70	66.5	14.4	860	2	AAAY41140	Mouse mam
71	66.5	14.4	1755	2	AAAY41139	Mouse mam
72	66	14.3	229	3	AAAB41703	Human ORF
73	66	14.3	318	5	ABG77906	High leve
74	66	14.3	503	2	AAW85085	Esterase
75	66	14.3	856	6	ABR39820	Human SCA

ALIGNMENTS

RESULT 1
ABB78148
ID ABB78148 standard; protein; 87 AA.

XX ABB78148;

AC ABB78148;

DT 05-NOV-2002 (first entry)

XX Amino acid sequence of a YggX homologue.

DE Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;

XX hydroxyl radical; DNA damage; YggX homologue.

OS Bordetella parapertussis.

XX US2002072118-A1.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502a-3

Perfect score: 461
Sequence: 1 MSRIVNCVKLKREAEGLDFP.....QQMERFLFEDGTVEAGGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	290	62.9	88	2	H81014	conserved hypotnet
2	256	55.5	90	2	C64013	hypothetical prote
3	255	55.3	91	2	A85954	hypothetical prote
4	255	55.3	91	2	A65082	hypothetical prote
5	255	55.3	91	2	P91108	hypothetical prote
6	249	54.0	90	2	C82320	conserved hypotnet
7	249	54.0	91	2	AH0879	conserved hypotnet
8	240	52.1	90	2	H83003	conserved hypotnet
9	226	49.0	90	2	AI0116	conserved hypotnet
10	205	44.5	105	2	C82624	conserved hypotnet
11	200	43.4	93	2	B84994	hypothetical prote
12	76.5	16.6	207	2	B89952	conserved hypotnet
13	76.5	16.6	749	2	B86774	hypothetical prote
14	71.5	15.5	855	2	A45713	Env transmembrane
15	69	15.0	429	2	AE2501	hypothetical prote
16	68.5	14.9	241	2	SI9999	hypothetical prote
17	68	14.8	134	2	T37027	hypothetical prote
18	67.5	14.6	312	2	H82399	hypothetical prote
19	67.5	14.6	522	1	ISBYSS	protein disulfide-
20	67.5	14.6	714	2	S77385	nitrate reductase
21	67	14.5	389	2	T14751	hypothetical prote
22	67	14.5	678	2	AB1130	penicillin-binding
23	66.5	14.4	591	1	FOMVMM	gag polyprotein -
24	66	14.3	318	2	S77153	transcription init
25	66	14.3	1276	2	T09204	probable tail-host
26	65.5	14.2	164	2	E75293	hypothetical prote
27	65	14.1	238	1	LRRTB2	clathrin light cha
28	65	14.1	323	2	UT0755	ethylene-forming e
29	65	14.1	323	2	A86184	hypothetical prote

30	65	14.1	393	2	S03576	DNA-directed RNA p
31	64.5	14.0	228	2	C26599	clathrin light cha
32	64.5	14.0	229	2	B31775	clathrin light cha
33	64.5	14.0	393	2	T49257	protein kinase-lik
34	64.5	14.0	560	1	HMIWT7	hemagglutinin prec
35	64.5	14.0	622	2	T23804	hypothetical prote
36	64.5	14.0	805	2	A46266	aryl hydrocarbon r
37	64.5	14.0	2291	1	A46147	spectrin beta chai
38	64.5	14.0	3063	2	S55505	fatty-acid synthas
39	64	13.9	133	2	G75385	hypothetical prote
40	64	13.9	299	2	T29546	protein SPB-11 - C
41	64	13.9	451	2	B64312	signal recognition
42	64	13.9	1068	2	S73091	hypothetical prote
43	63.5	13.8	353	1	FOMVGR	gag polyprotein -
44	63.5	13.8	563	1	A45539	hemagglutinin prec
45	63.5	13.8	853	2	S58375	aryl hydrocarbon r
46	63.5	13.8	920	2	JC7313	WD-repeat protein
47	63	13.7	506	2	T50211	hypothetical prote
48	63	13.7	569	2	T47358	hypothetical prote
49	62.5	13.6	388	2	T38810	hypothetical prote
50	62.5	13.6	563	1	HMITVF	hemagglutinin prec
51	62.5	13.6	694	2	A95866	probable transketo
52	62.5	13.6	897	2	G02529	dynein heavy chain
53	62.5	13.6	1675	2	S70770	hypothetical prote
54	62	13.4	337	2	AG2423	hypothetical prote
55	62	13.4	416	2	C47017	probable transcrip
56	62	13.4	416	2	AF2017	RNA polymerase sig
57	62	13.4	563	2	T17316	hypothetical prote
58	62	13.4	989	2	T46183	zinc proteinase (E
59	62	13.4	1291	2	T09273	probable tail-host
60	61.5	13.3	188	2	C87216	probable hemagglut
61	61.5	13.3	283	4	FOHUB1	retrovirus-related
62	61.5	13.3	310	2	P64311	hypothetical prote
63	61.5	13.3	320	2	S69547	transcription init
64	61.5	13.3	1464	2	T07050	hypothetical prote
65	61.5	13.3	4644	2	A38905	dynein heavy chain
66	61	13.2	143	2	D70003	general stress pro
67	61	13.2	320	2	S11879	ethylene-forming e
68	61	13.2	321	2	T02754	probable 1-aminocy
69	61	13.2	372	2	B81952	probable type II r
70	61	13.2	504	1	O4RTD5	cytochrome P450 2D
71	61	13.2	678	2	AB1490	penicillin-binding
72	61	13.2	865	2	B84718	hypothetical prote
73	61	13.2	1138	2	T24635	hypothetical prote
74	61	13.2	1245	2	T18211	delta endotoxin -
75	60.5	13.1	138	2	T10309	hypothetical prote

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014; F81958
R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Bisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Mastignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: AB1000; MUID:20175755; PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TET>
A/Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AB002098; NID:g7227279; PIDN..
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jags, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

```

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: AB1775; MUID:20222556; PMID:10761919
A;Accession: F81958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB2021; MMA0419
C;Superfamily: fe(II) trafficking protein YggX

Query Match      62.9%; Score 290; DB 2; Length 88;
Best Local Similarity 60.9%; Pred. No. 4.6e-23;
Matches 53; Conservative 14; Mismatches 20; Indels 0; Gaps 0;

OY 1 MSRVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNLADA 60
   |||:|||||:||||:|||||:|||||:|:|:|||||:||||
Db 1 MARWVCVKLNKEAGMKRPPLPNELGKRIFENVSOEAWAAWTRHQTMLINENRSLADP 60
   |||:|||||:||||:|||||:|||||:|:|:|||||:||||

OY 61 RARKYLQQOMERFLFEDGTVEAQGYVP 87
   |||:|||||:||||:|||||:|||||:|:|:|||||:||||
Db 61 RAREYLAQOMEQYFFGDGADVQGYVP 87

RESULT 2
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C;Accession: C64013
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A.;
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J.;
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <TIGR>
A;Cross-references: UNIPROT:P4048; UNIPARC:UPI000013B0A4; GB:U32760; GB:L42023; NID:g15
C;Superfamily: fe(II) trafficking protein YggX

Query Match      55.5%; Score 256; DB 2; Length 90;
Best Local Similarity 57.5%; Pred. No. 1.5e-19;
Matches 50; Conservative 12; Mismatches 25; Indels 0; Gaps 0;

OY 1 MSRVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRLNLADA 60
   |||:|||||:|||||:|||||:|:|:|||||:||||:|
Db 1 MARTVFCEYLKKEAEGLDFOLYPGELGKRIFDSVSQAQGWGIKKQTMLVNEKKLMMNA 60
   |||:|||||:|||||:|||||:|:|:|||||:||||

OY 61 RARKYLQQOMERFLFEDGTVEAQGYVP 87
   |||:|||||:||||:|||||:|||||:|:|:|||||:||||
Db 61 EHRRKLLEQEMVNFLFEKGDVHIEGYVP 87

RESULT 3
A85954
hypothetical protein YggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
Miller, L.; Groetbeck, E.J.; Davis, N.W.; Lim, A.; Dialanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>

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C/Genetics:
A;Gene: yggX
C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

OY      1 MSRVNCVKLKREAEGLDPPYPGELGTRIWQISKEAEEWKQIQTRLVNNRLNLADA 60
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Db      1 MSRTIFCTFLGREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLTMMNA 60
C/Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;/Reference number: A99629; MUID:21156231; PMID:11258796
A;/Accession: F91108
A;/Status: preliminary
A;/Molecule type: DNA
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A;/Experimental source: strain O157:H7, substrain RIMD 0509952
C/Genetics:
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C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
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Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;/Reference number: A99629; MUID:21156231; PMID:11258796
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C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
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A;/Status: preliminary
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C;Superfamily: fe(II) trafficking protein YggX

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Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
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A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g1
A;/Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX

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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
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A;/Molecule type: DNA
A;/Residues: 1-91 <HAY>
A;/Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE000378; GB:U00096; NID:g1
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C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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DNA Res. 8, 11-22, 2001
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A;/Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

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DNA Res. 8, 11-22, 2001
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A;/Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX

Query Match          55.3%; Score 255; DB 2; Length 91;
Best Local Similarity 55.2%; Pred. No. 2e-19;
Matches 48; Conservative 13; Mismatches 26; Indels 0; Gaps 0;

OY      1 MSRVNCVKLKREAEGLDPPYPGELGTRIWQISKEAEEWKQIQTRLVNNRLNLADA 60
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gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
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A;/Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:46 ; Search time 79.9886 Seconds
(without alignments)
767.371 Million cell updates/sec

Title: US-09-955-502A-3

Perfect score: 461

Sequence: 1 MSRIVNCVTKLKREAEGLDFP.....QQMERFLFEDGTVEAGGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 75 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	461	100.0	90	1	FETP_BORBR
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4	313	67.9	91	1	FETP_RALSO
5	304	65.9	91	2	Q4LS19_9BURK
6	300	65.1	91	1	FETP_BURMA
7	300	65.1	91	1	FETP_BURPS
8	297	64.4	90	1	FETP_CHRVO
9	290	62.9	88	1	FETP_NEIG1
10	290	62.9	88	1	FETP_NEIMA
11	290	62.9	88	1	FETP_NEIMB
12	286	62.0	90	1	FETP_NITEU
13	260	56.4	90	1	FETP_METCA
14	256	55.5	90	1	FETP_HAEIN
15	256	55.5	90	2	Q4QMD9_HAEI8
16	256	55.5	91	1	FETP_MANSN
17	256	55.5	92	1	FETP_SHEON
18	255	55.3	90	1	FETP_VIBPA
19	254	55.1	90	1	FETP_IDILO
20	252	54.7	90	1	FETP_VIBF1
21	251	54.4	90	1	FETP_PASMU
22	250	54.2	90	1	FETP_BCO57
23	250	54.2	90	1	FETP_BCOLI
24	250	54.2	90	1	FETP_SHIFL
25	250	54.2	90	1	FETP_VIBVU
26	250	54.2	90	1	FETP_VIBVY
27	249	54.0	89	1	FETP_LEGPA
28	249	54.0	89	1	FETP_LEGPH
29	249	54.0	90	1	FETP_VIBCH
30	248	53.8	89	1	FETP_LEGPH
31	247	53.6	90	1	FETP_PHOPR

32	246	53.4	90	1	FETP_BCOL6	Q8fe19 escherichia
33	246	53.4	90	1	FETP_PHOLL	Q7n711 photorhabdu
34	244	52.9	90	1	FETP_SALCH	Q57K04 salmonella
35	244	52.9	90	1	FETP_SALPA	Q5pmn1 salmonella
36	244	52.9	90	1	FETP_SALTI	P67618 salmonella
37	244	52.9	90	1	FETP_SALTY	P67617 salmonella
38	243	52.7	94	1	FETP_HABDU	Q7vrb6 haemophilus
39	240	52.1	90	1	FETP_PSEAB	Q9nu36 pseudomonas
40	239	51.8	90	1	FETP_ERMCT	Q6d819 erwinia car
41	239	51.8	90	2	Q4J228_AZOVI	Q4j228 azotobacter
42	234	50.8	90	1	FETP_YERPS	Q66fm3 yersinia ps
43	231.5	50.2	90	1	FETP_AC1AD	Q6fEb3 acinetobact
44	231	50.1	91	1	FETP_XANAC	Q8pj17 xanthomonas
45	230	49.9	90	1	FETP_COXBU	Q83d06 coxiella bu
46	226	49.0	90	1	FETP_YERPE	Q8zhe7 yersinia pe
47	223	48.4	92	1	FETP_XANOR	Q5gy22 xanthomonas
48	222	48.2	90	1	FETP_PSEPK	Q88r49 pseudomonas
49	222	48.2	92	1	FETP_XANCP	Q8p829 xanthomonas
50	222	48.2	92	2	Q4UW14_XANCP	Q4uw14 xanthomonas
51	220	47.7	78	1	FETP_BUCAP	Q8k925 buchnera ap
52	218	47.3	90	1	FETP_PSESM	Q87vts pseudomonas
53	218	47.3	90	2	Q4ZLF3_PSESY	Q4zlp3 pseudomonas
54	214	46.4	90	2	Q6T7F6_PSEFL	Q6t7f6 pseudomonas
55	214	46.4	90	2	Q4KJT2_PSEFS	Q4kjt2 pseudomonas
56	213	46.2	79	1	FETP_CANBF	Q7vrg9 candidatus
57	212	46.0	90	1	FETP_XYLF1	Q87d06 xyella fas
58	205	44.5	90	1	FETP_XYLF1	Q9pc73 xyella fas
59	200	43.4	77	1	FETP_BUCAI	P57618 buchnera ap
60	193	41.9	78	1	FETP_WIGBR	Q8d3c5 wigleswort
61	184	39.9	87	1	FETP_FRATP	Q5nh18 francisella
62	178	38.6	92	2	Q4NW04_9DELT	Q4nwq4 anaeromyxob
63	175	38.0	96	2	Q4FVJ7_9GAMM	Q4fvj7 psychrobact
64	157	34.1	87	1	FETP_BUCBP	Q89444 buchnera ap
65	79.5	17.2	116	2	Q6UFK7_9HIV1	Q6ufk7 human immun
66	77	16.7	330	2	Q5DA35_SCHUA	Q5da35 schistosoma
67	77	16.7	2410	2	Q5AZ49_EMENT	Q5az49 aspergillus
68	76.5	16.6	207	1	COAB_STAM	P63830 staphylococ
69	76.5	16.6	207	1	COAB_STAN	P63831 staphylococ
70	76.5	16.6	207	1	COAB_STAAR	Q6g918 staphylococ
71	76.5	16.6	207	1	COAB_STAAS	P63832 staphylococ
72	76.5	16.6	207	1	COAB_STAAW	Q5n185 staphylococ
73	76.5	16.6	207	2	Q5HF85_STAAC	Q5hfg5 lactococcus
74	76.5	16.6	749	2	Q9CGA2_LACLA	Q9cga2 lactococcus
75	75.5	16.4	116	2	Q6WS71_9HIV1	Q6ws71 human immun

ALIGNMENTS

RESULT 1
FETP_BORBR
ID FETP_BORBR STANDARD; PRT; 90 AA.
AC Q7WH06;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DB Probable Fe(2+) trafficking protein.
GN OrderedLocusNames=BB3405;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
[1]
RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.B., Holden M.T.G., Churcher C.M., Harris B., Quail M.A.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris N., Cherevach I.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltham T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,


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RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; BX640447; CAB33897.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MSRIYVCVKLKREAEGLDPPYPGELGTRIWQISKEAWEEWKQIQTRLVNNRLNLADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAOGYVP 87
DB 61 RARKYLQOQMERFLFEDGTVEAOGYVP 87

RESULT 2
FETP BORPA
ID FETP BORPA STANDARD; PRT; 90 AA.
AC Q7W9Q2;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP1703;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=519;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
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CC removed.
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DR EMBL; BX640428; CAB37004.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
DR Pfam; PF04362; DUF495; 1.
DR PIRSF; PIRSF029827; Fe_traffic_Y9GX; 1.
DR ProDom; PD029191; DUF495; 1.
KW Complete proteome; Iron.
SQ SEQUENCE 90 AA; 10568 MW; 7187EA3FB0420388 CRC64;

Query Match 100.0%; Score 461; DB 1; Length 90;
Best Local Similarity 100.0%; Pred. No. 1.6e-40;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIYVCVKLKREAEGLDPPYPGELGTRIWQISKEAWEEWKQIQTRLVNNRLNLADA 60
DB 1 MSRIYVCVKLKREAEGLDPPYPGELGTRIWQISKEAWEEWKQIQTRLVNNRLNLADA 60

QY 61 RARKYLQOQMERFLFEDGTVEAOGYVP 87
DB 61 RARKYLQOQMERFLFEDGTVEAOGYVP 87

RESULT 3
FETP BORPE
ID FETP BORPE STANDARD; PRT; 90 AA.
AC Q7WC4;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Probable Fe(2+) trafficking protein.
GN OrderedLocustNames=BP2336;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=520;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
CC -1- FUNCTION: Could be a mediator in iron transactions between iron
CC acquisition and iron-requiring processes, such as synthesis and/or
CC repair of Fe-S clusters in biosynthetic enzymes (By similarity).
CC -1- SIMILARITY: Belongs to the Fe(2+) trafficking protein family.
-----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
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DR EMBL; BX640418; CAB42609.1; -; Genomic_DNA.
DR HAMAP; MF_00686; -; 1.
DR InterPro; IPR007457; Y9GX.
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OM protein - protein search, using SW model

Run on: February 28, 2006, 20:09:58 ; Search time 20.3428 Seconds
(without alignments)
353.579 Million cell updates/sec

Title: US-09-955-502A-3
Perfect score: 461

Sequence: 1 MSRIVNCVKIKREAEGLDFP.....QOMERFLFEDGTVEAGGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	243	52.7	107	2	US-09-489-039A-11962
2	242	52.5	93	2	US-09-543-681A-5443
3	240	52.1	122	2	US-09-252-991A-23355
4	230.5	50.0	92	2	US-09-328-352-5456
5	164	35.6	110	2	US-09-540-236-2859
6	72.5	15.7	303	2	US-09-902-540-13601
7	70.5	15.3	200	2	US-09-710-279-1186
8	70.5	15.3	200	2	US-09-710-279-2390
9	70.5	15.3	208	2	US-09-134-001C-3785
10	67.5	14.6	504	1	US-08-441-139-18
11	67.5	14.6	521	1	US-08-557-122A-32
12	67.5	14.6	522	2	US-09-262-666-32
13	67.5	14.6	522	2	US-09-368-588-2
14	67.5	14.6	530	1	US-08-557-122A-35
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16	67	14.5	381	2	US-09-949-016-9788
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18	66.5	14.4	591	2	US-09-370-368-8
19	66	14.3	503	2	US-09-928-260-26
20	65	14.1	366	2	US-08-928-213B-59
21	64.5	14.0	805	1	US-08-045-806-2
22	64.5	14.0	805	1	US-08-366-051B-2
23	64	13.9	856	2	US-09-252-991A-17850
24	64	13.9	1493	2	US-09-713-273A-20
25	63.5	13.8	219	2	US-08-928-213B-61
26	63.5	13.8	498	2	US-09-058-260-16
27	63.5	13.8	503	1	US-08-761-802-2

28	63.5	13.8	503	1	US-08-761-802-10	Sequence 10, Appl
29	63.5	13.8	503	1	US-08-761-802-12	Sequence 12, Appl
30	63.5	13.8	503	2	US-08-694-078-2	Sequence 2, Appli
31	63.5	13.8	503	2	US-09-058-260-2	Sequence 2, Appli
32	63.5	13.8	503	2	US-09-058-260-10	Sequence 10, Appl
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34	63.5	13.8	503	2	US-09-058-260-28	Sequence 28, Appl
35	63.5	13.8	503	2	US-09-058-260-30	Sequence 30, Appl
36	63.5	13.8	1242	2	US-09-107-532A-5241	Sequence 5241, Ap
37	63	13.7	581	2	US-09-713-273A-12	Sequence 12, Appl
38	63	13.7	2532	2	US-09-215-694-10	Sequence 10, Appl
39	63	13.7	2532	2	US-10-109-310-10	Sequence 10, Appl
40	62.5	13.6	666	2	US-09-270-767-62249	Sequence 62249, A
41	62.5	13.6	721	2	US-09-270-767-46645	Sequence 46645, A
42	62.5	13.6	839	2	US-09-489-039A-13252	Sequence 13252, A
43	62	13.4	862	1	US-08-685-118-2	Sequence 2, Appli
44	62	13.4	862	1	US-08-915-495-2	Sequence 2, Appli
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46	62	13.4	862	2	US-09-853-180B-4	Sequence 4, Appli
47	62	13.4	864	2	US-09-949-016-7758	Sequence 7758, Ap
48	62	13.4	979	2	US-09-543-681A-5466	Sequence 5466, Ap
49	61.5	13.3	391	2	US-09-489-039A-7804	Sequence 7804, Ap
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57	61	13.2	312	2	US-09-605-703B-2656	Sequence 2656, Ap
58	61	13.2	1245	1	US-08-158-232-8	Sequence 8, Appli
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60	61	13.2	1245	1	US-08-611-928-8	Sequence 8, Appli
61	61	13.2	1245	2	US-09-173-891-8	Sequence 8, Appli
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66	60	13.0	713	2	US-09-540-236-3595	Sequence 3595, Ap
67	59.5	12.9	447	2	US-09-902-540-13195	Sequence 13195, A
68	59.5	12.9	623	2	US-10-104-047-3378	Sequence 3378, Ap
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72	59	12.8	309	2	US-09-248-796A-14939	Sequence 14939, A
73	59	12.8	371	2	US-10-104-047-3421	Sequence 3421, Ap
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ALIGNMENTS

RESULT 1
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; Sequence 11962, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489, 039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117, 747
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 11962
; LENGTH: 107
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-11962

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 1, 2006, 00:01:31 ; Search time 66.1635 Seconds
(without alignments)
549.414 Million cell updates/sec

Title: US-09-955-502A-3

Perfect score: 461
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	461	100.0	87	3	US-09-955-502-2 Sequence 2, Appli
2	461	100.0	87	3	US-09-955-502-3 Sequence 3, Appli
3	443.5	96.2	86	3	US-09-955-502-4 Sequence 4, Appli
4	300	65.1	87	3	US-09-955-502-29 Sequence 29, Appl
5	300	65.1	87	3	US-09-955-502-30 Sequence 30, Appl
6	290	62.9	88	3	US-09-955-502-26 Sequence 26, Appl
7	290	62.9	88	3	US-09-955-502-27 Sequence 27, Appl
8	290	62.9	88	3	US-09-955-502-28 Sequence 28, Appl
9	275	59.7	87	3	US-09-955-502-31 Sequence 31, Appl
10	260	56.4	87	3	US-09-955-502-32 Sequence 32, Appl
11	260	56.4	87	3	US-09-955-502-5 Sequence 5, Appli
12	256	55.5	87	3	US-09-955-502-7 Sequence 7, Appli
13	256	55.5	88	3	US-09-955-502-9 Sequence 9, Appli
14	255	55.3	91	3	US-09-955-502-11 Sequence 11, Appl
15	255	55.3	91	3	US-09-955-502-12 Sequence 12, Appl
16	255	55.3	91	3	US-09-955-502-13 Sequence 13, Appl
17	251	54.4	87	3	US-09-955-502-6 Sequence 6, Appli
18	249	54.0	88	3	US-09-955-502-15 Sequence 15, Appl
19	249	54.0	90	3	US-09-955-502-10 Sequence 10, Appl
20	249	54.0	91	3	US-09-955-502-14 Sequence 14, Appl
21	249	54.0	91	3	US-09-955-502-16 Sequence 16, Appl
22	249	54.0	91	3	US-09-955-502-17 Sequence 17, Appl
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24	242	52.5	91	3	US-09-955-502-18 Sequence 18, Appl
25	240	52.1	87	3	US-09-955-502-25 Sequence 25, Appl
26	230	49.9	88	3	US-09-955-502-33 Sequence 33, Appl
27	226	49.0	90	3	US-09-955-502-20 Sequence 20, Appl

28	222	48.2	78	3	US-09-955-502-19	Sequence 19, Appl
29	222	48.2	87	3	US-09-955-502-24	Sequence 24, Appl
30	218	47.3	90	3	US-09-955-502-23	Sequence 23, Appl
31	205	44.5	89	3	US-09-955-502-22	Sequence 22, Appl
32	200	43.4	76	3	US-09-955-502-21	Sequence 21, Appl
33	76.5	16.6	207	5	US-10-857-625-698	Sequence 698, App
34	70.5	15.3	208	4	US-10-724-972A-6021	Sequence 6021, Ap
35	69.5	15.1	1733	4	US-10-437-963-181840	Sequence 181840,
36	69	15.0	373	4	US-10-437-963-107538	Sequence 107538,
37	69	15.0	428	4	US-10-437-963-146305	Sequence 146305,
38	69	15.0	527	5	US-10-501-282-46	Sequence 46, Appl
39	69	15.0	528	5	US-10-501-282-48	Sequence 48, Appl
40	68.5	14.9	87	4	US-10-424-599-281616	Sequence 281616,
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42	68	14.8	558	4	US-10-425-115-217061	Sequence 217061,
43	67.5	14.6	559	4	US-10-425-115-338828	Sequence 338828,
44	67.5	14.6	714	4	US-10-369-493-2684	Sequence 2684, Ap
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46	67	14.5	381	5	US-10-975-523-13	Sequence 4, Appli
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49	66.5	14.4	591	4	US-09-827-822-8	Sequence 129763,
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51	66	14.3	318	4	US-10-047-260-20	Sequence 117, App
52	66	14.3	997	5	US-10-485-710-117	Sequence 10030, A
53	65.5	14.2	348	4	US-10-437-963-121938	Sequence 121938,
54	65.5	14.2	596	4	US-10-437-963-130475	Sequence 130475,
55	65.5	14.2	1360	4	US-10-437-963-201860	Sequence 201860,
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71	64.5	14.0	805	4	US-10-415-255-2	Sequence 2, Appli
72	64.5	14.0	805	4	US-10-744-544-14	Sequence 14, Appl
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74	64.5	14.0	890	4	US-10-437-963-156221	Sequence 156221,
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ALIGNMENTS

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; Sequence 2, Application US/09955502
; Patent No. US20020072118A1
; GENERAL INFORMATION:
; APPLICANT: Downs, Diana M.
; APPLICANT: Gralnick, Jeff A.
; TITLE OF INVENTION: Method for Preventing Superoxide Damage to Cells and
; TITLE OF INVENTION: Oxygen-Labile Proteins
; FILE REFERENCE: 960296.97559
; CURRENT APPLICATION NUMBER: US/09/955,502
; PRIOR FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: 60/234,588
; PRIOR FILING DATE: 2000-09-22
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 87
; TYPE: PRT
; ORGANISM: Bordetella pertussis

GenCore version 5.1.7
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Run on: March 1, 2006, 00:02:41 ; Search time 5.92509 Seconds
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Title: US-09-955-502a-3
Perfect score: 461
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Gapop 10.0 , Gapext 0.5

Searched: 117670 seqs, 14887254 residues

Total number of hits satisfying chosen parameters: 117670

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
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Listing first 75 summaries

Database : Published Applications AA New:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	62.9	88	6	US-10-467-657-968
2	70.5	15.3	200	6	US-10-793-626-1186
3	70.5	15.3	200	6	US-10-793-626-2390
4	67	14.5	1320	7	US-11-098-686-10831
5	64.5	14.0	805	7	US-11-033-039-1279
6	64.5	14.0	805	7	US-11-108-539-2
7	62.5	13.6	483	7	US-11-137-465-40
8	61.5	13.3	832	7	US-11-098-686-10182
9	60	13.0	240	7	US-11-044-111-10
10	59.5	12.9	623	7	US-11-072-512-3378
11	59	12.8	226	7	US-11-072-512-3820
12	59	12.8	265	6	US-10-793-626-174
13	59	12.8	371	7	US-11-072-512-3421
14	59	12.8	805	6	US-10-927-641-77
15	58.5	12.7	662	7	US-11-072-175-184
16	58	12.6	919	6	US-10-821-234-951
17	57.5	12.5	104	7	US-11-120-308-74
18	57.5	12.5	398	6	US-10-793-626-44
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23	57	12.4	239	7	US-11-044-111-5
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27	57	12.4	809	7	US-11-072-512-3367	Sequence 3367, Ap
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29	56	12.1	183	7	US-11-072-512-3180	Sequence 3180, Ap
30	56	12.1	702	7	US-11-072-512-2154	Sequence 2154, Ap
31	56	12.1	1076	6	US-10-467-657-7916	Sequence 7916, Ap
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34	55.5	12.0	522	7	US-11-072-512-3665	Sequence 3665, Ap
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37	55.5	12.0	3353	7	US-11-037-243-64	Sequence 64, Appl
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40	54.5	11.8	356	7	US-11-143-986-9	Sequence 9, Appli
41	54.5	11.8	1275	6	US-10-724-598-49	Sequence 49, Appl
42	54.5	11.8	1340	7	US-11-070-575-6	Sequence 6, Appli
43	54.5	11.8	1344	7	US-11-091-643-20	Sequence 20, Appli
44	54.5	11.8	1659	7	US-11-072-175-205	Sequence 205, App
45	54.5	11.8	2080	7	US-11-124-367A-364	Sequence 364, App
46	54.5	11.8	2542	7	US-11-124-367A-363	Sequence 363, App
47	54	11.7	331	7	US-11-098-686-10431	Sequence 10431, A
48	53.5	11.6	372	6	US-10-467-657-2318	Sequence 2318, Ap
49	53.5	11.6	599	7	US-11-109-157A-3	Sequence 3, Appli
50	53.5	11.6	1373	7	US-11-098-686-11150	Sequence 11150, A
51	53.5	11.6	1686	7	US-11-109-157A-1	Sequence 1, Appli
52	53.5	11.6	1686	7	US-11-226-701-2	Sequence 2, Appli
53	53.5	11.6	2250	6	US-10-922-232B-57	Sequence 57, Appl
54	53.5	11.6	2630	7	US-11-186-731-2	Sequence 2, Appli
55	53.5	11.6	4060	6	US-10-922-232B-55	Sequence 55, Appl
56	53.5	11.6	6738	6	US-10-922-232B-56	Sequence 56, Appl
57	53.5	11.6	7968	7	US-11-186-731-5	Sequence 5, Appli
58	53	11.5	200	7	US-11-194-246-402	Sequence 402, App
59	53	11.5	240	7	US-11-007-282-8	Sequence 8, Appli
60	53	11.5	240	7	US-11-007-282-13	Sequence 13, Appl
61	53	11.5	240	7	US-11-007-282-14	Sequence 14, Appl
62	53	11.5	258	7	US-11-007-282-6	Sequence 6, Appli
63	53	11.5	342	7	US-11-156-084-25	Sequence 25, Appl
64	53	11.5	342	7	US-11-156-084-44	Sequence 44, Appl
65	53	11.5	369	7	US-11-156-084-45	Sequence 45, Appl
66	53	11.5	384	7	US-11-098-686-10752	Sequence 10752, A
67	53	11.5	453	7	US-11-072-512-3394	Sequence 3394, Ap
68	53	11.5	618	6	US-10-454-437-396	Sequence 396, App
69	53	11.5	784	6	US-11-156-084-24	Sequence 24, Appl
70	53	11.5	784	7	US-10-517-939-324	Sequence 324, App
71	52.5	11.4	143	6	US-10-793-626-1714	Sequence 1714, Ap
72	52.5	11.4	237	7	US-11-044-111-11	Sequence 11, Appl
73	52.5	11.4	362	6	US-10-517-939-88	Sequence 88, Appl
74	52.5	11.4	471	6	US-10-770-726-68	Sequence 68, Appl
75	52.5	11.4	471	7	US-11-152-366-31	Sequence 31, Appl

ALIGNMENTS

RESULT 1
US-10-467-657-968
; Sequence 968, Application US/10467657
; Publication No. US20050260581A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; APPLICANT: FONTANA Maria Rita
; APPLICANT: PIZZA Mariagrazia
; APPLICANT: MASIGNANI Vega
; APPLICANT: MONACI Elisabetta
; TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: US/10/467,657
; CURRENT FILING DATE: 2003-08-11
; PRIOR APPLICATION NUMBER: GB-0103424.8
; PRIOR FILING DATE: 2001-02-12
; NUMBER OF SEQ ID NOS: 9218
; SOFTWARE: SeqWin99, version 1.04

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; SEQ ID NO 968
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; LENGTH: 88
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; TYPE: PRT
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; ORGANISM: Neisseria gonorrhoeae
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US-10-467-657-968
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; Sequence 1186, Application US/10793626
; Publication No. US20050255478A1

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1  APPLICANT: KIMBERLY, WILLIAM JOHN
2  TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
3  FILE REFERENCE: PU3480US
4  CURRENT APPLICATION NUMBER: US/10/793,626
5  CURRENT FILING DATE: 2004-03-04
6  PRIOR APPLICATION NUMBER: 60/164,258
7  PRIOR FILING DATE: 1999-11-09
8  NUMBER OF SEQ ID NOS: 4472
9  SOFTWARE: PatentIn Ver. 2.1
10 SEQ ID NO 1186
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12 LENGTH: 200
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14 TYPE: PRT
15
16 ORGANISM: Artificial Sequence
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18 FEATURE:
19
20 OTHER INFORMATION: Description of Artificial Sequence: synthetic
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22 OTHER INFORMATION: amino acid sequence
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24 US-10-793-626-1186

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; APPLICANT: KIMMERLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PU3480US
; CURRENT APPLICATION NUMBER: US/10/793,626
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: 60/164,258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2390
; LENGTH: 200
; TYPE: PR1
; ORGANISM: Artificial Sequence

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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: amino acid sequence
US-10-793-626-2390

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Best Local Similarity	26.3%	Pred. No. 0.38;		
Matches 25; Conservative	15;	Mismatches	22;	Indels 33; Gaps 5;

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RESULT 4
US-11-098-686-10831
; Sequence 10831, Application US/11098686
; Publication No. US20060024696A1

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; APPLICANT: Kapur, Vivek and Gebhart, Connie J.
; TITLE OF INVENTION: NUCLEIC ACID AND POLYPEPTIDE SEQUENCES
; TITLE OF INVENTION: FROM LAWSONIA INTRACELLULARIS AND METHODS OF USING
; FILE REFERENCE: 09531-128001
; CURRENT APPLICATION NUMBER: US/11/098,686
; CURRENT FILING DATE: 2005-04-04
; PRIOR APPLICATION NUMBER: PCT/US03/31318
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: US 60/416,395
; PRIOR FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 11433
; SOFTWARE: FastSeq for windows Version 4.0
; SEQ ID NO 10831
; LENGTH: 1320
; TYPE: PRT
; ORGANISM: Lawsonia intracellularis
US-11-098-686-10831

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; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 81.9977 Seconds
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Title: US-09-955-502A-4
Perfect score: 454
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Gapop 10.0 , Gapext 0.5

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Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	282.5	62.2	87	5	ABB78175 Amino aci
5	276.5	60.9	87	5	ABB78174 Amino aci
6	272.5	60.0	88	5	ABB78171 Amino aci
7	272.5	60.0	88	5	ABB78172 Amino aci
8	272.5	60.0	88	5	ABB78173 Amino aci
9	272.5	60.0	88	6	ABP77219 N. gonorr
10	257.5	56.7	87	5	ABB78176 Amino aci
11	246	54.2	91	5	ABB78150 Amino aci
12	242.5	53.4	87	5	ABB78177 Amino aci
13	242.5	53.4	88	5	ABB78154 Amino aci
14	242	53.3	89	9	AEB41576 L. pneumo
15	242	53.3	95	9	AEB38294
16	241	53.1	91	5	ABB78158 Amino aci
17	241	53.1	91	5	ABB78163 Amino aci
18	241	53.1	91	5	ABB78157 Amino aci
19	241	53.1	91	5	ABB78156 Amino aci
20	238.5	52.5	87	5	ABB78152 Amino aci
21	235	51.8	88	5	ABB78160 Amino aci
22	235	51.8	90	5	ABB78155 Amino aci
23	235	51.8	91	5	ABB78161 Amino aci
24	235	51.8	91	5	ABB78159 Amino aci

25	235	51.8	91	5	ABB78162	Abb78162 Amino aci
26	233.5	51.4	87	5	ABB78151	Abb78151 Amino aci
27	229	50.4	107	7	ABO65445	AbO65445 Klebsiell
28	228	50.2	93	7	ADFO5158	AdfO5158 Bacterial
29	225.5	49.7	87	5	ABB78153	Abb78153 Amino aci
30	223.5	49.2	92	6	ADA34169	Ada34169 Acinetoba
31	223	49.1	88	5	ABB78178	Abb78178 Amino aci
32	222.5	49.0	87	5	ABB78170	Abb78170 Amino aci
33	222.5	49.0	122	7	ABO74609	AbO74609 Pseudomon
34	222	48.9	78	5	ABB78164	Abb78164 Amino aci
35	212	46.7	90	5	ABB78165	Abb78165 Amino aci
36	204.5	45.0	87	5	ABB78169	Abb78169 Amino aci
37	200.5	44.2	90	5	ABB78168	Abb78168 Amino aci
38	200	44.1	76	5	ABB78166	Abb78166 Amino aci
39	187.5	41.3	90	5	ABB78167	Abb78167 Amino aci
40	157.5	34.7	110	8	ADL05173	Adl05173 M. catar
41	76.5	16.9	749	5	ABB54524	Abb54524 Lactococc
42	72.5	16.0	303	9	ABM94402	Abm94402 M. xanthu
43	71.5	15.7	207	6	ABM73508	Abm73508 Staphyloc
44	71.5	15.7	207	9	ADV16859	Adv16859 Staphyloc
45	71.5	15.7	207	9	ADW94758	Adw94758 Prolifera
46	70.5	15.5	200	4	AAg82648	Aag82648 S. epider
47	70.5	15.5	200	4	AAg82046	Aag82046 S. epider
48	70.5	15.5	208	5	ABP38940	Abp38940 Staphyloc
49	70.5	15.5	208	8	ADS06726	Ads06726 Staphyloc
50	70.5	15.5	308	6	ABM70179	Abm70179 Phototrab
51	70.5	15.5	366	2	AAy05922	Aay05922 DNA polym
52	69.5	15.3	1233	8	ADQ66727	Adq66727 Novel hum
53	69	15.2	124	9	ADX40209	Adx40209 HIV Rev p
54	69	15.2	522	2	AAW69726	Aaw69726 Saccharom
55	69	15.2	522	9	AEB13006	Aeb13006 Yeast pro
56	69	15.2	522	9	AEB50108	Aeb50108 Yeast dis
57	69	15.2	526	2	AAR26174	Aar26174 Protein d
58	69	15.2	527	6	ADB06106	Adb06106 Alloiococ
59	69	15.2	528	6	ADB06108	Adb06108 Alloiococ
60	69	15.2	530	9	AEB13007	Aeb13007 Yeast alt
61	69	15.2	530	9	AEB50109	Aeb50109 Yeast dis
62	68.5	15.1	529	5	AAE26857	Aae26857 Anabaena
63	67.5	14.9	714	8	ADN20031	Adn20031 Bacterial
64	67	14.8	381	5	AAO20498	Aao20498 Human amy
65	67	14.8	389	4	AAm80170	Aam80170 Human pro
66	67	14.8	593	6	ABR39276	AbR39276 Protein s
67	66.5	14.6	591	2	AAy41141	Aay41141 Mouse mam
68	66.5	14.6	860	2	AAy41140	Aay41140 Mouse mam
69	66.5	14.6	1221	2	AAy05940	Aay05940 Thermophi
70	66.5	14.6	1240	6	ABU29661	Abu29661 Protein e
71	66.5	14.6	1242	7	ADC95614	Adc95614 E. faeciu
72	66.5	14.6	1245	8	ADJ67857	Adj67857 T. thermo
73	66.5	14.6	1245	8	ADJ68069	Adj68069 T. thermo
74	66.5	14.6	1245	8	ADK01147	Adk01147 DNA polym
75	66.5	14.6	1245	8	ADJ79366	Adj79366 T. thermo

ALIGNMENTS

RESULT 1
ABB78149
ID ABB78149 standard; protein; 86 AA.
XX ABB78149;
AC
XX
DT 05-NOV-2002 (first entry)
XX
XX Amino acid sequence of a YggX homologue.
DE
XX
XX Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
XX Bordetella bronchiseptica.
OS
XX
XX
PN US2002072118-A1.
XX

PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 86 AA;
XX
Query Match 100.0%; Score 454; DB 5; Length 86;
Best Local Similarity 100.0%; Pred. No. 9.8e-47;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
Db 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
QY 61 RARKYLQQQMERFLFEDGTVEAGVVP 86
Db 61 RARKYLQQQMERFLFEDGTVEAGVVP 86
RESULT 2
ABB78148
ID ABB78148 standard; protein; 87 AA.
XX
AC ABB78148;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella parapertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
SQ Sequence 87 AA;
XX
Query Match 97.7%; Score 443.5; DB 5; Length 87;
Best Local Similarity 98.9%; Pred. No. 1.8e-45;
Matches 86; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
QY 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
Db 1 MSRIVNCVKLKREAGLDPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
QY 61 RARKYLQQQMERFLFEDGTVEAG-VVP 86
Db 61 RARKYLQQQMERFLFEDGTVEAGVVP 87
RESULT 3
ABB78147
ID ABB78147 standard; protein; 87 AA.
XX
AC ABB78147;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella pertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
PT Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
PS Example; Fig 1A; 16pp; English.
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.2758 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-4
Perfect score: 454
Sequence: 1 MSRIVNCVKLKREABGLDFP.....QQQMERFLFEDGTVEAQGV 86

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	272.5	60.0	88	2	H81014	conserved hypothet
2	241	53.1	91	2	A85954	hypothetical prote
3	241	53.1	91	2	A65082	hypothetical prote
4	241	53.1	91	2	F91108	hypothetical prote
5	238.5	52.5	90	2	C64013	hypothetical prote
6	235	51.8	90	2	C82320	conserved hypothet
7	235	51.8	91	2	AH0879	conserved hypothet
8	222.5	49.0	90	2	H83003	conserved hypothet
9	212	46.7	90	2	AI0116	conserved hypothet
10	200	44.1	93	2	E84994	hypothetical prote
11	195	43.0	105	2	C82624	conserved hypothet
12	76.5	16.9	749	2	E86774	hypothetical prote
13	71.5	15.7	207	2	E89952	conserved hypothet
14	71.5	15.7	855	2	A45713	Env transmembrane
15	69	15.2	429	2	AE2501	hypothetical prote
16	69	15.2	522	1	ISBYSS	protein disulfide-
17	68.5	15.1	241	2	S19999	hypothetical prote
18	68	15.0	134	2	T37027	hypothetical prote
19	68	15.0	393	2	S03576	DNA-directed RNA p
20	67.5	14.9	714	2	S77385	nitrate reductase
21	67	14.8	389	2	T14751	hypothetical prote
22	66.5	14.6	591	1	FOMVM	gag polyprotein -
23	66	14.5	318	2	S77153	transcription init
24	65.5	14.4	164	2	E75293	hypothetical prote
25	65	14.3	323	2	UT0755	ethylene-forming e
26	65	14.3	323	2	A86184	hypothetical prote
27	65	14.3	837	2	B89583	protein K07B3.2 li
28	65	14.3	1276	2	T09204	probable tail-host
29	64.5	14.2	228	2	C26599	clathrin light cha

30	64.5	14.2	229	2	B31775	clathrin light cha
31	64.5	14.2	238	1	LRRTB2	clathrin light cha
32	64.5	14.2	393	2	T49257	protein kinase-lik
33	64.5	14.2	560	1	HMITV7	hemagglutinin prec
34	64.5	14.2	622	2	T23804	hypothetical prote
35	64.5	14.2	688	2	AG3124	ATP-dependent DNA
36	64.5	14.2	706	2	B99163	ATP-dependent DNA
37	64.5	14.2	2291	1	A46147	spectrin beta chai
38	64	14.1	133	2	G75385	hypothetical prote
39	64	14.1	451	2	E64312	signal recognition
40	64	14.1	1068	2	S73091	hypothetical prote
41	63.5	14.0	353	1	FOMVGR	gag polyprotein -
42	63.5	14.0	563	1	A45539	hemagglutinin prec
43	63.5	14.0	805	2	A46266	aryl hydrocarbon r
44	63	13.9	506	2	T50211	WD-repeat protein
45	63	13.9	563	2	T17316	hypothetical prote
46	63	13.9	569	2	T47358	hypothetical prote
47	62.5	13.8	165	1	XUBSM1	methyated-DNA-lpr
48	62.5	13.8	388	2	T38810	hypothetical prote
49	62.5	13.8	563	1	HMITV	hemagglutinin prec
50	62.5	13.8	694	2	A95866	probable transkeo
51	62.5	13.8	853	2	S58375	aryl hydrocarbon r
52	62.5	13.8	920	2	JC7313	hypothetical prote
53	62.5	13.8	1675	2	S70770	hypothetical prote
54	62	13.7	337	2	AG2423	hypothetical prote
55	62	13.7	416	2	C47017	probable transcrip
56	62	13.7	416	2	AF2017	RNA polymerase sig
57	62	13.7	432	2	B75638	hypothetical prote
58	62	13.7	559	2	AH1719	pheromone ABC tran
59	62	13.7	989	2	T46183	zinc proteinase (E
60	61.5	13.5	121	2	C97906	hypothetical prote
61	61.5	13.5	283	4	FOHUE1	retrovirus-related
62	61.5	13.5	310	2	F64311	hypothetical prote
63	61.5	13.5	320	2	S69547	transcription init
64	61.5	13.5	430	2	S75313	serine-tRNA ligase
65	61.5	13.5	897	2	G02529	dynein heavy chain
66	61.5	13.5	1464	2	T07050	hypothetical prote
67	61	13.4	143	2	D70003	general stress pro
68	61	13.4	320	2	S11879	probable l-aminocy
69	61	13.4	321	2	T02754	probable type II r
70	61	13.4	372	2	B81952	pheromone ABC tran
71	61	13.4	558	2	AD1349	hypothetical prote
72	61	13.4	865	2	E84718	hypothetical prote
73	61	13.4	1138	2	T24635	probable tail-host
74	61	13.4	1291	2	T09273	probable tail-host
75	61	13.4	3685	1	A27605	dystrophin, muscle

ALIGNMENTS

RESULT 1
H81014
conserved hypothetical protein NMB2021 [imported] - Neisseria meningitidis (strain MC58
C/Species: Neisseria meningitidis
C/Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C/Accession: H81014, F81958
R/Tetelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Yamathayan, J.; Gill, J.; Scariato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A/Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A/Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A/Reference number: AB1000, MUID:20175755, PMID:10710307
A/Accession: H81014
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-88 <TEXT>
A/Cross-references: UNIPARC:UPI00000C4E7F, GB:AE002552, GB:AE002098, NID:g7227279, PIDN:
A/Experimental source: serogroup B, strain MC58
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jags, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

```

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: F81958
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <PAR>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AL162753; GB:AL157959; NID:g7379120; PIDN:
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: NMB2021; MMA0419
C;Superfamily: fe(II) trafficking protein YggX

Query Match      60.0%; Score 272.5; DB 2; Length 88;
Best Local Similarity 59.8%; Pred. No. 1.7e-21;
Matches 52; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

OY 1 MSRIVNCVKLKREAGGLDPFPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRNLADA 60
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DB 1 MARWVFCVKLNKEAGEMKFPPLPNELGKRIFENVSGEAWAATRHQTMLINEKRLSLADP 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 PARKYLQOQMERFLFEDGTVEAOG-VP 86
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 RAREYLAQOMEQYFFGDADAVQGYVP 87
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RESULT 2
A85954
hypothetical protein yggX [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 05-Oct-2004
C;Accession: A85954
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: A85954
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <STO>
A;Cross-references: UNIPROT:P52065; UNIPARC:UPI0000163A04; GB:AE005174; NID:g12517511; F
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yggX
C;Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 241; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.4e-18;
Matches 46; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

OY 1 MSRIVNCVKLKREAGGLDPFPYPGELGTRIMQOISKEAWBEWKQIQTRLVNNRNLADA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 1 MSRTIIFCTPLQREAGQDFQLYPGLGKRIYNEISKEAWAQMWHKQTMLINEKRLNMNNA 60
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

OY 61 PARKYLQOQMERFLFEDGTVEAOG 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
DB 61 EHRKLLQEQEMVNFLEFGKEVHIEG 84
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
A65082
hypothetical protein b2962 - Escherichia coli (strain K-12)
C;Species: Escherichia coli
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 05-Oct-2004
C;Accession: A65082
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Cc
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: A65082
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA

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A;Residues: 1-91<BLAT>
A;Cross-references: UNIPROT:P52065, UNIPARC:UPI0000163A04, GB:AE000378, GB:U00096, NID:91
A;Experimental source: strain K-12, substrain MG1655
C;Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 241; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.4e-18;
Matches 46; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY      1 MSRIIVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWEEWKOIOTRLVNNENRLNLADA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLTMMNA 60

QY      61 PAKKYLQOQMERFLPEDGTVEAOG 84
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EHRKLLQOEMVNFLEGEKEVHIEG 84

RESULT 4
F91108
hypothetical protein ECs3838 [imported] - Escherichia coli (strain O157:H7, substrain R1)
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 05-Oct-2004
C;Accession: F91108
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genom
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: F91108
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-91 <HAY>
A;Cross-references: UNIPROT:P52065, UNIPARC:UPI0000163A04, GB:BA000007, PIDN:BA837261.1;
A;Experimental source: strain O157:H7, substrain R1MD 0509952
C;Genetics:
A;Gene: ECs3838
C;Superfamily: fe(II) trafficking protein YggX

Query Match      53.1%; Score 241; DB 2; Length 91;
Best Local Similarity 54.8%; Pred. No. 3.4e-18;
Matches 46; Conservative 13; Mismatches 25; Indels 0; Gaps 0;

QY      1 MSRIIVNCVKLKREAEGLDPPYPGELGTRIMQOISKEAWEEWKOIOTRLVNNENRLNLADA 60
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MSRTIFCTFLQREAEQDFQLYPGELGKRIYNEISKEAWAQWQHKTMLINEKLTMMNA 60

QY      61 PAKKYLQOQMERFLPEDGTVEAOG 84
      |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      61 EHRKLLQOEMVNFLEGEKEVHIEG 84

RESULT 5
C64013
hypothetical protein HI0760 - Haemophilus influenzae (strain Rd KW20)
C;Species: Haemophilus influenzae
C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 05-Oct-2004
C;Accession: C64013
R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, A
Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, J
D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhmann, J.L.; Geoghegan, N.S.M.
Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter,
A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630; PMID:7542800
A;Accession: C64013
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-90 <TIGR>
A;Cross-references: UNIPROT:P44048, UNIPARC:UPI000013B0A4, GB:U32760, GB:L42023, NID:915
C;Superfamily: fe(II) trafficking protein YggX

Query Match      52.5%; Score 238.5; DB 2; Length 90;

```

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension **.rup**) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (UniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.

When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or members of the public who may encounter UniProt temporary accession numbers.

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OM protein - protein search, using sw model

Run on: February 28, 2006, 20:05:33 ; Search time 13.4302 Seconds
(without alignments)
623.287 Million cell updates/sec

Title: US-09-955-502A-2
Perfect score: 461
Sequence: 1 MSRIIVNCVCLKREAEGLDFP.....QQMERFLFEDGTVEAQGYVP 87

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	290	62.9	88	2 H81014	conserved hypothet
2	256	55.5	90	2 C64013	hypothetical prote
3	255	55.3	91	2 A85954	hypothetical prote
4	255	55.3	91	2 A65082	hypothetical prote
5	255	55.3	91	2 F91108	hypothetical prote
6	249	54.0	90	2 C82320	conserved hypothet
7	249	54.0	91	2 AH0879	conserved hypothet
8	240	52.1	90	2 H83003	conserved hypothet
9	226	49.0	90	2 AI0116	conserved hypothet
10	205	44.5	105	2 C82624	conserved hypothet
11	200	43.4	93	2 E84994	hypothetical prote
12	76.5	16.6	207	2 E89952	conserved hypothet
13	76.5	16.6	749	2 E86774	hypothetical prote
14	71.5	15.5	855	2 A45713	Env transmembrane
15	69	15.0	429	2 AE2501	hypothetical prote
16	68.5	14.9	241	2 SI9999	hypothetical prote
17	68	14.8	134	2 T37027	hypothetical prote
18	67.5	14.6	312	2 H82399	hypothetical prote
19	67.5	14.6	522	1 ISBYSS	protein disulfide-
20	67.5	14.6	714	2 S77385	nitrate reductase
21	67	14.5	389	2 TI4751	hypothetical prote
22	67	14.5	678	2 AB1130	penicillin-binding
23	66.5	14.4	591	1 FOMVM	gag polyprotein -
24	66	14.3	318	2 S77153	transcription init
25	66	14.3	1276	2 T09204	probable tail-host
26	65.5	14.2	164	2 E75293	hypothetical prote
27	65	14.1	238	1 LRRTB2	clathrin light cha
28	65	14.1	323	2 JT0755	ethylene-forming e
29	65	14.1	323	2 A86184	hypothetical prote

30	65	14.1	393	2	S03576	DNA-directed RNA p
31	64.5	14.0	228	2	C26599	clathrin light cha
32	64.5	14.0	229	2	B31775	clathrin light cha
33	64.5	14.0	393	2	T49257	protein kinase-lik
34	64.5	14.0	560	1	HMITV7	hemagglutinin prec
35	64.5	14.0	622	2	T23804	hypothetical prote
36	64.5	14.0	805	2	A46266	aryl hydrocarbon r
37	64.5	14.0	2291	1	A46147	spectrin beta chai
38	64.5	14.0	3063	2	S55505	fatty-acid synthas
39	64	13.9	133	2	G75385	hypothetical prote
40	64	13.9	299	2	T29546	protein SPE-11 - C
41	64	13.9	451	2	E64312	signal recognition
42	64	13.9	1068	2	S73091	hypothetical prote
43	63.5	13.8	353	1	FOMVGR	gag polyprotein -
44	63.5	13.8	563	1	A45539	hemagglutinin prec
45	63.5	13.8	853	2	S58375	aryl hydrocarbon r
46	63.5	13.8	920	2	JC7313	aryl hydrocarbon r
47	63	13.7	506	2	T50211	WD-repeat protein
48	63	13.7	569	2	T47358	hypothetical prote
49	62.5	13.6	388	2	T38810	hypothetical prote
50	62.5	13.6	563	1	HMIVF	hemagglutinin prec
51	62.5	13.6	694	2	A95866	probable transketo
52	62.5	13.6	897	2	G02529	dynein heavy chain
53	62.5	13.6	1675	2	S70770	hypothetical prote
54	62	13.4	337	2	AG2423	hypothetical prote
55	62	13.4	416	2	C47017	probable transcrip
56	62	13.4	416	2	AF2017	RNA polymerase sig
57	62	13.4	563	2	T17316	hypothetical prote
58	62	13.4	989	2	T46183	zinc proteinase (E
59	62	13.4	1291	2	T09273	probable tail-host
60	61.5	13.3	188	2	C87216	probable hemagglut
61	61.5	13.3	283	4	FOHUE1	retrovirus-related
62	61.5	13.3	310	2	F64311	hypothetical prote
63	61.5	13.3	320	2	S69547	transcription init
64	61.5	13.3	1464	2	T07050	hypothetical prote
65	61.5	13.3	4644	1	A38905	dynein heavy chain
66	61	13.2	143	2	D70003	general stress pro
67	61	13.2	320	2	S11879	ethylene-forming e
68	61	13.2	321	2	T02754	probable 1-aminocy
69	61	13.2	372	2	B81952	probable type II r
70	61	13.2	504	1	O4RTD5	cytochrome P450 2D
71	61	13.2	678	2	AE1490	penicillin-binding
72	61	13.2	865	2	E84718	hypothetical prote
73	61	13.2	1138	2	T24635	hypothetical prote
74	61	13.2	1245	2	T18211	delta endotoxin -
75	60.5	13.1	138	2	T10309	hypothetical prote

ALIGNMENTS

RESULT 1
H81014

conserved hypothetical protein_NMB2021 [imported] - Neisseria meningitidis (strain MC58
C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 05-Oct-2004
C;Accession: H81014; F81958
R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.,
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: A81000; MUID:20175755; PMID:10710307
A;Accession: H81014
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-88 <TET>
A;Cross-references: UNIPARC:UPI00000C4E7F; GB:AE002552; GB:AE002098; NID:g7227279; PIDN
A;Experimental source: serogroup B, strain MC58
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000

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OM protein - protein search, using sw model

Run on: February 28, 2006, 18:23:22 ; Search time 82.9512 Seconds
(without alignments)
460.825 Million cell updates/sec

Title: US-09-955-502A-2
Perfect score: 461
Sequence: 1 MSRIVNCVKLKREAEGLDFP.....QMERFLFEDGTVEAQGYVP 87

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 segs, 439378781 residues
Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 75 summaries

Database : A_Geneseq_21:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	461	100.0	87	5	ABB78148 Amino aci
2	461	100.0	87	5	ABB78147 Amino aci
3	443.5	96.2	86	5	ABB78149 Amino aci
4	300	65.1	87	5	ABB78175 Amino aci
5	294	63.8	87	5	ABB78174 Amino aci
6	290	62.9	88	5	ABB78171 Amino aci
7	290	62.9	88	5	ABB78172 Amino aci
8	290	62.9	88	5	ABB78173 Amino aci
9	290	62.9	88	6	ABP77219 N. gonorr
10	275	59.7	87	5	ABB78176 Amino aci
11	260	56.4	87	5	ABB78177 Amino aci
12	260	56.4	91	5	ABB78150 Amino aci
13	256	55.5	87	5	ABB78152 Amino aci
14	256	55.5	88	5	ABB78154 Amino aci
15	255	55.3	91	5	ABB78158 Amino aci
16	255	55.3	91	5	ABB78157 Amino aci
17	255	55.3	91	5	ABB78156 Amino aci
18	251	54.4	87	5	ABB78151 Amino aci
19	249	54.0	88	5	ABB78160 Amino aci
20	249	54.0	89	9	AEB41576 L. pneumo
21	249	54.0	90	5	ABB78155 Amino aci
22	249	54.0	91	5	ABB78161 Amino aci
23	249	54.0	91	5	ABB78159 Amino aci
24	249	54.0	91	5	ABB78162 Amino aci

25	249	54.0	95	9	AEB38294 L. pneumo
26	243	52.7	87	5	ABB78153 Amino aci
27	243	52.7	107	7	ABO65445 Klebsiell
28	242	52.5	91	5	ABB78163 Amino aci
29	242	52.5	93	7	ADF05158 Bacteri
30	240	52.1	87	5	ABB78170 Amino aci
31	240	52.1	122	7	ABO74609 Pseudomon
32	230.5	50.0	92	6	ADA34169 Acinetoba
33	230	49.9	88	5	ABB78178 Amino aci
34	226	49.0	90	5	ABB78165 Amino aci
35	222	48.2	78	5	ABB78164 Amino aci
36	222	48.2	87	5	ABB78169 Amino aci
37	218	47.3	90	5	ABB78168 Amino aci
38	200	43.4	76	5	ABB78166 Amino aci
39	197.5	42.8	90	5	ABB78167 Amino aci
40	164	35.6	110	8	ADL05173 M. catarr
41	76.5	16.6	207	6	ABW73508 Staphyloc
42	76.5	16.6	207	9	ADY16859 Staphyloc
43	76.5	16.6	207	9	ADW94758 Prolifera
44	76.5	16.6	749	5	ABB54524 Lactococc
45	72.5	15.7	303	9	ABM94402 M. xanthu
46	70.5	15.3	200	4	AAQ82648 S. epider
47	70.5	15.3	200	4	AAQ82046 S. epider
48	70.5	15.3	208	5	ABP38940 Staphyloc
49	70.5	15.3	208	8	ADS06726 Staphyloc
50	70.5	15.3	308	6	ABW70179 Photorhab
51	69.5	15.1	1233	8	ADQ66727 Novel hum
52	69	15.0	124	9	ADX40209 HIV Rev p
53	69	15.0	527	6	ADB06106 Alloiococ
54	69	15.0	528	6	ADB06108 Alloiococ
55	68.5	14.9	529	5	AAE26857 Anaena
56	68.5	14.9	720	7	ADF29270 Bacteri
57	68.5	14.9	720	7	ADG32479 Pasteurel
58	67.5	14.6	522	2	AAW69726 Saccharom
59	67.5	14.6	522	9	AEB13006 Yeast pro
60	67.5	14.6	522	9	AEB50108 Yeast dis
61	67.5	14.6	526	2	AAR26174 Protein d
62	67.5	14.6	530	9	AEB13007 Yeast alt
63	67.5	14.6	530	9	AEB50109 Yeast dis
64	67.5	14.6	714	8	ADN20031 Bacteri
65	67	14.5	381	5	AAQ20498 Human amy
66	67	14.5	389	4	AAW80170 Human pro
67	67	14.5	593	6	ABR39276 Protein s
68	67	14.5	678	5	ABB47819 Listeria
69	66.5	14.4	591	2	AAV41141 Mouse mam
70	66.5	14.4	860	2	AAV41140 Mouse mam
71	66.5	14.4	1755	2	AAV41139 Mouse mam
72	66	14.3	229	3	AAB41703 Human ORF
73	66	14.3	318	5	ABG77906 High leve
74	66	14.3	503	2	AAW85085 Esterase
75	66	14.3	856	6	ABR39820 Human SCA

ALIGNMENTS

RESULT 1					
ABB78148					
ID	ABB78148	standard; protein; 87 AA.			
XX					
AC	ABB78148;				
DT					
XX	05-NOV-2002	(first entry)			
DE	Amino acid sequence of a YgXx homologue.				
XX					
KW	Superoxide damage; cell; YgXx; Salmonella enterica serovar typhimurium;				
XX	hydroxyl radical; DNA damage; YgXx homologue.				
OS	Bordetella parapertussis.				
XX					
PN	US2002072118-A1.				
XX					

PD 13-JUN-2002.
XX
XX 18-SEP-2001; 2001US-00955502.
PF
XX 22-SEP-2000; 2000US-0234588P.
PR
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX WPI; 2002-589476/63.
DR
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 100.0%; Score 461; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.1e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIIVNCVKLKREAEGLDFPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
|||
Db 1 MSRIIVNCVKLKREAEGLDFPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLOOQOMERFLFEDGTVEAOGYVP 87
|||
Db 61 RARKYLOOQOMERFLFEDGTVEAOGYVP 87

RESULT 2
ABB78147 standard; protein; 87 AA.
XX
AC ABB78147;
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella pertussis.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX

DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
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XX
XX Example; Fig 1A; 16pp; English.
PS
XX
XX
CC The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella
CC enterica serovar typhimurium) or its homolog, where the cells are
CC rendered more resistant to superoxide damage. YggX reduces the oxidation
CC of (Fe-S) clusters, and thus reduces the loss of Fe(II) ions from
CC clusters. The resulting decrease in free-iron levels generates fewer
CC hydroxyl radicals and thus reduced DNA damage. The method is useful for
CC reducing superoxide damage in a bacterial, yeast, mammalian or plant
CC cell. ABB78147-78 represent YggX homologues
XX
XX SQ Sequence 87 AA;

Query Match 100.0%; Score 461; DB 5; Length 87;
Best Local Similarity 100.0%; Pred. No. 3.1e-47;
Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSRIIVNCVKLKREAEGLDFPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60
|||
Db 1 MSRIIVNCVKLKREAEGLDFPPYPGELGTRIWQISKEAWBEWKQIQTRLVNNENRLNLADA 60

QY 61 RARKYLOOQOMERFLFEDGTVEAOGYVP 87
|||
Db 61 RARKYLOOQOMERFLFEDGTVEAOGYVP 87

RESULT 3
ABB78149 standard; protein; 86 AA.
XX
XX ABB78149;
AC
XX
DT 05-NOV-2002 (first entry)
XX
DE Amino acid sequence of a YggX homologue.
XX
KW Superoxide damage; cell; YggX; Salmonella enterica serovar typhimurium;
KW hydroxyl radical; DNA damage; YggX homologue.
XX
OS Bordetella bronchiseptica.
XX
PN US2002072118-A1.
XX
PD 13-JUN-2002.
XX
PF 18-SEP-2001; 2001US-00955502.
XX
PR 22-SEP-2000; 2000US-0234588P.
XX
PA (DOWN/) DOWNS D.
PA (GRAL/) GRALNICK J A.
XX
PI Downs D, Gralnick JA;
XX
DR WPI; 2002-589476/63.
XX
XX Reducing superoxide damage to a cell, e.g. bacterial, mammalian or plant
PT cell, comprises engineering the cell to produce more YggX protein, a
PT protein identified from Salmonella enterica Serovar Typhimurium.
XX
XX Example; Fig 1A; 16pp; English.
PS
XX
XX The specification describes a method for reducing superoxide damage to a
CC cell. The method comprises engineering the cell to produce more than the
CC native amount of YggX protein (a protein identified from Salmonella